

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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## GenCore version 5.1.6

OM protein - protein search, using sw model  
Run on: April 7, 2005, 00:34:03 ; Search time 176 Seconds  
(without alignments)  
966.901 Million cell updates/sec

Title: US-10-063-561-52

Perfect score: 440

Sequence: 1 MKFGQPLACLLALCLGSGE.....KLGFINWDINKDQRRSRIP 440

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Database : A\_Geneseq\_16Dec04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No. Score Match Length DB ID Description

## RESULT 1

ID AAY9354 standard; protein; 440 AA.

DE Human PRO1411 (UNQ729) amino acid sequence SEQ ID NO:52.

PD 09-MAR-2000.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 3; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 2

ID AAB66103 standard; protein; 440 AA.

DE Protein of the invention #15.

PD 28-DEC-2000.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 3; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 3

ID AAB31205 standard; protein; 440 AA.

DE Amino acid sequence of human polypeptide PRO1411.

PD 21-DEC-2000.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 4; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 4

ID AAU29124 standard; protein; 440 AA.

DE Human PRO polypeptide sequence #101.

PD 20-SEP-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 4; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 5

ID AAB87551 standard; protein; 440 AA.

DE Human PRO1411.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 4; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 6

ID AAU83669 standard; protein; 440 AA.

DE Human PRO protein, Seq ID No 156.

PD 31-JAN-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 4; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 7

ID ABB95497 standard; protein; 440 AA.

DE Human angiogenesis related protein PRO1411 SEQ ID NO: 150.

PD 31-JAN-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 5; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 8

ID ABB84891 standard; protein; 440 AA.

DE Human PRO1411 protein sequence SEQ ID NO:150.

PD 03-JAN-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 5; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 9

ID ABB95497 standard; protein; 440 AA.

DE Human angiogenesis related protein PRO1411 SEQ ID NO: 150.

PD 31-JAN-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 5; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 10

ID ABU58500 standard; protein; 440 AA.

DE Human PRO polypeptide #101.

PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 11

ID ABU88048 standard; protein; 440 AA.

DE Novel human secreted and transmembrane protein PRO1411.

PD 13-FEB-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 12

ID ABU84363 standard; protein; 440 AA.

DE Human secreted/transmembrane protein (PRO) #101.

PD 13-FEB-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 13

ID ABR66237 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

## RESULT 14

ID ABR65627 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

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PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 15
ID ABR94705 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 26
ID ABO25176 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO141.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 27
ID ABO33782 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 28
ID ABU85678 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 29
ID ABU98838 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 30
ID ABU98053 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 31
ID ABU91759 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 32
ID ABU89452 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 33
ID ABU86293 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 34
ID ABU67506 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036162-A1.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 16
ID ABU82806 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 17
ID ABU89927 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 18
ID ABR68176 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 19
ID ABU96229 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 20
ID ABU92660 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 21
ID ABU80816 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 22
ID ABO08737 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 23
ID ABO02789 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 24
ID ABR74943 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040056-A1.
PD 27-FEB-2003.
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PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 35  
ID ABU80534 standard; protein; 440 AA.  
DE Human PRO protein #101.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 36  
ID ABU90901 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 37  
ID ABO33960 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO411.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 38  
ID ABR99452 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 39  
ID ABR9842 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 40  
ID ABO16365 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 41  
ID ABR92265 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 42  
ID ABO18906 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 43  
ID ABR7827 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 44  
ID ABU71977 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 45  
ID ABU85063 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 46  
ID ABO00202 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 47  
ID ABO11534 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 48  
ID ABO02179 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 49  
ID ABU8753 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 50  
ID ABU67294 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032063-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 51  
ID ABU83448 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 52  
ID ABO06249 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 53  
ID ABR59285 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 54  
ID ABO09347 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.

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PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ABO19211 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ABO11229 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 57
ID ABR66847 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 58
ID ABO16060 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 59
ID ABO13766 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 60
ID ABU71531 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 61
ID ABU65669 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, SEQ ID 202.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 62
ID ABO07517 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ABO03704 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ABR67152 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ABO15755 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ABU56036 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO1411.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 67
ID ABU72312 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ABU65364 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ABU95309 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ABU71212 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ABO7822 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ABR70063 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ABR69396 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ABO01537 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003008353-A1.
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PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 75
ID ABU81339 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 76
ID ABR60136 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 77
ID ABU90985 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 78
ID ABR67871 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 79
ID ABR65259 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 80
ID ABR68481 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 81
ID ABR71893 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 82
ID ABU85373 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 83
ID ABU89063 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 84
ID ABU83143 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032105-A1.

PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 85
ID ABU94999 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 86
ID ABU90547 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 87
ID ABU84058 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 88
ID ABU93709 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 89
ID ABR64954 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 90
ID ABR68786 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 91
ID ABO06602 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 92
ID ABR99147 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 93
ID ABU57031 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 94
ID ABU72062 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 95  
ID ABR5983 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 96  
ID ABR2270 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 97  
ID ABR7281 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 98  
ID ABR7163 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032062-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 99  
ID ABR3753 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 100  
ID ABO8127 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 101  
ID ABR2501 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 102  
ID ABR1838 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 103  
ID ABR66002 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 104  
ID ABR1171 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 105  
ID ABR59831 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 106  
ID ABR4019 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 107  
ID ABR9872 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 108  
ID ABR2125 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 109  
ID ABR6542 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 110  
ID ABR90960 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 111  
ID ABO53286 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 112  
ID ABR4397 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 113  
ID ABR79269 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 114  
ID ABR6598 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032129-A1.  
PD 13-FEB-2003.

Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 115  
ID ABU86903 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 116  
ID ABU94692 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 117  
ID AB004619 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 118  
ID ABR70368 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 119  
ID ABU98533 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 120  
ID ABR65932 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 121  
ID ABR64649 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 122  
ID ABU79574 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 123  
ID ABU92965 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 124  
ID ABU95924 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;

RESULT 125  
ID ABU91144 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 126  
ID ABU90237 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 127  
ID AB009652 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 128  
ID AB010924 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 129  
ID ABR70978 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 130  
ID ABU98288 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 131  
ID ABU87586 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 132  
ID ABU91454 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 133  
ID ABU92993 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 134  
ID ABU84668 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;  
RESULT 135

ID ABR69758 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 136  
ID ABR80135 standard; protein; 440 AA.  
DE Human PRO protein #101.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 137  
ID ABR82500 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 138  
ID ABR93404 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 139  
ID ABO09957 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 140  
ID ABO09042 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 141  
ID ABR96464 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 142  
ID ABR10610 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein #101.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 143  
ID ABR72134 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 144  
ID ABR95619 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 145  
ID ABR79805 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003032057-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 146  
ID ABR96828 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 147  
ID ABR70673 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 148  
ID ABO05024 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 149  
ID ABO08432 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 150  
ID ABO05639 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 151  
ID ABR74028 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 152  
ID ABR95620 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 153  
ID ABR80917 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 154  
ID ABR81222 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049743-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 155  
ID ABM00918 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 156  
ID ABR88520 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 157  
ID ABM77341 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 158  
ID ABO28825 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 159  
ID ABO31570 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 160  
ID ABR07987 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 161  
ID ABO40467 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 162  
ID ABO35892 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 163  
ID ABO44031 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 164  
ID ADA77954 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 165  
ID ABM24826 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 166  
ID ABO03094 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 167  
ID ABR90350 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 168  
ID ABM17264 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 169  
ID ABR95010 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 170  
ID ABR95315 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 171  
ID ABR72305 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 172  
ID ADB17109 standard; protein; 440 AA.  
DE Human transmembrane PRO polypeptide (SeqID 52).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 173  
ID ABO21553 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.

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PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ABR97817 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ABR87605 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176
ID ABR77646 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 177
ID ABR27876 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 178
ID ABR06157 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 179
ID ABR03663 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 180
ID ABR35114 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 181
ID ABR26351 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 182
ID ABR048133 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 183
ID ABR92875 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 184
ID ABO24636 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003085159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 185
ID ABR11647 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 186
ID ABR02748 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 187
ID ABR16044 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003084463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 188
ID ABO27605 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 189
ID ABR29096 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 190
ID ABR07072 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003086899-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 191
ID ABR21166 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 192  
ID ABM09512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 193  
ID ABO41382 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 194  
ID ABO36197 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 195  
ID ABO43726 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 196  
ID ABM76426 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 197  
ID ABM76122 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 198  
ID ABM25741 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 199  
ID ABM26046 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 200  
ID ABO03399 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 201  
ID ABO02484 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 202  
ID ABO44264 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO 1411.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 203  
ID ABR90655 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 204  
ID ABR73723 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 205  
ID ABO16975 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 206  
ID ABR94400 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 207  
ID ABR75907 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 208  
ID ABR71283 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 209  
ID ABR93180 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 210  
ID ABR93485 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 211  
ID ABO39552 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 212  
ID ABO3596 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073130-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 213  
ID ABO27910 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 214  
ID ABO30045 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 215  
ID ABO33254 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 216  
ID ABO4942 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 217  
ID ABO8902 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 218  
ID ABO36502 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 219  
ID ABO3587 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 220  
ID ABR86995 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

ID ABO39552 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 221  
ID ABO10427 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 222  
ID ABO11952 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 223  
ID ABO52098 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 224  
ID ABO52403 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 225  
ID ADA19914 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 226  
ID ABO23721 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 227  
ID ADB17297 standard; protein; 440 AA.  
DE Human transmembrane PRO polypeptide (SeqID 52).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 228  
ID ABR97207 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 229  
ID ABR86995 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

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PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 230
ID ABM11037 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 231
ID ABM28181 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 232
ID ABO32180 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 233
ID ABM15307 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 234
ID ABM06462 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 235
ID ABM04273 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 236
ID ABM22386 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 237
ID ABM07682 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 238
ID ABO40772 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068684-A1.

PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 239
ID ABM35419 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 240
ID ABM33182 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 241
ID ABO52708 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 242
ID ABO50268 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 243
ID ABU99262 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 244
ID ABO04314 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 245
ID ABO05944 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 246
ID ABM18484 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 247
ID ABR97512 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 248
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ID ABR80612 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 249  
ID ABM01223 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 250  
ID ABR88825 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 251  
ID ABM13477 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 252  
ID ABM20861 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 253  
ID ABO41992 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 254  
ID ABO42602 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 255  
ID ABM10122 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 256  
ID ABO38637 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 257  
ID ABR32877 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 258  
ID ABM22691 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 259  
ID ABM74902 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 260  
ID ADA9746 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 261  
ID ABR96292 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 262  
ID ABM02443 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 263  
ID ABR86385 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 264  
ID ABR86690 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 265  
ID ABM16654 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 266  
ID ABM29706 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;

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RESULT 267
ID ABO29130 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 268
ID ABM23911 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 269
ID ABM23301 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 270
ID ADA47278 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 271
ID ABM22081 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 272
ID ABO37722 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 273
ID ABM28486 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 274
ID ABM28791 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 275
ID ABM66435 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 276
ID ABM75817 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 277
ID ABM34097 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 278
ID ABM34402 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 279
ID ABO20333 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 280
ID ABO21248 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 281
ID ABO22163 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 282
ID ADA20086 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 283
ID ABR9597 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 284
ID ABR85775 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 285
ID ABR99757 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 286
ID ABO0613 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 287
ID ABO0308 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 288
ID ABO29740 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 289
ID ABO23606 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ABO29401 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ABO38332 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 292
ID ABO45632 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ABO20556 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ABO81473 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ABO16670 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 296
ID ABO18296 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ABO22723 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ABO23028 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ABR92570 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ABR81527 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 301
ID ABM77951 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ABR89740 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 303
ID ABM26656 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 304
ID ABM13782 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 305
ID ABO28520 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ABO30350 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ABO7377 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 308
ID ABO3968 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 309
ID ABO37112 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 310
ID ABO41687 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 311
ID ABO35282 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 312
ID ABO25131 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 313
ID ABO47523 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 314
ID ABO47828 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 315
ID ABO48438 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 316
ID ABO51488 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 317
ID ABO51793 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 318
ID ABO50573 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 319
ID ABR79697 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 320
ID ABM16959 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 321
ID ABO17991 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 322
ID ABO20943 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 323
ID ABR96902 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054462-A1.
PD 20-MAR-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 324  
ID ABM12257 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 325  
ID ABM16349 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 326  
ID ABM24216 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 327  
ID ABM14697 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 328  
ID ABM04578 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 329  
ID ABM06767 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 330  
ID ABM09207 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 331  
ID ABO39247 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 332  
ID ABM75512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 333  
ID ABM25436 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 334  
ID ABM19946 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 335  
ID ABO46852 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 336  
ID ABO47157 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 337  
ID ADA83271 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 338  
ID ABR71588 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 339  
ID ABR72198 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 340  
ID ABR98537 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 341  
ID ABO06907 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 342  
ID ABR84860 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;



Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 343  
ID ABR73418 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 344  
ID ABR76512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044532-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 345  
ID ABR73113 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 346  
ID ABJ72433 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 347  
ID ABM18179 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 348  
ID ABO20638 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 349  
ID ABO25381 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 350  
ID ABO25686 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 351  
ID ABR94095 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 352  
ID ABR80002 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068759-A1.  
PD 10-APR-2003.

PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 353  
ID ABM1342 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 354  
ID ABO32949 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 355  
ID ABO30655 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 356  
ID ABO30960 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 357  
ID ABR27266 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 358  
ID ABR30011 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 359  
ID ABR05547 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 360  
ID ABR15612 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 361  
ID ABR08597 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068759-A1.  
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 362
ID ABO42297 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 363
ID ABO38027 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 364
ID ABO45937 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 365
ID ABM66740 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 366
ID ADB20314 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 367
ID ABM19641 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 368
ID ABO49353 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 369
ID ABO49658 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 370
ID ADA78566 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 371
ID ABO34328 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO 1411.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 372
ID ABR88215 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 373
ID ADA00383 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO 411.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 374
ID ABM28961 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 375
ID ABM03358 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 376
ID ABO39857 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003086889-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 377
ID ABO49963 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 378
ID ABO50878 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 379
ID ABO5334 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 380
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
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ID ABR74538 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 381  
ID ABO44449 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 382  
ID ABR77117 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 383  
ID ABR17874 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 384  
ID ABR95925 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 385  
ID ABO21858 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 386  
ID ABO20028 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 387  
ID ABO24331 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 388  
ID ABR86080 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 389  
ID ABR10732 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 390  
ID ABR76731 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 391  
ID ABR89435 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 392  
ID ABR12562 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 393  
ID ABR05852 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 394  
ID ABO34977 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 395  
ID ABR03053 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 396  
ID ABR19031 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 397  
ID ABR19336 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 398  
ID ABO46547 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 399  
ID ABR05852 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;  
Pred. No. 0;  
RESULT 399

ID ABO49048 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049757-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 400  
ID ABR69091 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 401  
ID ABR89130 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 402  
ID ABR72503 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 403  
ID ABR74333 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 404  
ID ABO18601 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 405  
ID ABR80307 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 406  
ID ABO1528 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 407  
ID ABO2138 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 408  
ID ABR87300 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068687-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 409  
ID ABM12867 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073186-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 410  
ID ABM30621 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003084443-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 411  
ID ABM24521 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003084444-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 412  
ID ABO29435 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068697-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 413  
ID ABO31265 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068710-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 414  
ID ABM14392 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068686-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 415  
ID ABM09817 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073178-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 416  
ID ABO38942 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068774-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 417  
ID ABM34707 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 418  
ID ABO51183 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 419  
ID ABO04009 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 420  
ID ABO10479 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 421  
ID ABR7722 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 422  
ID ABR78932 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 423  
ID ABO24026 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 424  
ID ABR93790 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 425  
ID ABO1833 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 426  
ID ABR78256 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 427  
ID ABO33473 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073129-A1.  
PD 17-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 428  
ID ABR90045 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 429  
ID ABR27571 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 430  
ID ABR13172 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 431  
ID ABO31875 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 432  
ID ABR14087 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068683-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 433  
ID ABR08292 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 434  
ID ABO40162 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068681-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 435  
ID ABR74597 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 436  
ID ABR33792 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 437	Query Match	100.0%;	Score 440;	DB 7;	Length 440;
ID	ABM20251 standard; protein; 440 AA.				
DE	Human secreted polypeptide PRO1411, SEQ ID NO:202.				
PN	US2003104556-A1.				
PD	05-JUN-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 440;	DB 7;	Length 440;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 438	Query Match	100.0%;	Score 440;	DB 7;	Length 440;
ID	ABO48743 standard; protein; 440 AA.				
DE	Human secreted/transmembrane protein (PRO) #101.				
PN	US2003049756-A1.				
PD	13-MAR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 440;	DB 7;	Length 440;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 439	Query Match	100.0%;	Score 440;	DB 7;	Length 440;
ID	ABR72808 standard; protein; 440 AA.				
DE	Human secreted polypeptide PRO1411, SEQ ID NO:202.				
PN	US2003036122-A1.				
PD	20-FEB-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 440;	DB 7;	Length 440;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 440	Query Match	100.0%;	Score 440;	DB 7;	Length 440;
ID	ABO15450 standard; protein; 440 AA.				
DE	Human secreted/transmembrane protein (PRO) #101.				
PN	US2003036121-A1.				
PD	20-FEB-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 440;	DB 7;	Length 440;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 441	Query Match	100.0%;	Score 440;	DB 7;	Length 440;
ID	ABR85165 standard; protein; 440 AA.				
DE	Human secreted polypeptide PRO1411, SEQ ID NO:202.				
PN	US2003040065-A1.				
PD	27-FEB-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 440;	DB 7;	Length 440;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 442	Query Match	100.0%;	Score 440;	DB 7;	Length 440;
ID	ABO15145 standard; protein; 440 AA.				
DE	Human secreted/transmembrane protein (PRO) #101.				
PN	US2003044919-A1.				
PD	06-MAR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 440;	DB 7;	Length 440;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 443	Query Match	100.0%;	Score 440;	DB 7;	Length 440;
ID	ABO17280 standard; protein; 440 AA.				
DE	Human secreted/transmembrane protein (PRO) #101.				
PN	US2003040077-A1.				
PD	27-FEB-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 440;	DB 7;	Length 440;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 444	Query Match	100.0%;	Score 440;	DB 7;	Length 440;
ID	ABO19863 standard; protein; 440 AA.				
DE	Human secreted/transmembrane protein PRO1411.				
PN	US2003044902-A1.				
PD	06-MAR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 440;	DB 7;	Length 440;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 445	Query Match	100.0%;	Score 440;	DB 7;	Length 440;
ID	ABM17569 standard; protein; 440 AA.				
DE	Human secreted polypeptide PRO1411, SEQ ID NO:202.				
PN	US2003044928-A1.				
PD	06-MAR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 440;	DB 7;	Length 440;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 446	Query Match	100.0%;	Score 440;	DB 7;	Length 440;
ID	ABE72135 standard; protein; 440 AA.				
DE	Human membrane bound receptor/protein PRO1411 amino acid sequence.				
PN	US2003065147-A1.				
PD	03-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 440;	DB 7;	Length 440;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 447	Query Match	100.0%;	Score 440;	DB 7;	Length 440;
ID	ABR85470 standard; protein; 440 AA.				
DE	Human secreted polypeptide PRO1411, SEQ ID NO:202.				
PN					

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 456  
ID ABO36807 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 457  
ID ABO37417 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 458  
ID ABO75207 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 459  
ID ABO33487 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 460  
ID ABO46242 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 461  
ID ADA82637 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 462  
ID ADB85625 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 463  
ID ADB83646 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 464  
ID ADB80752 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 465  
ID ADB73293 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 466  
ID ABO31841 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 467  
ID ABO78375 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 468  
ID ABO31231 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 469  
ID ADB85023 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 470  
ID ADB78129 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 471  
ID ADB85945 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 472  
ID ABO32146 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 473  
ID ABO32451 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 474  
ID ADB87195 standard; protein; 440 AA.

DE Human PRO polypeptide #78.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 475  
ID ADB84777 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 476  
ID ADB68304 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 477  
ID ADB68111 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 478  
ID ADB31536 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 479  
ID ABM30926 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 480  
ID ADB83892 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 481  
ID ADB73047 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 482  
ID ADB90928 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003083473-A1.  
PD 03-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 483  
ID ADC07008 standard; protein; 440 AA.  
DE Human PRO1411 protein.

PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 484  
ID ADC17921 standard; protein; 440 AA.  
DE Human PRO polypeptide #15.  
PN US2003084925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 485  
ID ADC17187 standard; protein; 440 AA.  
DE Mammalian PRO polypeptide (SeqID 52).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 486  
ID ADC14885 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 487  
ID ADC36885 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003088085-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 488  
ID ADC52380 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 489  
ID ADC21875 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 490  
ID ADC49906 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 491  
ID ADC49105 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 492  
ID ADC49622 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088071-A1.



PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 493  
ID ADC47483 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 494  
ID ADC47228 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 495  
ID ADC78103 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 496  
ID ADD06338 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 497  
ID ADD05675 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 498  
ID ADD10439 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 499  
ID ADC77857 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 500  
ID ADD11399 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 501  
ID ADD50820 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 502  
ID ADD51066 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 503  
ID ADD70567 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 504  
ID ADD39644 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 505  
ID ADD70090 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 506  
ID ADD37192 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 507  
ID ADD36056 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 508  
ID ADD38211 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 509  
ID ADD39167 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 510  
ID ADD50547 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.

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Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 511
ID ADD50301 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 512
ID ADD38690 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 513
ID ADD40121 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 514
ID ADD51312 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 515
ID ADE50342 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 516
ID ADE19954 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 517
ID ADE49865 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 518
ID ADE21423 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 519
ID ADF29848 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US20031204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 520
ID ADF55741 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US20031204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 521
ID ADG01057 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 522
ID ADG08610 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 523
ID ADG02670 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 524
ID ADG01377 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 525
ID ADF95552 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 526
ID ADF95231 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 527
ID ADG12367 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 528
ID ADH24084 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 529
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ID ADH34110 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 530  
ID ADH29943 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 531  
ID ADH23914 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 532  
ID ADH09027 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 533  
ID ADG85318 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 534  
ID ADH24594 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 535  
ID ADH37450 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO411.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 536  
ID ADH02039 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 537  
ID ADH37620 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO411.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 538  
ID ADG85658 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.

DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 539  
ID ADH24254 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 540  
ID ADH38548 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 541  
ID ADG63787 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO1411.  
PN US2003170721-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 542  
ID ADG83669 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 543  
ID ADH29477 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 544  
ID ADH27593 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 545  
ID ADH37790 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO1411.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 546  
ID ADH37967 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO411.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 547  
ID ADH57387 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.

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PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 548
ID ADH53529 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 549
ID ADH53699 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 550
ID ADH52035 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 551
ID ADH49890 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 552
ID ADI25400 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 553
ID ADH90193 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 554
ID ADI25570 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 555
ID ADH97744 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 556
ID ADH99245 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003065142-A1.

PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 557
ID ADI03592 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 558
ID ADI11949 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 559
ID ADH90023 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 560
ID ADH98424 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 561
ID ADI11099 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 562
ID ADI11609 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 563
ID ADH98254 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 564
ID ADH98594 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 565
ID ADH98084 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181673-A1.
PD 25-SEP-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 566  
ID ADI05072 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 567  
ID ADI03422 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO411.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 568  
ID ADI04817 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 569  
ID ADH78271 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 570  
ID ADI19615 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 571  
ID ADH90363 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 572  
ID ADI03082 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 573  
ID ADH77931 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 574  
ID ADH97914 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 575  
ID ADI01299 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 576  
ID ADI01994 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 577  
ID ADI03252 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 578  
ID ADI11439 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 579  
ID ADI02341 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 580  
ID ADI11779 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 581  
ID ADI05416 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 582  
ID ADH79488 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 583  
ID ADI19445 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 584  
ID ADH97914 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 584
ID ADI05246 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 585
ID ADH79658 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 586
ID ADI01484 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 587
ID ADI01654 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 588
ID ADI01824 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 589
ID ADH79828 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 590
ID ADI04646 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 591
ID ADI02782 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 592
ID ADH78101 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 593
ID ADI25740 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 594
ID ADI25910 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 595
ID ADK65422 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 596
ID ADH98764 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 597
ID ADH80005 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 598
ID ADM30342 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 599
ID ADL91736 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 600
ID ADC48859 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 601
ID ADC52190 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 602
ID ADH78101 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
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ID ADE21030 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 603  
ID ADE05874 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 604  
ID ADD75103 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 605  
ID ADD75849 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 606  
ID ADD85081 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 607  
ID ADD86907 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 608  
ID ADE20784 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 609  
ID ADE39081 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 610  
ID ADE05628 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 611  
ID ADD73613 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 612  
ID ADD78453 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 613  
ID ADE41400 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 614  
ID ADE74339 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 615  
ID ADE21276 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100736-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 616  
ID ADD77391 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100732-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 617  
ID ADE20538 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100733-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 618  
ID ADD75603 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100064-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 619  
ID ADD74119 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100708-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 620  
ID ADD74365 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100709-A1.

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PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 630
ID ADD77637 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 631
ID ADD77883 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 632
ID ADD77883 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 633
ID ADD73873 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 634
ID ADD74611 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 635
ID ADD77139 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 636
ID ADD85833 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 637
ID ADE05382 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 638
ID ADD74857 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 639
ID ADE74951 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003211574-A1.
PD 13-NOV-2003.

PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 621
ID ADD76095 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 622
ID ADD8587 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 623
ID ADE05136 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 624
ID ADD75349 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 625
ID ADD76893 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 626
ID ADD86661 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 627
ID ADE41201 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
PN US2003104558-A1.
PD 03-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 628
ID ADD78129 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 629
ID ADE74951 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003211574-A1.
PD 13-NOV-2003.
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Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 639  
ID ADE96425 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 640  
ID ADF25736 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 641  
ID ADF24635 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 642  
ID ADF29371 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 643  
ID ADE96902 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 644  
ID ADG05669 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 645  
ID ADG27223 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 646  
ID ADF96164 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 647  
ID ADG11286 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 648  
ID ADH25104 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 649  
ID ADG12065 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 650  
ID ADG00595 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 651  
ID ADF94622 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 652  
ID ADG06718 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 653  
ID ADH06622 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 654  
ID ADH06452 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 655  
ID ADG68873 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 656  
ID ADH27763 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 657  
ID ADH25104 standard; protein; 440 AA.

DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 658  
ID ADH33736 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 659  
ID ADG82851 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 660  
ID ADH02940 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 661  
ID ADH02379 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 662  
ID ADH07986 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 663  
ID ADG69383 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 664  
ID ADH39204 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 665  
ID ADH03894 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 666  
ID ADH03417 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.

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PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 667  
ID ADH26132 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 668  
ID ADG83944 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 669  
ID ADH39062 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 670  
ID ADG8548 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 671  
ID ADG63636 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO1411.  
PN US2003180796-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 672  
ID ADH06282 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 673  
ID ADH30112 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 674  
ID ADH24424 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 675  
ID ADH33101 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068768-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 676  
ID ADG6953 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 677  
ID ADH07816 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 678  
ID ADG85928 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 679  
ID ADH39374 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 680  
ID ADH33566 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 681  
ID ADH33906 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 682  
ID ADH01116 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 683  
ID ADG69723 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 684  
ID ADH02209 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 685  
ID ADG69213 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 686  
ID ADG85998 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 687  
ID ADH24934 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 688  
ID ADH39551 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 689  
ID ADH02549 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 690  
ID ADG69043 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 691  
ID ADH07646 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 692  
ID ADG86168 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;  
RESULT 693  
ID ADH24764 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.



RESULT 712  
ID ADJ98578 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 713  
ID ADJ98748 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 714  
ID ADH78907 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 715  
ID ADJ99141 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 716  
ID ADJ99311 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 717  
ID ADJ98929 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 718  
ID ADH79077 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 719  
ID ADK00937 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 720  
ID ADK14458 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 721  
ID ADN37967 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US200404179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 722  
ID ADK82928 standard; protein; 440 AA.  
DE Human PRO polypeptide #75.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 723  
ID ADJ64611 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 724  
ID ADK66632 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 725  
ID ADM31507 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 726  
ID ADM36554 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 727  
ID ADM40359 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 728  
ID ADM80907 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 729  
ID ADL94571 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 730  
ID ADN37967 standard; protein; 440 AA.

DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 440; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 731  
ID ABL32808 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 78.4%; Score 345; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 6.5e-291;  
RESULT 732  
ID ABO27306 standard; protein; 372 AA.  
DE Human secreted/transmembrane polypeptide PRO411.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 77.3%; Score 340; DB 6; Length 372;  
Best Local Similarity 100.0%; Pred. No. 1.2e-286;  
RESULT 733  
ID ABO34192 standard; protein; 372 AA.  
DE Human secreted/transmembrane polypeptide PRO 1411.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 77.3%; Score 340; DB 6; Length 372;  
Best Local Similarity 100.0%; Pred. No. 1.2e-286;  
RESULT 734  
ID AAB3824 standard; protein; 387 AA.  
DE Human secreted protein encoded by gene 4 clone HKAJK47.  
PN WO2000061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 40.5%; Score 178; DB 3; Length 387;  
Best Local Similarity 99.6%; Pred. No. 7.1e-146;  
RESULT 735  
ID AAY50939 standard; protein; 358 AA.  
DE Human adult skin cDNA clone vd3\_1 derived protein #1.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 31.8%; Score 140; DB 3; Length 358;  
Best Local Similarity 100.0%; Pred. No. 6.9e-113;  
RESULT 736  
ID AAY50940 standard; protein; 369 AA.  
DE Human adult skin cDNA clone vd3\_1 derived protein #2.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 31.8%; Score 140; DB 3; Length 369;  
Best Local Similarity 100.0%; Pred. No. 7.1e-113;  
RESULT 737  
ID AAY50941 standard; protein; 479 AA.  
DE Human adult skin cDNA clone vd4\_1 derived protein.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 31.8%; Score 140; DB 3; Length 479;  
Best Local Similarity 100.0%; Pred. No. 8.9e-113;  
RESULT 738  
ID ADP07783 standard; protein; 186 AA.  
DE Human secreted protein, seq id 266.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 20.5%; Score 90; DB 8; Length 186;  
Best Local Similarity 100.0%; Pred. No. 1.1e-69;  
RESULT 739  
ID AAY60056 standard; protein; 230 AA.  
DE Human endometrium tumour EST encoded protein 116.

PN DE19817948-A1.  
PD 21-OCT-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 19.5%; Score 86; DB 2; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3.8e-66;  
RESULT 740  
ID AAM94219 standard; protein; 116 AA.  
DE Human reproductive system related antigen SEQ ID NO: 2877.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.5%; Score 55; DB 4; Length 116;  
Best Local Similarity 100.0%; Pred. No. 1.8e-39;  
RESULT 741  
ID ADE28209 standard; protein; 203 AA.  
DE Human MDDT protein - SEQ ID 59.  
PN WO2003046152-A2.  
PD 05-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.1%; Score 40; DB 7; Length 203;  
Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
RESULT 742  
ID AAY12417 standard; protein; 76 AA.  
DE Human 5' EST secreted protein SEQ ID NO:448.  
PN WO9906548-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 8.0%; Score 35; DB 2; Length 76;  
Best Local Similarity 100.0%; Pred. No. 2.9e-22;  
RESULT 743  
ID AAG01482 standard; protein; 72 AA.  
DE Human secreted protein, SEQ ID NO: 5563.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST ) GENSET.  
Query Match 5.7%; Score 25; DB 3; Length 72;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
RESULT 744  
ID AAG01483 standard; protein; 72 AA.  
DE Human secreted protein, SEQ ID NO: 5564.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST ) GENSET.  
Query Match 5.7%; Score 25; DB 3; Length 72;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
RESULT 745  
ID AAB73503 standard; protein; 123 AA.  
DE Human transferase HTFS-10, SEQ ID NO:10.  
PN WO200132888-A2.  
PD 10-MAY-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 5.7%; Score 25; DB 4; Length 123;  
Best Local Similarity 100.0%; Pred. No. 2.2e-13;  
RESULT 746  
ID ABU25709 standard; protein; 1751 AA.  
DE Protein encoded by Prokaryotic essential gene #11236.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 3.4%; Score 15; DB 6; Length 1751;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
RESULT 747  
ID AAB35982 standard; peptide; 16 AA.  
DE Linker peptide #2 used in the exemplification of the invention.  
PN WO2002101079-A2.  
PD 19-DEC-2002.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 3.0%; Score 13; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00098;  
RESULT 748  
ID ADQ66425 standard; protein; 120 AA.  
DE Novel human protein sequence #1398.  
PN EP1440981-A2.

PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 3.0%; Score 13; DB 8; Length 120;  
Best Local Similarity 100.0%; Pred. No. 0.0057;  
RESULT 749  
ID AAW37241 standard; protein; 476 AA.  
DE Heterodera glycines cellulase HG-engl.  
FN WO9801569-A1.  
PD 15-JAN-1998.  
PA (RIJK-) RIJSLANDBOUWHOGESCHOOL.  
Query Match 3.0%; Score 13; DB 2; Length 476;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 750  
ID AAW43910 standard; protein; 484 AA.  
DE Heterodera glycines svp encoded cellulase.  
FN EP818538-A1.  
PD 14-JAN-1998.  
PA (RIJK-) RIJSLANDBOUWHOGESCHOOL.  
Query Match 3.0%; Score 13; DB 2; Length 484;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 751  
ID ABB68240 standard; protein; 828 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 31512.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 2.7%; Score 12; DB 4; Length 828;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
RESULT 752  
ID ADA20331 standard; protein; 214 AA.  
DE Mutant human CITED2 protein amino acids 1-214.  
FN WO2003038441-A2.  
PD 08-MAY-2003.  
PA (ISIS-) ISIS INNOVATION LTD.  
Query Match 2.5%; Score 11; DB 6; Length 214;  
Best Local Similarity 100.0%; Pred. No. 0.52;  
RESULT 753  
ID ABB69351 standard; protein; 252 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 34845.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 2.5%; Score 11; DB 4; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.6;  
RESULT 754  
ID AAB60461 standard; protein; 270 AA.  
DE Human cell cycle and proliferation protein CCYPR-9, SEQ ID NO:9.  
FN WO200107471-A2.  
PD 01-FEB-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 2.5%; Score 11; DB 4; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
RESULT 755  
ID ADA20318 standard; protein; 270 AA.  
DE Human CITED2 protein.  
FN WO2003038441-A2.  
PD 08-MAY-2003.  
PA (ISIS-) ISIS INNOVATION LTD.  
Query Match 2.5%; Score 11; DB 6; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
RESULT 756  
ID ADD18604 standard; protein; 270 AA.  
DE Human disease related protein SeqID35.  
FN WO2003018621-A2.  
PD 06-MAR-2003.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 2.5%; Score 11; DB 7; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
RESULT 757  
ID ABE60370 standard; protein; 270 AA.  
DE Human Protein Q99967, SEQ ID NO 6278.  
FN WO2003016475-A2.  
PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 2.5%; Score 11; DB 7; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
RESULT 758  
ID ADE60373 standard; protein; 270 AA.  
DE Human Protein Q99967, SEQ ID NO 6282.  
FN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 2.5%; Score 11; DB 7; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
RESULT 759  
ID ADD45931 standard; protein; 270 AA.  
DE Human Protein Q99967, SEQ ID NO 11603.  
FN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 2.5%; Score 11; DB 7; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
RESULT 760  
ID ADN95881 standard; protein; 270 AA.  
DE Human BEC/LEC-related protein sequence SeqID805.  
FN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
Query Match 2.5%; Score 11; DB 7; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
RESULT 761  
ID ADO19714 standard; protein; 270 AA.  
DE Human PRO polypeptide #320.  
FN WO2004043361-A2.  
PD 27-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 2.5%; Score 11; DB 8; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
RESULT 762  
ID ADO19616 standard; protein; 270 AA.  
DE Human PRO polypeptide #273.  
FN WO2004043361-A2.  
PD 27-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 2.5%; Score 11; DB 8; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
RESULT 763  
ID ADR14659 standard; protein; 270 AA.  
DE Human NF-kappaB pathway-associated protein SeqID660.  
FN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 2.5%; Score 11; DB 8; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
RESULT 764  
ID ADP54707 standard; protein; 270 AA.  
DE Human PRO protein sequence SEQ ID NO:683.  
FN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 2.5%; Score 11; DB 8; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
RESULT 765  
ID ADJ35152 standard; protein; 445 AA.  
DE Xylanase from an environmental sample seq id 368.  
FN WO2003106654-A2.  
PD 24-DEC-2003.  
PA (DIVE-) DIVERSA CORP.  
Query Match 2.5%; Score 11; DB 8; Length 445;  
Best Local Similarity 100.0%; Pred. No. 0.98;  
RESULT 766  
ID ABR55544 standard; protein; 452 AA.

DE Amino acid sequence of mature murine mucinase AMCase.  
PN W02003038079-A2.  
PD 08-MAY-2003.  
PA (MACR-) MACROZYME BV. 2.5%; Score 11; DB 7; Length 452;  
Query Match 100.0%; Pred. No. 1;  
Best Local Similarity 100.0%; Pred. No. 1;  
RESULT 767  
ID ABR55543 standard; protein; 473 AA.  
DE Amino acid sequence of murine mucinase AMCase.  
PN W02003038079-A2.  
PD 08-MAY-2003.  
PA (MACR-) MACROZYME BV. 2.5%; Score 11; DB 7; Length 473;  
Query Match 100.0%; Pred. No. 1;  
Best Local Similarity 100.0%; Pred. No. 1;  
RESULT 768  
ID ADC51464 standard; protein; 473 AA.  
DE Chitinase 52.03 protein SEQ ID NO:2.  
PN CN1382800-A.  
PD 04-DEC-2002.  
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI. 2.5%; Score 11; DB 7; Length 473;  
Query Match 100.0%; Pred. No. 1;  
Best Local Similarity 100.0%; Pred. No. 1;  
RESULT 769  
ID ABU09914 standard; protein; 520 AA.  
DE Partial mouse acidic mammalian chitinase (AMCase) precursor.  
PN W02003031582-A2.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
PA (CURA-) CURAGEN CORP.  
PA (STEW) STEWART T A.  
PA (KELL) KELLY K M.  
Query Match 2.5%; Score 11; DB 6; Length 520;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
RESULT 770  
ID ABB70436 standard; protein; 644 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 38100.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 2.5%; Score 11; DB 4; Length 644;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
RESULT 771  
ID ADH48368 standard; protein; 718 AA.  
DE Human KPP protein SEQ ID NO:26.  
PN W02004001008-A2.  
PD 31-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 2.5%; Score 11; DB 8; Length 718;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
RESULT 772  
ID ADB09224 standard; protein; 844 AA.  
DE Allostococcus otitis antigenic protein SEQ ID NO:3164.  
PN W02003048304-A2.  
PD 12-JUN-2003.  
PA (AWHP) WYETH HOLDINGS CORP.  
Query Match 2.5%; Score 11; DB 6; Length 844;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
RESULT 773  
ID ADB09226 standard; protein; 871 AA.  
DE Allostococcus otitis antigenic protein SEQ ID NO:3166.  
PN W02003048304-A2.  
PD 12-JUN-2003.  
PA (AWHP) WYETH HOLDINGS CORP.  
Query Match 2.5%; Score 11; DB 6; Length 871;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
RESULT 774  
ID ABW85183 standard; protein; 923 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5432.  
PN W02004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 2.5%; Score 11; DB 8; Length 923;  
Best Local Similarity 100.0%; Pred. No. 1.9;

RESULT 775  
ID ABP70836 standard; protein; 953 AA.  
DE Human serine/threonine kinase-related protein.  
PN W02003018786-A2.  
PD 06-MAR-2003.  
PA (FARB) BAYER AG.  
Query Match 2.5%; Score 11; DB 6; Length 953;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
RESULT 776  
ID ADC77693 standard; protein; 953 AA.  
DE Human 16314 protein SEQ ID NO:56.  
PN W02003073983-A2.  
PD 12-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.5%; Score 11; DB 7; Length 953;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
RESULT 777  
ID ADO01049 standard; protein; 954 AA.  
DE Human homologue of Fruit fly AD-related protein CG8789 #3.  
PN US2004067535-A1.  
PD 08-APR-2004.  
PA (LIFE-) LIFE SCI DEV CORP.  
Query Match 2.5%; Score 11; DB 8; Length 954;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
RESULT 778  
ID RAG94132 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 326.  
PN W0200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 2.3%; Score 10; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.26;  
RESULT 779  
ID ADO43232 standard; peptide; 10 AA.  
DE Bioactivation peptide extension used to solubilise quantum dot.  
PN W02004039830-A2.  
PD 13-MAY-2004.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 2.3%; Score 10; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.26;  
RESULT 780  
ID ADO57970 standard; peptide; 15 AA.  
DE MHC multimer linker peptide SEQ ID 5.  
PN DE10247014-A1.  
PD 22-APR-2004.  
PA (ERFL) ERFLE V.  
Query Match 2.3%; Score 10; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
RESULT 781  
ID ADO43228 standard; peptide; 20 AA.  
DE Bioactivation peptide used to solubilise quantum dot.  
PN W02004039830-A2.  
PD 13-MAY-2004.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 2.3%; Score 10; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
RESULT 782  
ID AAU77733 standard; protein; 119 AA.  
DE Novel human secreted protein #5.  
PN W0200214341-A1.  
PD 21-FEB-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.3%; Score 10; DB 5; Length 119;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
RESULT 783  
ID RAM92862 standard; protein; 203 AA.  
DE Human digestive system antigen SEQ ID NO: 2211.  
PN W0200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.3%; Score 10; DB 4; Length 203;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
RESULT 784



ID ADQ97309 standard; protein; 214 AA.  
DE Human cancer associated sequence HP08-029, SEQ ID 286.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 2.3%; Score 10; DB 8; Length 214;  
Best Local Similarity 100.0%; Pred. No. 3.8;  
RESULT 785  
ID ABG08358 standard; protein; 324 AA.  
DE Novel human diagnostic protein #8349.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.3%; Score 10; DB 4; Length 324;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
RESULT 786  
ID ABB97580 standard; protein; 368 AA.  
DE Novel human protein SEQ ID NO: 848.  
PN WO200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.3%; Score 10; DB 5; Length 368;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
RESULT 787  
ID ABU09916 standard; protein; 368 AA.  
DE Human eosinophil chemotactic-like cytokine.  
PN WO2003031582-A2.  
PD 17-APR-2003.  
PA (GETH-) GENENTECH INC.  
PA (CURA-) CURAGEN CORP.  
PA (STEW/) STEWART T A.  
PA (KELL/) KELLY K M.  
Query Match 2.3%; Score 10; DB 6; Length 368;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
RESULT 788  
ID ADP69059 standard; protein; 368 AA.  
DE Human NOV6f protein SEQ ID NO:54.  
PN WO2004055158-A2.  
PD 01-JUL-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.3%; Score 10; DB 8; Length 368;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
RESULT 789  
ID ADP69057 standard; protein; 368 AA.  
DE Human NOV6e protein SEQ ID NO:52.  
PN WO2004055158-A2.  
PD 01-JUL-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.3%; Score 10; DB 8; Length 368;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
RESULT 790  
ID ADP69061 standard; protein; 368 AA.  
DE Human NOV6g protein SEQ ID NO:56.  
PN WO2004055158-A2.  
PD 01-JUL-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.3%; Score 10; DB 8; Length 368;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
RESULT 791  
ID ADP69053 standard; protein; 368 AA.  
DE Human NOV6c protein SEQ ID NO:48.  
PN WO2004055158-A2.  
PD 01-JUL-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.3%; Score 10; DB 8; Length 368;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
RESULT 792  
ID ADP69055 standard; protein; 368 AA.  
DE Human NOV6d protein SEQ ID NO:50.  
PN WO2004055158-A2.  
PD 01-JUL-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.3%; Score 10; DB 8; Length 368;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
RESULT 793  
ID ADP69049 standard; protein; 368 AA.  
DE Human NOV6a protein SEQ ID NO:44.  
PN WO2004055158-A2.  
PD 01-JUL-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.3%; Score 10; DB 8; Length 368;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
RESULT 794  
ID ABUS6729 standard; protein; 441 AA.  
DE Lung cancer-associated polypeptide #322.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 2.3%; Score 10; DB 6; Length 441;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
RESULT 795  
ID ADD45205 standard; protein; 441 AA.  
DE Human Protein S34118, SEQ ID NO 10638.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match 2.3%; Score 10; DB 7; Length 441;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
RESULT 796  
ID ADE55546 standard; protein; 441 AA.  
DE Human Protein S34118, SEQ ID NO 1363.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match 2.3%; Score 10; DB 7; Length 441;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
RESULT 797  
ID ADN39194 standard; protein; 441 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:512.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 2.3%; Score 10; DB 7; Length 441;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
RESULT 798  
ID ADQ21597 standard; protein; 441 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4417.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.3%; Score 10; DB 8; Length 441;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
RESULT 799  
ID AAG62541 standard; protein; 455 AA.  
DE Disease treatment related protein SEQ ID NO: 1.  
PN WO200136633-A1.  
PD 25-MAY-2001.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 2.3%; Score 10; DB 4; Length 455;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
RESULT 800  
ID AAG62543 standard; protein; 476 AA.  
DE Disease treatment related protein SEQ ID NO: 5.  
PN WO200136633-A1.  
PD 25-MAY-2001.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 2.3%; Score 10; DB 4; Length 476;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
RESULT 801  
ID ABU09915 standard; protein; 476 AA.  
DE Human acidic mammalian chitinase (AMCase) precursor.  
PN WO2003031582-A2.  
PD 17-APR-2003.  
PA (GETH-) GENENTECH INC.

PA (CURA-) CURAGEN CORP. 2.3%; Score 10; DB 6; Length 476;  
PA (STEW/) STEWART T A.  
PA (KELL/) KELLY K M.  
Query Match 2.3%; Score 10; DB 6; Length 476;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
RESULT 802  
ID ABR55542 standard; protein; 476 AA.  
DE Amino acid sequence of human mucinase AMCase.  
PN WO2003038079-A2.  
PD 08-MAY-2003.  
PA (MACR-) MACROZYME BV. 2.3%; Score 10; DB 7; Length 476;  
Query Match 2.3%; Score 10; DB 7; Length 476;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
RESULT 803  
ID ADP69051 standard; protein; 476 AA.  
DE Human NOV6b protein SEQ ID NO:46.  
PN WO2004055158-A2.  
PD 01-JUL-2004.  
PA (CURA-) CURAGEN CORP. 2.3%; Score 10; DB 8; Length 476;  
Query Match 2.3%; Score 10; DB 8; Length 476;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
RESULT 804  
ID AAB68273 standard; protein; 501 AA.  
DE Amino acid sequence of an Arabidopsis thaliana PMR6 gene.  
PN WO200129230-A2.  
PD 26-APR-2001.  
PA (CARN-) CARNEGIE INST WASHINGTON. 2.3%; Score 10; DB 4; Length 501;  
Query Match 2.3%; Score 10; DB 4; Length 501;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
RESULT 805  
ID ADN74843 standard; protein; 501 AA.  
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 2738.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPDISEIGN NV. 2.3%; Score 10; DB 8; Length 501;  
Query Match 2.3%; Score 10; DB 8; Length 501;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
RESULT 806  
ID AAE19445 standard; protein; 537 AA.  
DE Hansenula polymorpha GPI cell wall anchor protein, HpgAslp.  
PN WO200212509-A1.  
PD 14-FEB-2002.  
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG. 2.3%; Score 10; DB 5; Length 537;  
Query Match 2.3%; Score 10; DB 5; Length 537;  
Best Local Similarity 100.0%; Pred. No. 8.6;  
RESULT 807  
ID ABB92667 standard; protein; 542 AA.  
DE Herbicidally active polypeptide SEQ ID NO 1878.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB-) BAYER AG. 2.3%; Score 10; DB 5; Length 542;  
Query Match 2.3%; Score 10; DB 5; Length 542;  
Best Local Similarity 100.0%; Pred. No. 8.6;  
RESULT 808  
ID AAU12046 standard; protein; 626 AA.  
DE Clostridium difficile S-layer protein cell wall binding portion (ORFG).  
PN WO200194599-A1.  
PD 13-DEC-2001.  
PA (SMIT-) SMITTSKYDINSITTUTET. 2.3%; Score 10; DB 5; Length 626;  
Query Match 2.3%; Score 10; DB 5; Length 626;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
RESULT 809  
ID ABU25345 standard; protein; 628 AA.  
DE Protein encoded by Prokaryotic essential gene #10872.  
PN WO200271183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC. 2.3%; Score 10; DB 6; Length 628;  
Query Match 2.3%; Score 10; DB 6; Length 628;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
RESULT 810  
ID ABU03140 standard; protein; 866 AA.  
DE Alpha amylase polypeptide #101.  
PN WO200268589-A2.

PD 06-SEP-2002.  
PA (DIVE-) DIVERSA CORP. 2.3%; Score 10; DB 6; Length 866;  
Query Match 2.3%; Score 10; DB 6; Length 866;  
Best Local Similarity 100.0%; Pred. No. 13;  
RESULT 811  
ID ABB69760 standard; protein; 952 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 36072.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY. 2.3%; Score 10; DB 4; Length 952;  
Query Match 2.3%; Score 10; DB 4; Length 952;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 812  
ID ABB59829 standard; protein; 1893 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 6279.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY. 2.3%; Score 10; DB 4; Length 1893;  
Query Match 2.3%; Score 10; DB 4; Length 1893;  
Best Local Similarity 100.0%; Pred. No. 26;  
RESULT 813  
ID ABB64682 standard; protein; 2090 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 20838.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY. 2.3%; Score 10; DB 4; Length 2090;  
Query Match 2.3%; Score 10; DB 4; Length 2090;  
Best Local Similarity 100.0%; Pred. No. 28;  
RESULT 814  
ID AAG94130 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 324.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD. 2.0%; Score 9; DB 4; Length 10;  
Query Match 2.0%; Score 9; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
RESULT 815  
ID ABW00721 standard; peptide; 10 AA.  
DE Peptide spacer #1 used in the invention.  
PN US2002168375-A1.  
PD 14-NOV-2002.  
PA (CHIR-) CHIRON CORP. 2.0%; Score 9; DB 7; Length 10;  
Query Match 2.0%; Score 9; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
RESULT 816  
ID ADH88625 standard; protein; 60 AA.  
DE Enterococcus faecalis polypeptide #3105.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A. 2.0%; Score 9; DB 7; Length 60;  
PA (BUSH/) BUSH D. 2.0%; Score 9; DB 7; Length 60;  
Query Match 2.0%; Score 9; DB 7; Length 60;  
Best Local Similarity 100.0%; Pred. No. 9.3;  
RESULT 817  
ID ADC32840 standard; protein; 96 AA.  
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:2922.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC. 2.0%; Score 9; DB 7; Length 96;  
Query Match 2.0%; Score 9; DB 7; Length 96;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 818  
ID ABJ39196 standard; protein; 111 AA.  
DE Fragment d, glycine rich sticky domain 1 of the human S protein.  
PN WO2003050311-A2.  
PD 19-JUN-2003.  
PA (WELA-) WELIA AG. 2.0%; Score 9; DB 7; Length 111;  
Query Match 2.0%; Score 9; DB 7; Length 111;  
Best Local Similarity 100.0%; Pred. No. 16;  
RESULT 819  
ID ABJ39195 standard; protein; 146 AA.  
DE Fragment c, cleavage product of human S (corneodesmosin skin) protein.  
PN WO2003050311-A2.

PD 19-JUN-2003.  
PA (WELA ) WELLA AG.  
Query Match 2.0%; Score 9; DB 7; Length 146;  
Best Local Similarity 100.0%; Pred. No. 20;  
RESULT 820  
ID ADJ92311 standard; protein; 167 AA.  
DE Mouse hair keratin-associated-protein SEQ ID NO:170.  
PN WO2003042387-A1.  
PD 22-MAY-2003.  
PA (UYKE-) UNIV KEIO.  
PA (NIPR-) JAPAN SOC PROMOTION SCI.  
Query Match 2.0%; Score 9; DB 7; Length 167;  
Best Local Similarity 100.0%; Pred. No. 23;  
RESULT 821  
ID AAB54279 standard; protein; 175 AA.  
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:731.  
PN WO200055320-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.0%; Score 9; DB 3; Length 175;  
Best Local Similarity 100.0%; Pred. No. 24;  
RESULT 822  
ID ADC96370 standard; protein; 184 AA.  
DE E. faecium protein sequence SEQ ID 5997.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 2.0%; Score 9; DB 7; Length 184;  
Best Local Similarity 100.0%; Pred. No. 25;  
RESULT 823  
ID AAU16338 standard; protein; 199 AA.  
DE Human novel secreted protein, Seq ID 1291.  
PN WO200155322-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.0%; Score 9; DB 4; Length 199;  
Best Local Similarity 100.0%; Pred. No. 27;  
RESULT 824  
ID ABU55407 standard; protein; 199 AA.  
DE Human novel polypeptide #494.  
PN US2002132753-A1.  
PD 19-SEP-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 2.0%; Score 9; DB 6; Length 199;  
Best Local Similarity 100.0%; Pred. No. 27;  
RESULT 825  
ID AAU15883 standard; protein; 201 AA.  
DE Human novel secreted protein, Seq ID 836.  
PN WO200155322-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.0%; Score 9; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 27;  
RESULT 826  
ID ABU54952 standard; protein; 201 AA.  
DE Human novel polypeptide #39.  
PN US2002132753-A1.  
PD 19-SEP-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 2.0%; Score 9; DB 6; Length 201;  
Best Local Similarity 100.0%; Pred. No. 27;  
RESULT 827  
ID ABO60412 standard; protein; 219 AA.  
DE Human genome derived single exon protein #6646.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.

Query Match 2.0%; Score 9; DB 8; Length 219;  
Best Local Similarity 100.0%; Pred. No. 29;  
RESULT 828  
ID ABB70402 standard; protein; 253 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 37998.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 2.0%; Score 9; DB 4; Length 253;  
Best Local Similarity 100.0%; Pred. No. 33;  
RESULT 829  
ID ABB70259 standard; protein; 280 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 37569.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 2.0%; Score 9; DB 4; Length 280;  
Best Local Similarity 100.0%; Pred. No. 36;  
RESULT 830  
ID ADE55544 standard; protein; 396 AA.  
DE Rat Protein AJ004858, SEQ ID NO 1361.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 2.0%; Score 9; DB 7; Length 396;  
Best Local Similarity 100.0%; Pred. No. 48;  
RESULT 831  
ID ADD45203 standard; protein; 396 AA.  
DE Rat Protein AJ004858, SEQ ID NO 10636.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 2.0%; Score 9; DB 7; Length 396;  
Best Local Similarity 100.0%; Pred. No. 48;  
RESULT 832  
ID ADQ97306 standard; protein; 464 AA.  
DE Mouse cancer associated sequence MP08-029, SEQ ID 283.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 2.0%; Score 9; DB 8; Length 464;  
Best Local Similarity 100.0%; Pred. No. 56;  
RESULT 833  
ID AAB57004 standard; protein; 476 AA.  
DE Human prostate cancer antigen protein sequence SEQ ID NO:1582.  
PN WO200055174-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match 2.0%; Score 9; DB 3; Length 476;  
Best Local Similarity 100.0%; Pred. No. 57;  
RESULT 834  
ID AAB95574 standard; protein; 480 AA.  
DE Human protein sequence SEQ ID NO:18225.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 2.0%; Score 9; DB 4; Length 480;  
Best Local Similarity 100.0%; Pred. No. 57;  
RESULT 835  
ID ABJ39147 standard; protein; 486 AA.  
DE Human S protein encoded by the skin corneodesmosin (CDSN) gene (S-gene).  
PN WO2003050311-A2.  
PD 19-JUN-2003.  
PA (WELA ) WELLA AG.  
Query Match 2.0%; Score 9; DB 7; Length 486;  
Best Local Similarity 100.0%; Pred. No. 58;  
RESULT 836  
ID ADQ21504 standard; protein; 486 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4324.  
PN WO2004048938-A2.

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PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.0%; Score 9; DB 8; Length 486;
Best Local Similarity 100.0%; Pred. No. 58;
RESULT 837
ID ADR51219 standard; protein; 504 AA.
DE Anti-biofilm polypeptide #5.
PN WO2004066945-A2.
PD 12-AUG-2004.
PA (DIVE-) DIVERSA CORP.
Query Match 2.0%; Score 9; DB 8; Length 504;
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 838
ID AAW80498 standard; protein; 529 AA.
DE A protein designated corneodesmosin.
PN FR2761362-A1.
PD 02-OCT-1998.
PA (OREA ) L'OREAL SA.
Query Match 2.0%; Score 9; DB 2; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 839
ID AAW85055 standard; protein; 529 AA.
DE Human protein designated corneodesmosin.
PN FR2761363-A1.
PD 02-OCT-1998.
PA (OREA ) L'OREAL SA.
Query Match 2.0%; Score 9; DB 2; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 840
ID AAY44989 standard; protein; 529 AA.
DE Human epidermal protein-6.
PN WO200006727-A2.
PD 10-FEB-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 2.0%; Score 9; DB 3; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 841
ID AAG64152 standard; protein; 529 AA.
DE Polypeptide #1 for vulgar psoriasis diagnosis.
PN WO200142458-A1.
PD 14-JUN-2001.
PA (INOK/) INOKO H.
Query Match 2.0%; Score 9; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 842
ID AAU27550 standard; protein; 529 AA.
DE Corneodesmosin.
PN WO200162788-A2.
PD 30-AUG-2001.
PA (OXAG-) OXAGEN LTD.
Query Match 2.0%; Score 9; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 843
ID ABJ39148 standard; protein; 529 AA.
DE Human corneodesmosin (CDSN) protein.
PN WO2003050311-A2.
PD 19-JUN-2003.
PA (WELA ) WELLA AG.
Query Match 2.0%; Score 9; DB 7; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 844
ID AUN04226 standard; protein; 529 AA.
DE Antipsoriatic protein sequence #308.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 2.0%; Score 9; DB 8; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 845
ID ADP12525 standard; protein; 529 AA.
DE Protein encoded by mRNA of the invention #135.
PN WO2004042346-A2.
PD 21-MAY-2004.

PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 2.0%; Score 9; DB 8; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 846
ID ABB69163 standard; protein; 596 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 34281.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 2.0%; Score 9; DB 4; Length 596;
Best Local Similarity 100.0%; Pred. No. 69;
RESULT 847
ID ADA35429 standard; protein; 607 AA.
DE Acinetobacter baumannii protein #2590.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.0%; Score 9; DB 6; Length 607;
Best Local Similarity 100.0%; Pred. No. 70;
RESULT 848
ID AAB92857 standard; protein; 624 AA.
DE Human protein sequence SEQ ID NO:11428.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.0%; Score 9; DB 4; Length 624;
Best Local Similarity 100.0%; Pred. No. 72;
RESULT 849
ID ADM04489 standard; protein; 634 AA.
DE Human protein of the invention SEQ ID NO:3174.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.0%; Score 9; DB 7; Length 634;
Best Local Similarity 100.0%; Pred. No. 73;
RESULT 850
ID AAW55483 standard; protein; 668 AA.
DE H. pylori ORF 14ap10815_20585777_ci_13 cell envelope OMP.
PN WO9737044-A1.
PD 09-OCT-1997.
PA (ASTR ) ASTRA AB.
Query Match 2.0%; Score 9; DB 2; Length 668;
Best Local Similarity 100.0%; Pred. No. 77;
RESULT 851
ID AAB46377 standard; protein; 668 AA.
DE H. pylori HPN137 protein.
PN WO200073502-A2.
PD 07-DEC-2000.
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (CREA-) CREATOGEN GMBH.
Query Match 2.0%; Score 9; DB 4; Length 668;
Best Local Similarity 100.0%; Pred. No. 77;
RESULT 852
ID ADJ49662 standard; protein; 675 AA.
DE Oil-associated gene related protein #1162.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 2.0%; Score 9; DB 8; Length 675;
Best Local Similarity 100.0%; Pred. No. 77;
RESULT 853
ID AAW55328 standard; protein; 677 AA.
DE H. pylori ORF hp3el0349orf27 protein.
PN WO9737044-A1.
PD 09-OCT-1997.
PA (ASTR ) ASTRA AB.
Query Match 2.0%; Score 9; DB 2; Length 677;
Best Local Similarity 100.0%; Pred. No. 78;
RESULT 854
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ID ABB60904 standard; protein; 688 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 9504.  
PN WO200171042-A2.  
PA (PEKE ) PE CORP NY.  
Query Match 2.0%; Score 9; DB 4; Length 688;  
Best Local Similarity 100.0%; Pred. No. 79;  
RESULT 855  
ID ABB68902 standard; protein; 729 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 33498.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 2.0%; Score 9; DB 4; Length 729;  
Best Local Similarity 100.0%; Pred. No. 83;  
RESULT 856  
ID ADR10276 standard; protein; 972 AA.  
DE Human protein useful for treating neurological disease Seq 3782.  
PN EPI447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 2.0%; Score 9; DB 8; Length 972;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 857  
ID ABB67028 standard; protein; 1046 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 27876.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 2.0%; Score 9; DB 4; Length 1046;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 858  
ID ABB59068 standard; protein; 1064 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 3996.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 2.0%; Score 9; DB 4; Length 1097;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
RESULT 859  
ID ABB62237 standard; protein; 1097 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 13503.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 2.0%; Score 9; DB 4; Length 1097;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
RESULT 860  
ID ABB64387 standard; protein; 1171 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 19953.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 2.0%; Score 9; DB 4; Length 1171;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
RESULT 861  
ID ABB70775 standard; protein; 1357 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39117.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 2.0%; Score 9; DB 4; Length 1357;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
RESULT 862  
ID ABB59325 standard; protein; 1486 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 4767.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 2.0%; Score 9; DB 4; Length 1486;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 863  
ID AAE36104 standard; protein; 1709 AA.  
DE Human chromodomain helicase DNA binding protein (CHD) #2.  
PN WO200298899-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 2.0%; Score 9; DB 6; Length 1709;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 864  
ID ABO07199 standard; protein; 1709 AA.  
DE Human p53 modifying protein, SEQ ID 159.  
PN WO200299122-A1.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 2.0%; Score 9; DB 6; Length 1709;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 865  
ID ADP23690 standard; protein; 1709 AA.  
DE PRO polypeptide SEQ ID NO:868.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 9; DB 8; Length 1709;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
RESULT 867  
ID ADB80349 standard; protein; 1839 AA.  
DE Human MDT protein SEQ ID NO:36.  
PN WO2003016497-A2.  
PD 27-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 2.0%; Score 9; DB 7; Length 1839;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
RESULT 868  
ID AAG94122 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 316.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.8%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 869  
ID AAG97122 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 3316.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.8%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 870  
ID AAG97134 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 3328.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.8%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 871  
ID AAG93958 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 152.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.8%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 872  
ID AAG87504 standard; peptide; 10 AA.  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2453.

PN WO200142276-A1.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.8%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 873  
ID AAG87505 standard; peptide; 10 AA.  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2454.  
PN WO200142276-A1.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.8%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 874  
ID AAG87506 standard; peptide; 10 AA.  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2455.  
PN WO200142276-A1.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.8%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 875  
ID AAG85279 standard; peptide; 10 AA.  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 228.  
PN WO200142276-A1.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.8%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 876  
ID AAG85067 standard; peptide; 10 AA.  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 16.  
PN WO200142276-A1.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.8%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 877  
ID AAG85633 standard; peptide; 10 AA.  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 582.  
PN WO200142276-A1.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.8%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 878  
ID AAG85099 standard; peptide; 10 AA.  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 48.  
PN WO200142276-A1.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.8%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 879  
ID AAG87507 standard; peptide; 10 AA.  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2456.  
PN WO200142276-A1.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.8%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 880  
ID AAE38484 standard; peptide; 10 AA.  
DE Peptide linker #3.  
PN WO2003068802-A2.  
PD 21-AUG-2003.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 1.8%; Score 8; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
RESULT 881  
ID AAE38483 standard; peptide; 16 AA.  
DE Peptide linker #2.  
PN WO2003068802-A2.

PD 21-AUG-2003.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 1.8%; Score 8; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 22;  
RESULT 882  
ID AAB37493 standard; peptide; 17 AA.  
DE Peptide linker #2 used as a control peptide.  
PN WO200066182-A1.  
PD 09-NOV-2000.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 1.8%; Score 8; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 23;  
RESULT 883  
ID ADT91223 standard; peptide; 17 AA.  
DE Radiation-inducible alpha2beta3 integrin binding control peptide #4.  
PN US2004191249-A1.  
PD 30-SEP-2004.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 1.8%; Score 8; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 23;  
RESULT 884  
ID ADT91222 standard; peptide; 22 AA.  
DE Radiation-inducible alpha2beta3 integrin binding control peptide #3.  
PN US2004191249-A1.  
PD 30-SEP-2004.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 1.8%; Score 8; DB 8; Length 22;  
Best Local Similarity 100.0%; Pred. No. 28;  
RESULT 885  
ID AAY59113 standard; peptide; 28 AA.  
DE N. clavipes spider silk protein 1 repeat fragment.  
PN US5989894-A.  
PD 23-NOV-1999.  
PA (UYWY-) UNIV WYOMING.  
Query Match 1.8%; Score 8; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 35;  
RESULT 886  
ID ADB83483 standard; peptide; 28 AA.  
DE Selected BLIP Mask peptide sequence, HB501-2.  
PN WO2003069312-A2.  
PD 21-AUG-2003.  
PA (KALO-) KALOBIO INC.  
Query Match 1.8%; Score 8; DB 7; Length 28;  
Best Local Similarity 100.0%; Pred. No. 35;  
RESULT 887  
ID AAY59121 standard; peptide; 30 AA.  
DE N. clavipes spider silk protein 1 repeat fragment.  
PN US5989894-A.  
PD 23-NOV-1999.  
PA (UYWY-) UNIV WYOMING.  
Query Match 1.8%; Score 8; DB 3; Length 30;  
Best Local Similarity 100.0%; Pred. No. 37;  
RESULT 888  
ID ADB83489 standard; peptide; 30 AA.  
DE Selected BLIP Mask peptide sequence, HB501-8.  
PN WO2003069312-A2.  
PD 21-AUG-2003.  
PA (KALO-) KALOBIO INC.  
Query Match 1.8%; Score 8; DB 7; Length 30;  
Best Local Similarity 100.0%; Pred. No. 37;  
RESULT 889  
ID AAY59109 standard; peptide; 31 AA.  
DE N. clavipes spider silk protein 1 repeat fragment.  
PN US5989894-A.  
PD 23-NOV-1999.  
PA (UYWY-) UNIV WYOMING.  
Query Match 1.8%; Score 8; DB 3; Length 31;  
Best Local Similarity 100.0%; Pred. No. 38;  
RESULT 890  
ID ADB83485 standard; peptide; 32 AA.  
DE Selected BLIP Mask peptide sequence, HB501-4.  
PN WO2003069312-A2.  
PD 21-AUG-2003.

PA (KALO-) KALOBIOUS INC.  
 Query Match 1.8%; Score 8; DB 7; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 RESULT 891  
 ID ADB83490 standard; peptide; 32 AA.  
 DE Selected BLIP Mask peptide sequence, HB501-9.  
 PN W02003069312-A2.  
 PD 21-AUG-2003.  
 PA (KALO-) KALOBIOUS INC.  
 Query Match 1.8%; Score 8; DB 7; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 RESULT 892  
 ID ADB83488 standard; peptide; 32 AA.  
 DE Selected BLIP Mask peptide sequence, HB501-7.  
 PN W02003069312-A2.  
 PD 21-AUG-2003.  
 PA (KALO-) KALOBIOUS INC.  
 Query Match 1.8%; Score 8; DB 7; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 RESULT 893  
 ID ADB83486 standard; peptide; 32 AA.  
 DE Selected BLIP Mask peptide sequence, HB501-5.  
 PN W02003069312-A2.  
 PD 21-AUG-2003.  
 PA (KALO-) KALOBIOUS INC.  
 Query Match 1.8%; Score 8; DB 7; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 RESULT 894  
 ID ADB83484 standard; peptide; 32 AA.  
 DE Selected BLIP Mask peptide sequence, HB501-3.  
 PN W02003069312-A2.  
 PD 21-AUG-2003.  
 PA (KALO-) KALOBIOUS INC.  
 Query Match 1.8%; Score 8; DB 7; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 RESULT 895  
 ID ADB83482 standard; peptide; 32 AA.  
 DE Selected BLIP Mask peptide sequence, HB501-1.  
 PN W02003069312-A2.  
 PD 21-AUG-2003.  
 PA (KALO-) KALOBIOUS INC.  
 Query Match 1.8%; Score 8; DB 7; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 RESULT 896  
 ID ADB83487 standard; peptide; 32 AA.  
 DE Selected BLIP Mask peptide sequence, HB501-6.  
 PN W02003069312-A2.  
 PD 21-AUG-2003.  
 PA (KALO-) KALOBIOUS INC.  
 Query Match 1.8%; Score 8; DB 7; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 RESULT 897  
 ID ADM08430 standard; peptide; 32 AA.  
 DE Canine immunoglobulin group 3 VL species framework 3 peptide 15.  
 PN W02003060080-A2.  
 PD 24-JUL-2003.  
 PA (IDEX-) IDEX LAB INC.  
 Query Match 1.8%; Score 8; DB 7; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 RESULT 898  
 ID ADM08336 standard; peptide; 32 AA.  
 DE Canine immunoglobulin group 3 VL subgenus framework 3 peptide 6.  
 PN W02003060080-A2.  
 PD 24-JUL-2003.  
 PA (IDEX-) IDEX LAB INC.  
 Query Match 1.8%; Score 8; DB 7; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 RESULT 899  
 ID ADL27343 standard; peptide; 33 AA.  
 DE Eitope used to test prethrombin adzymes.  
 PN W02004018878-A2.  
 PD 11-MAR-2004.  
 PA (COMP-) COMPOUND THERAPEUTICS INC.

PA (AFXY/) AFEYAN N B.  
 Query Match 1.8%; Score 8; DB 8; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 RESULT 900  
 ID AAU48534 standard; protein; 58 AA.  
 DE Protonibacterium acnes immunogenic protein #9430.  
 PN W0200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.8%; Score 8; DB 4; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 RESULT 901  
 ID AEM45053 standard; protein; 58 AA.  
 DE Protonibacterium acnes predicted ORF-encoded polypeptide #9729.  
 PN W02003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.8%; Score 8; DB 6; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 RESULT 902  
 ID AAY59696 standard; protein; 62 AA.  
 DE Secreted protein 57-19-2-G8-CL1\_3.  
 PN W0940189-A2.  
 PD 12-AUG-1999.  
 PA (GEST-) GENSET.  
 Query Match 1.8%; Score 8; DB 2; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 71;  
 RESULT 903  
 ID ADM77846 standard; protein; 62 AA.  
 DE Human protein #43.  
 PN US2003162176-A1.  
 PD 28-AUG-2003.  
 PA (EDWA/) EDWARDS J D M.  
 PA (DUC/) DUCLETT A.  
 PA (BOUG/) BOUGUELERET L.  
 Query Match 1.8%; Score 8; DB 7; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 71;  
 RESULT 904  
 ID ADP19527 standard; protein; 62 AA.  
 DE Human secreted polypeptide #378.  
 PN US2004110939-A1.  
 PD 10-JUN-2004.  
 PA (GEST-) GENSET SA.  
 Query Match 1.8%; Score 8; DB 8; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 71;  
 RESULT 905  
 ID AAM21759 standard; protein; 63 AA.  
 DE Peptide #8193 encoded by probe for measuring cervical gene expression.  
 PN W0200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 1.8%; Score 8; DB 4; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 72;  
 RESULT 906  
 ID ABB44131 standard; peptide; 63 AA.  
 DE Peptide #11637 encoded by human foetal liver single exon probe.  
 PN W0200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 1.8%; Score 8; DB 4; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 72;  
 RESULT 907  
 ID AAM38081 standard; protein; 63 AA.  
 DE Peptide #12118 encoded by probe for measuring placental gene expression.  
 PN W0200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 1.8%; Score 8; DB 4; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 72;  
 RESULT 908  
 ID ABB27013 standard; protein; 63 AA.  
 DE Protein #9012 encoded by probe for measuring heart cell gene expression.  
 PN W0200157274-A2.

PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.8%; Score 8; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 72;  
RESULT 909  
ID AAM77859 standard; protein; 63 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 38165.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.8%; Score 8; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 72;  
RESULT 910  
ID AAM65154 standard; protein; 63 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 37259.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.8%; Score 8; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 72;  
RESULT 911  
ID ABG59511 standard; peptide; 63 AA.  
DE Human liver peptide, SEQ ID No 38159.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.8%; Score 8; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 72;  
RESULT 912  
ID ABG46887 standard; peptide; 63 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 36552.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.8%; Score 8; DB 5; Length 63;  
Best Local Similarity 100.0%; Pred. No. 72;  
RESULT 913  
ID AAU37867 standard; protein; 67 AA.  
DE Streptococcus pneumoniae cellular proliferation protein #296.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 8; DB 4; Length 67;  
Best Local Similarity 100.0%; Pred. No. 76;  
RESULT 914  
ID ABU02289 standard; protein; 67 AA.  
DE S. pneumoniae type 4 strain protein from coding region #1857.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 1.8%; Score 8; DB 6; Length 67;  
Best Local Similarity 100.0%; Pred. No. 76;  
RESULT 915  
ID ABU46220 standard; protein; 67 AA.  
DE Protein encoded by Prokaryotic essential gene #31747.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 8; DB 6; Length 67;  
Best Local Similarity 100.0%; Pred. No. 76;  
RESULT 916  
ID ADK46533 standard; protein; 67 AA.  
DE Streptococcus pneumoniae protein, Seq ID No 3048.  
PN US6699703-B1.  
PD 02-MAR-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.8%; Score 8; DB 8; Length 67;  
Best Local Similarity 100.0%; Pred. No. 76;  
RESULT 917  
ID AAU38017 standard; protein; 68 AA.  
DE Streptococcus pneumoniae cellular proliferation protein #446.  
PN WO200170955-A2.

PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 8; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 77;  
RESULT 918  
ID ADR94888 standard; protein; 77 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 3523.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.8%; Score 8; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 85;  
RESULT 919  
ID AAM86130 standard; protein; 82 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:13723.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.8%; Score 8; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 90;  
RESULT 920  
ID ADB09048 standard; protein; 91 AA.  
DE Alloicoccus otitis antigenic protein SEQ ID NO:2988.  
PN WO2003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP) WYETH HOLDINGS CORP.  
Query Match 1.8%; Score 8; DB 6; Length 91;  
Best Local Similarity 100.0%; Pred. No. 99;  
RESULT 921  
ID AAG03015 standard; protein; 95 AA.  
DE Human secreted protein, SEQ ID NO: 7096.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST) GENSET.  
Query Match 1.8%; Score 8; DB 3; Length 95;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
RESULT 922  
ID AAU47045 standard; protein; 95 AA.  
DE Propionibacterium acnes immunogenic protein #7941.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.8%; Score 8; DB 4; Length 95;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
RESULT 923  
ID ABM43564 standard; protein; 95 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #8240.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.8%; Score 8; DB 6; Length 95;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
RESULT 924  
ID AAG03558 standard; protein; 103 AA.  
DE Human secreted protein, SEQ ID NO: 7639.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST) GENSET.  
Query Match 1.8%; Score 8; DB 3; Length 103;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 925  
ID ABB41967 standard; peptide; 103 AA.  
DE Peptide #9473 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.8%; Score 8; DB 4; Length 103;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 926  
ID AAM35768 standard; protein; 103 AA.  
DE Peptide #9805 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.



PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 1.8%; Score 8; DB 4; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 RESULT 927  
 ID AAW75658 standard; protein; 103 AA.  
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35964.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 1.8%; Score 8; DB 4; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 RESULT 928  
 ID AAW62844 standard; protein; 103 AA.  
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34949.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 1.8%; Score 8; DB 4; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 RESULT 929  
 ID AAW57399 standard; peptide; 103 AA.  
 DE Human liver peptide, SEQ ID NO 36047.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 1.8%; Score 8; DB 4; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 RESULT 930  
 ID AAW45161 standard; peptide; 103 AA.  
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 34826.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 1.8%; Score 8; DB 5; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 RESULT 931  
 ID AAW11848 standard; protein; 104 AA.  
 DE Saccharomyces cerevisiae acetamidase internal consensus fragment.  
 PN EP758020-A2.  
 PD 12-FEB-1997.  
 PA (KONN ) GIST-BROCADES BV.  
 Query Match 1.8%; Score 8; DB 2; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 RESULT 932  
 ID AAW50034 standard; protein; 104 AA.  
 DE N. clavipes epidroin synthetic homologue SBI protein.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 1.8%; Score 8; DB 5; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 RESULT 933  
 ID AAW11849 standard; protein; 111 AA.  
 DE Aspergillus niger acetamidase internal consensus fragment.  
 PN EP758020-A2.  
 PD 12-FEB-1997.  
 PA (KONN ) GIST-BROCADES BV.  
 Query Match 1.8%; Score 8; DB 2; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 RESULT 934  
 ID AAY35937 standard; protein; 112 AA.  
 DE Extended human secreted protein sequence, SEQ ID NO. 186.  
 PN WO931236-A2.  
 PD 24-JUN-1999.  
 PA (GEST ) GENSET.  
 Query Match 1.8%; Score 8; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 RESULT 935  
 ID ADP19245 standard; protein; 112 AA.  
 DE Human secreted polypeptide #96.  
 PN US2004110939-A1.  
 PD 10-JUN-2004.  
 PA (GEST ) GENSET SA.

Query Match 1.8%; Score 8; DB 8; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 RESULT 936  
 ID ABB62125 standard; protein; 125 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 13167.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 1.8%; Score 8; DB 4; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 RESULT 937  
 ID AAG92718 standard; protein; 137 AA.  
 DE C. glutamicum protein fragment SEQ ID NO: 6472.  
 PN EP1108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Query Match 1.8%; Score 8; DB 4; Length 137;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 RESULT 938  
 ID AAM50036 standard; protein; 137 AA.  
 DE N. clavipes epidroin synthetic homologue SD1 protein.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 1.8%; Score 8; DB 5; Length 137;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 RESULT 939  
 ID ABB70412 standard; protein; 139 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 38028.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 1.8%; Score 8; DB 4; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 RESULT 940  
 ID AAG26489 standard; protein; 142 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 30963.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 1.8%; Score 8; DB 3; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 RESULT 941  
 ID AAG26488 standard; protein; 146 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 30962.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 1.8%; Score 8; DB 3; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 RESULT 942  
 ID AAG54787 standard; protein; 152 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 69975.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 1.8%; Score 8; DB 3; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 RESULT 943  
 ID AAB63563 standard; protein; 154 AA.  
 DE Human gastric cancer associated antigen protein sequence SEQ ID NO: 925.  
 PN WO200073801-A2.  
 PD 07-DEC-2000.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 Query Match 1.8%; Score 8; DB 4; Length 154;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 RESULT 944  
 ID AAW82486 standard; protein; 159 AA.  
 DE Ehrlichia sp. E74.1 protein.  
 PN WO9849312-A2.  
 PD 05-NOV-1998.  
 PA (AQU-) AQUILA BIOPHARMACEUTICALS INC.  
 Query Match 1.8%; Score 8; DB 2; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 RESULT 945  
 ID AAG26487 standard; protein; 161 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 30961.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 161;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
RESULT 946  
ID ABUL1844 standard; protein; 178 AA.  
DE Human MDT polypeptide SEQ ID 791.  
PN W0200279449-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.8%; Score 8; DB 6; Length 178;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
RESULT 947  
ID ADN99741 standard; protein; 178 AA.  
DE Novel human protein sequence #557.  
PN W02004038003-A2.  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 1.8%; Score 8; DB 8; Length 178;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
RESULT 948  
ID AAM93486 standard; protein; 180 AA.  
DE Human polypeptide, SEQ ID NO: 3175.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 1.8%; Score 8; DB 4; Length 180;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
RESULT 949  
ID ADL31142 standard; protein; 180 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 3175.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 1.8%; Score 8; DB 8; Length 180;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
RESULT 950  
ID AAG07583 standard; protein; 182 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4792.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 182;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
RESULT 951  
ID ADN74835 standard; protein; 190 AA.  
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 2730.  
PN W02004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPEDESIGN NV.  
Query Match 1.8%; Score 8; DB 8; Length 190;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
RESULT 952  
ID AAG07582 standard; protein; 194 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4791.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 194;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
RESULT 953  
ID AAY95937 standard; protein; 202 AA.  
DE Porcine adenovirus 3 E1B-202R protein.  
PN W0200050076-A1.  
PD 31-AUG-2000.  
PA (PURD) PURDUE RES FOUND.  
Query Match 1.8%; Score 8; DB 3; Length 202;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
RESULT 954  
ID AAB64527 standard; protein; 215 AA.  
DE Gene 32 human secreted protein homologous amino acid sequence #165.  
PN W0200077255-A1.  
PD 21-DEC-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.8%; Score 8; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
RESULT 955  
ID AAM50040 standard; protein; 219 AA.  
DE N. clavipes spidroin synthetic homologue FA2 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 1.8%; Score 8; DB 5; Length 219;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
RESULT 956  
ID AAM50035 standard; protein; 230 AA.  
DE N. clavipes spidroin synthetic homologue SE1 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 1.8%; Score 8; DB 5; Length 230;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
RESULT 957  
ID ABJ26668 standard; protein; 232 AA.  
DE Human protein modification + maintenance molecule protein SEQ ID NO 22.  
PN W0200300844-A2.  
PD 03-JAN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.8%; Score 8; DB 6; Length 232;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
RESULT 958  
ID ADC39240 standard; protein; 232 AA.  
DE Novel human NOVX polypeptide SEQ ID NO: 184.  
PN W02003010327-A2.  
PD 06-FEB-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.8%; Score 8; DB 7; Length 232;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
RESULT 959  
ID ADC31414 standard; protein; 232 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1496.  
PN W02003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.8%; Score 8; DB 7; Length 232;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
RESULT 960  
ID ADQ66777 standard; protein; 232 AA.  
DE Novel human protein sequence #1750.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 1.8%; Score 8; DB 8; Length 232;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
RESULT 961  
ID ADQ66668 standard; protein; 232 AA.  
DE Novel human protein sequence #1641.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 1.8%; Score 8; DB 8; Length 232;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
RESULT 962  
ID ADC87119 standard; protein; 235 AA.  
DE Human GPCR protein SEQ ID NO:1572.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Query Match 1.8%; Score 8; DB 7; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
RESULT 963  
ID ABP45001 standard; protein; 255 AA.  
DE Human Blys binding scrv SEQ ID 1012.  
PN W0200202641-A1.  
PD 10-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.

PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 Query Match 1.8%; Score 8; DB 5; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 RESULT 964  
 ID AUC95828 standard; protein; 255 AA.  
 DE Single chain antibody that immunospecifically binds Blys SeqID 1012.  
 PN WO2003055979-A2.  
 PD 10-JUL-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.8%; Score 8; DB 7; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 RESULT 965  
 ID AAM50048 standard; protein; 264 AA.  
 DE N. clavipes epididymal synthetic homologue FA2 protein #2.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 1.8%; Score 8; DB 5; Length 264;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 RESULT 966  
 ID AAU17599 standard; protein; 267 AA.  
 DE Novel signal transduction pathway protein, Seq ID 1164.  
 PN WO200154733-A1.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.8%; Score 8; DB 4; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 RESULT 967  
 ID AAM95431 standard; protein; 267 AA.  
 DE Human reproductive system related antigen SEQ ID NO: 4089.  
 PN WO200155320-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.8%; Score 8; DB 4; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 RESULT 968  
 ID ABB96121 standard; protein; 267 AA.  
 DE Human testicular antigen SEQ ID NO: 1505.  
 PN WO200155317-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.8%; Score 8; DB 4; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 RESULT 969  
 ID ADB94307 standard; protein; 267 AA.  
 DE Human novel protein #541.  
 PN US2002168711-A1.  
 PD 14-NOV-2002.  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 Query Match 1.8%; Score 8; DB 7; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 RESULT 970  
 ID AAM50044 standard; protein; 271 AA.  
 DE N. clavipes epididymal synthetic homologue SFI protein.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 1.8%; Score 8; DB 5; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 RESULT 971  
 ID ABB68131 standard; protein; 273 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 31185.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 1.8%; Score 8; DB 4; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 RESULT 972  
 ID ABB69618 standard; protein; 276 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 35646.  
 PN WO200171042-A2.

PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 1.8%; Score 8; DB 4; Length 276;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 RESULT 973  
 ID AAY81909 standard; protein; 278 AA.  
 DE Pseudomonas fluorescens xylanase protein sequence.  
 PN JP11318474-A.  
 PD 24-NOV-1999.  
 PA (BIOT-) DEV CENT BIOTECHNOLOGY.  
 Query Match 1.8%; Score 8; DB 3; Length 278;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 RESULT 974  
 ID ABB70296 standard; protein; 288 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 37680.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 1.8%; Score 8; DB 4; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 RESULT 975  
 ID AAM20066 standard; protein; 297 AA.  
 DE Thielavia terrestris NRRL 8126 xylanase.  
 PN WO9727293-A1.  
 PD 31-JUL-1997.  
 PA (NOVO) NOVO-NORDISK AS.  
 Query Match 1.8%; Score 8; DB 2; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 RESULT 976  
 ID ADJ34998 standard; protein; 303 AA.  
 DE Xylanase from an environmental sample seq id 214.  
 PN WO200310654-A2.  
 PD 24-DEC-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match 1.8%; Score 8; DB 8; Length 303;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 RESULT 977  
 ID ABO52944 standard; protein; 305 AA.  
 DE Human spliceosome associated protein (SAP) #49.  
 PN US2003068803-A1.  
 PD 10-APR-2003.  
 PA (REED/) REED R.  
 PA (ZHOU/) ZHOU Z.  
 Query Match 1.8%; Score 8; DB 6; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 RESULT 978  
 ID AEM81703 standard; protein; 305 AA.  
 DE Tumour-associated antigenic target (TAT) polypeptide PRO82532, SEQ:4393.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 1.8%; Score 8; DB 8; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 RESULT 979  
 ID AEM80558 standard; protein; 305 AA.  
 DE Tumour-associated antigenic target (TAT) polypeptide PRO81124, SEQ:1411.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 1.8%; Score 8; DB 8; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 RESULT 980  
 ID AEM81704 standard; protein; 305 AA.  
 DE Tumour-associated antigenic target (TAT) polypeptide PRO82533, SEQ:4395.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 1.8%; Score 8; DB 8; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 RESULT 981  
 ID AAG72184 standard; protein; 311 AA.  
 DE Human olfactory receptor polypeptide, SEQ ID NO: 1865.  
 PN WO200127158-A2.

PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
Query Match 1.8%; Score 8; DB 4; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 982  
ID AAG72566 standard; protein; 311 AA.  
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2247.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
Query Match 1.8%; Score 8; DB 4; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 983  
ID AAU24692 standard; protein; 311 AA.  
DE Human olfactory receptor AOLF191.  
PN WO200168805-A2.  
PD 20-SEP-2001.  
PA (SENO-) SENOWYX INC.  
Query Match 1.8%; Score 8; DB 4; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 984  
ID ABG76795 standard; protein; 311 AA.  
DE Human G-protein coupled receptor (GPCR) protein #29.  
PN WO200259313-A2.  
PD 01-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.8%; Score 8; DB 5; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 985  
ID ABP51596 standard; protein; 311 AA.  
DE Human G-protein coupled receptor SEQ ID NO:74.  
PN WO200250276-A2.  
PD 27-JUN-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.8%; Score 8; DB 5; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 986  
ID ABP95818 standard; protein; 311 AA.  
DE Human GPCR polypeptide SEQ ID NO 446.  
PN WO200216548-A2.  
PD 28-FEB-2002.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 1.8%; Score 8; DB 5; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 987  
ID AAU95661 standard; protein; 311 AA.  
DE Human olfactory and pheromone G protein-coupled receptor #148.  
PN WO200224726-A2.  
PD 28-MAR-2002.  
PA (CHEM-) CHEMCOM SA.  
Query Match 1.8%; Score 8; DB 5; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 988  
ID AAU85312 standard; protein; 311 AA.  
DE G-coupled olfactory receptor #173.  
PN WO200198526-A2.  
PD 27-DEC-2001.  
PA (SENO-) SENOWYX INC.  
Query Match 1.8%; Score 8; DB 5; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 989  
ID ADC85819 standard; protein; 311 AA.  
DE Human GPCR protein SEQ ID NO:272.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 1.8%; Score 8; DB 7; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 990  
ID ADI04317 standard; protein; 311 AA.

DE Human G-protein coupled receptor #37.  
PN US2003198955-A1.  
PD 23-OCT-2003.  
PA (LILL-) LI L.  
PA (PADI-) PADIGARU M.  
PA (BALL-) BALLINGER R A.  
PA (KEKU-) KEKUDA R.  
PA (COLM-) COLMAN S D.  
PA (SPYT-) SPYTEK K A.  
PA (CASW-) CASHMAN S J.  
PA (EDIN-) EDINGER S R.  
PA (GERL-) GERLACH V.  
PA (SCIO-) SCIORE P.  
PA (SMIT-) SMITHSON G.  
PA (PEYN-) PEYMAN J A.  
PA (MACD-) MACDOUGALL J R.  
PA (STON-) STONE D J.  
PA (VERN-) VERNET C A M.  
PA (SHEN-) SHENOY S G.  
PA (GUNT-) GUNTHER E.  
PA (MILL-) MILLET I.  
PA (TCHE-) TCHERNEV V T.  
PA (ANDE-) ANDERSON D W.  
PA (GUSE-) GUSEV V Y.  
PA (MALY-) MALYANKAR U M.  
PA (ZHON-) ZHONG H.  
PA (ELLE-) ELLERMAN K.  
PA (WOLE-) WOLENC A R.  
Query Match 1.8%; Score 8; DB 7; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 991  
ID ADG83404 standard; protein; 311 AA.  
DE Human Olfactory and pheromone GPCR #59.  
PN US2003221205-A1.  
PD 27-NOV-2003.  
PA (VEIT-) VEITHEN A.  
Query Match 1.8%; Score 8; DB 8; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 992  
ID ABB80187 standard; protein; 313 AA.  
DE A. fumigatus AfXYL3.  
PN WO2003012071-A2.  
PD 13-FEB-2003.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 8; DB 6; Length 313;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 993  
ID AAG70693 standard; protein; 315 AA.  
DE S cerevisiae apoptosis associated protein YCR073WA.  
PN WO200102550-A2.  
PD 11-JAN-2001.  
PA (JANC-) JANSSEN PHARM NV.  
Query Match 1.8%; Score 8; DB 4; Length 315;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 994  
ID ABR01623 standard; protein; 315 AA.  
DE Human G-protein coupled receptor SEQ ID 106.  
PN WO2003000735-A2.  
PD 03-JAN-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 1.8%; Score 8; DB 6; Length 315;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 995  
ID ADQ19957 standard; protein; 316 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2777.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.8%; Score 8; DB 8; Length 316;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 996  
ID ABB69613 standard; protein; 319 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 35631.

PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 1.8%; Score 8; DB 4; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 RESULT 997  
 ID ADQ19814 standard; protein; 332 AA.  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2633.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 1.8%; Score 8; DB 8; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 RESULT 998  
 ID ADR99168 standard; protein; 333 AA.  
 DE AMMECR1, SEQ ID 174.  
 PN WO2004078035-A2.  
 PD 16-SEP-2004.  
 PA (FARB) BAYER PHARM CORP.  
 Query Match 1.8%; Score 8; DB 8; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 RESULT 999  
 ID AAY29904 standard; protein; 334 AA.  
 DE Human MDC and human scfV fusion protein.  
 PN WO9946392-A1.  
 PD 16-SEP-1999.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 1.8%; Score 8; DB 2; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 RESULT 1000  
 ID ADM03842 standard; protein; 334 AA.  
 DE Human protein of the invention SEQ ID NO:2527.  
 PN EPI347046-A1.  
 PD 24-SEP-2003.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 1.8%; Score 8; DB 7; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 RESULT 1001  
 ID AAY29905 standard; protein; 339 AA.  
 DE Human SDF-1 and human scfV fusion protein.  
 PN WO9946392-A1.  
 PD 16-SEP-1999.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 1.8%; Score 8; DB 2; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 RESULT 1002  
 ID ABB62884 standard; protein; 346 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 15444.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 1.8%; Score 8; DB 4; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 RESULT 1003  
 ID AAY29903 standard; protein; 348 AA.  
 DE Human MCP-3 and human scfV fusion protein.  
 PN WO9946392-A1.  
 PD 16-SEP-1999.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 1.8%; Score 8; DB 2; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 RESULT 1004  
 ID ADJ35000 standard; protein; 354 AA.  
 DE Xylanase from an environmental sample seq id 216.  
 PN WO2003106654-A2.  
 PD 24-DEC-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match 1.8%; Score 8; DB 8; Length 354;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 RESULT 1005  
 ID ABB68677 standard; protein; 355 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 32823.  
 PN WO200171042-A2.

PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 1.8%; Score 8; DB 4; Length 355;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 RESULT 1006  
 ID ADO65824 standard; protein; 359 AA.  
 DE Novel human protein sequence #797.  
 PN EPI40981-A2.  
 PD 28-JUL-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 1.8%; Score 8; DB 8; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 RESULT 1007  
 ID AAW30267 standard; protein; 360 AA.  
 DE Amino acid sequence of an enzyme with xylanase activity.  
 PN WO9736995-A2.  
 PD 09-OCT-1997.  
 PA (PACI-) PACIFIC ENZYMES LTD.  
 Query Match 1.8%; Score 8; DB 2; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 RESULT 1008  
 ID ABG25391 standard; protein; 361 AA.  
 DE Novel human diagnostic protein #25382.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 1.8%; Score 8; DB 4; Length 361;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 RESULT 1009  
 ID ABG22687 standard; protein; 363 AA.  
 DE Novel human diagnostic protein #22678.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 1.8%; Score 8; DB 4; Length 363;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 RESULT 1010  
 ID ADN9674 standard; protein; 363 AA.  
 DE Novel human protein sequence #490.  
 PN WO2004038003-A2.  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 1.8%; Score 8; DB 8; Length 363;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 RESULT 1011  
 ID AAM50043 standard; protein; 364 AA.  
 DE N. clavipes epidroin synthetic homologue SM12 protein.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 1.8%; Score 8; DB 5; Length 364;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 RESULT 1012  
 ID AAR87012 standard; protein; 368 AA.  
 DE Xylanase D.  
 PN WO9534662-A1.  
 PD 21-DEC-1995.  
 PA (KONN) GIST-BROCADES BV.  
 Query Match 1.8%; Score 8; DB 2; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 RESULT 1013  
 ID AAU54062 standard; protein; 372 AA.  
 DE Propionibacterium acnes immunogenic protein #14958.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.8%; Score 8; DB 4; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 RESULT 1014  
 ID ASM65617 standard; protein; 372 AA.  
 DE Propionibacterium acnes immunogenic polypeptide #30293.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.

PA (CORI-) CORIXA CORP.  
Query Match 1.8%; Score 8; DB 6; Length 372;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 1015  
ID ABM50581 standard; protein; 372 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #15257.  
PN W02003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.8%; Score 8; DB 6; Length 372;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 1016  
ID ABB67616 standard; protein; 380 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 29640.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 380;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 1017  
ID ABU33267 standard; protein; 380 AA.  
DE Protein encoded by Prokaryotic essential gene #18794.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 8; DB 6; Length 380;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 1018  
ID ADS29129 standard; protein; 380 AA.  
DE Bacterial polypeptide #18162.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.8%; Score 8; DB 8; Length 380;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 1019  
ID ADN39342 standard; protein; 381 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:B36.  
PN W02003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 1.8%; Score 8; DB 7; Length 381;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 1020  
ID ABP62776 standard; protein; 391 AA.  
DE Protein fragment #13 of S. roseosporus biosynthetic gene cluster.  
PN W0200259322-A2.  
PD 01-AUG-2002.  
PA (MIAO/) MIAO V P W.  
PA (BRIA/) BRIAN P.  
PA (BALZ/) BALZ R H.  
PA (SILV/) SILVA C J.  
Query Match 1.8%; Score 8; DB 5; Length 391;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 1021  
ID ADJ72187 standard; protein; 391 AA.  
DE S. roseosporus daptomycin biosynthesis gene cluster protein #13.  
PN W02003014297-A2.  
PD 20-FEB-2003.  
PA (CUBI-) CUBIST PHARM INC.  
Query Match 1.8%; Score 8; DB 7; Length 391;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 1022  
ID AAG31490 standard; protein; 392 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37825.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 392;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
RESULT 1023  
ID ADN04966 standard; protein; 392 AA.  
DE Antipsoriatic protein sequence #663.  
PN W02004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 1.8%; Score 8; DB 8; Length 392;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
RESULT 1024  
ID ADQ20013 standard; protein; 392 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2833.  
PN W02004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.8%; Score 8; DB 8; Length 392;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
RESULT 1025  
ID AAB70913 standard; protein; 396 AA.  
DE Polyoma virus coat protein VP1 variant PyVP1-RGD148 protein.  
PN W0200132851-A2.  
PD 10-MAY-2001.  
PA (ACGT-) ACGT PROGENOMICS AG.  
Query Match 1.8%; Score 8; DB 4; Length 396;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
RESULT 1026  
ID ABR63546 standard; protein; 396 AA.  
DE Danio rerio foxd3 homologue chicken CWH3.  
PN W02003048196-A2.  
PD 12-JUN-2003.  
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.  
Query Match 1.8%; Score 8; DB 6; Length 396;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
RESULT 1027  
ID AAG45048 standard; protein; 397 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 56505.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 397;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
RESULT 1028  
ID ABB67545 standard; protein; 397 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 29427.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 397;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
RESULT 1029  
ID AAE37147 standard; protein; 405 AA.  
DE Drosophila melanogaster salvador mutant protein #3.  
PN W02003035845-A2.  
PD 01-MAY-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 1.8%; Score 8; DB 6; Length 405;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1030  
ID ADB65137 standard; protein; 406 AA.  
DE Human protein encoded by clone SPLEN20063250.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 1.8%; Score 8; DB 7; Length 406;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1031  
ID ADR09419 standard; protein; 406 AA.  
DE Human protein useful for treating neurological disease Seq 2925.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 1.8%; Score 8; DB 8; Length 406;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1032

ID ABB64734 standard; protein; 410 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 20994.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 410;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1033  
ID AAW94998 standard; protein; 412 AA.  
DE Serine/threonine protein kinase-HTLAR33 (EST derived sequence).  
PN EPB94863-A1.  
PD 03-FEB-1999.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match 1.8%; Score 8; DB 2; Length 412;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1034  
ID AAG31489 standard; protein; 415 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37824.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 415;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1035  
ID ABB59727 standard; protein; 415 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 5973.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 415;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1036  
ID AAG45047 standard; protein; 420 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 56504.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 420;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
RESULT 1037  
ID AAG41764 standard; protein; 422 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52003.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 422;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
RESULT 1038  
ID AAR14186 standard; protein; 427 AA.  
DE 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase.  
PN WO9113978-A.  
PD 19-SEP-1991.  
PA (TRIN-) TRINITY COLLEGE DUB.  
Query Match 1.8%; Score 8; DB 2; Length 427;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
RESULT 1039  
ID AAU93074 standard; protein; 430 AA.  
DE Arabidopsis transcription factor #112.  
PN WO200215575-A1.  
PD 28-FEB-2002.  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
PA (PILG/) PILGRIM M.  
PA (CREE/) CREELMAN R.  
PA (DUBE/) DUBELL A J.  
PA (HEAR/) HEARD J.  
PA (JIAN/) JIANG C.  
PA (KEDD/) KEDDIE J.  
PA (ADAM/) ADAM L.  
PA (RATC/) RATCLIFF O.  
PA (REUB/) REUBER J L.  
PA (RIEC/) RIECHMANN J L.  
PA (YUGG/) YU G.  
PA (PINE/) PINEDA O.  
Query Match 1.8%; Score 8; DB 5; Length 430;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 1040

ID ABR39479 standard; protein; 430 AA.  
DE A. thaliana phytochrome interacting protein PIF4.  
PN WO2003018777-A1.  
PD 06-MAR-2003.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 1.8%; Score 8; DB 6; Length 430;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 1041  
ID ADD30128 standard; protein; 430 AA.  
DE Plant yield-related protein from clone G1494.  
PN WO2003013227-A2.  
PD 20-FEB-2003.  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
Query Match 1.8%; Score 8; DB 7; Length 430;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 1042  
ID ADI41829 standard; protein; 430 AA.  
DE Plant transcription factor #146.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER/) SHERMAN B K.  
PA (RIEC/) RIECHMANN J L.  
PA (JIAN/) JIANG C.  
PA (HEAR/) HEARD J E.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J.  
PA (BROU/) BROUN P E.  
PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match 1.8%; Score 8; DB 8; Length 430;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 1043  
ID ADO3453 standard; protein; 430 AA.  
DE Thalecraea transcription factor protein #558.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN/) ZHANG J.  
PA (FROM/) FROMM M E.  
PA (HEAR/) HEARD J E.  
PA (RIEC/) RIECHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIAN/) JIANG C.  
PA (SAMA/) SAMAHA R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
Query Match 1.8%; Score 8; DB 8; Length 430;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 1044  
ID ABO81890 standard; protein; 436 AA.  
DE Pseudomonas aeruginosa polypeptide #14065.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.8%; Score 8; DB 7; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 1045  
ID ABB92544 standard; protein; 441 AA.  
DE Herbicidally active polypeptide SEQ ID NO 1755.

PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 1.8%; Score 8; DB 5; Length 441;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 1046  
ID AAW46790 standard; protein; 442 AA.  
DE Arabidopsis thaliana UFO gene product.  
PD 12-FEB-1998.  
PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
Query Match 1.8%; Score 8; DB 2; Length 442;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 1047  
ID ABR42684 standard; protein; 442 AA.  
DE Arabidopsis unusual floral organs (UFO) protein.  
PN WO2003033714-A1.  
PD 24-APR-2003.  
PA (TECH-) TECHNOLOGIESTICHTING STW.  
Query Match 1.8%; Score 8; DB 6; Length 442;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 1048  
ID AAG29728 standard; protein; 447 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35420.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 447;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 1049  
ID ABR54251 standard; protein; 450 AA.  
DE Human NOV39b protein SEQ ID NO:170.  
PN WO2003023001-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.8%; Score 8; DB 6; Length 450;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 1050  
ID ABB68662 standard; protein; 452 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 32778.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 452;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 1051  
ID ABO77072 standard; protein; 452 AA.  
DE Pseudomonas aeruginosa polypeptide #9247.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.8%; Score 8; DB 7; Length 452;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 1052  
ID ADP04829 standard; protein; 453 AA.  
DE Sea squirt protein with tissue specific expression in development. Seq424.  
PN JF2004057129-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 1.8%; Score 8; DB 8; Length 453;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 1053  
ID AAG29727 standard; protein; 468 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35419.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 468;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
RESULT 1054  
ID AAG31488 standard; protein; 471 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37823.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 471;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 1055  
ID ADO57237 standard; protein; 472 AA.  
DE Kidney development associated protein seqid 4.  
PN US2004068763-A1.  
PD 08-APR-2004.  
PA (HOPK/) HOPKINS N.  
PA (GOLL/) GOLLING G.  
PA (AMST/) AMSTERDAM A.  
PA (SUNZ/) SUN Z.  
Query Match 1.8%; Score 8; DB 8; Length 472;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 1056  
ID AAG45045 standard; protein; 476 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 56503.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 476;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 1057  
ID ABU48976 standard; protein; 477 AA.  
DE Protein encoded by Prokaryotic essential gene #34503.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 8; DB 6; Length 477;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 1058  
ID ADR39740 standard; protein; 482 AA.  
DE Human kinase and phosphatase KPP-13 protein SEQ ID NO:13.  
PN WO200407453-A2.  
PD 02-SEP-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 1.8%; Score 8; DB 8; Length 482;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
RESULT 1059  
ID ABU33313 standard; protein; 483 AA.  
DE Protein encoded by Prokaryotic essential gene #18840.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 8; DB 6; Length 483;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
RESULT 1060  
ID ABM15873 standard; protein; 484 AA.  
DE Mycobacterium tuberculosis mycobacterial antigen protein SEQ ID NO:111.  
PN WO2003033530-A2.  
PD 24-APR-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Query Match 1.8%; Score 8; DB 6; Length 484;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
RESULT 1061  
ID ABU36943 standard; protein; 484 AA.  
DE Protein encoded by Prokaryotic essential gene #22470.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 8; DB 6; Length 484;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
RESULT 1062  
ID ABO23518 standard; protein; 484 AA.  
DE Mycobacterium tuberculosis outlier protein #2.  
PN US2003039963-A1.  
PD 27-FEB-2003.  
PA (BRAH/) BRAHMACHARI S K.  
PA (RAMA/) RAMACHANDRAN S.  
PA (NAND/) NANDI T.  
PA (BHIM/) BHIMARAO C.  
Query Match 1.8%; Score 8; DB 7; Length 484;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
RESULT 1063  
ID ADR08508 standard; protein; 488 AA.  
DE Human protein useful for treating neurological disease Seq 2014.



PD 03-OCT-2002.  
PA Query Match 1.8%; Score 8; DB 6; Length 506;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
RESULT 1073  
ID A8M68647 standard; protein; 512 AA.  
DE Photorhabdus luminescens protein sequence #1744.  
FN W0200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 1.8%; Score 8; DB 6; Length 512;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
RESULT 1074  
ID AAB82611 standard; protein; 528 AA.  
DE Spider recombinant silk protein *PETN*CDs.  
FN W0200153333-A1.  
PD 26-JUL-2001.  
PA (MELL/) MELLO C M.  
PA (ARCI/) ARCIADIACONO S.  
PA (BUTL/) BUTLER M M.  
PA (USSA ) US SEC OF ARMY.  
Query Match 1.8%; Score 8; DB 4; Length 528;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
RESULT 1075  
ID A8M68676 standard; protein; 532 AA.  
DE Photorhabdus luminescens protein sequence #1773.  
FN W0200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 1.8%; Score 8; DB 6; Length 532;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
RESULT 1076  
ID ADA35942 standard; protein; 532 AA.  
DE Acinetobacter baumannii protein #3103.  
FN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.8%; Score 8; DB 6; Length 532;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
RESULT 1077  
ID AAY00865 standard; protein; 536 AA.  
DE Cellobiohydrolase CBH B protein sequence.  
FN W09906574-A1.  
PD 11-FEB-1999.  
PA (KONN ) GIST-BROCADES BV.  
Query Match 1.8%; Score 8; DB 2; Length 536;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
RESULT 1078  
ID ABB68621 standard; protein; 541 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 32655.  
FN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 541;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
RESULT 1079  
ID AAW07702 standard; protein; 543 AA.  
DE Mouse ETS2 repressor factor (ERF).  
FN W09639517-A1.  
PD 12-DEC-1996.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 1.8%; Score 8; DB 2; Length 543;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
RESULT 1080  
ID AAW07700 standard; protein; 548 AA.  
DE Human ETS2 repressor factor (ERF).  
FN W09639517-A1.  
PD 12-DEC-1996.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 1.8%; Score 8; DB 2; Length 548;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;

RESULT 1081  
ID ADD14028 standard; protein; 548 AA.  
DE Human src biomarker polypeptide SEQ ID NO:217.  
PN WO2003062395-A2.  
PD 31-JUL-2003.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 1.8%; Score 8; DB 7; Length 548;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
RESULT 1082  
ID ADD18620 standard; protein; 548 AA.  
DE Human disease related protein SeqID51.  
PN WO2003018621-A2.  
PD 06-MAR-2003.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 1.8%; Score 8; DB 7; Length 548;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
RESULT 1083  
ID ARM82121 standard; protein; 548 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO12892, SEQ:5477.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 1.8%; Score 8; DB 8; Length 548;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
RESULT 1084  
ID ARM84614 standard; protein; 566 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4863.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 1.8%; Score 8; DB 8; Length 566;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
RESULT 1085  
ID AAG41763 standard; protein; 568 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52002.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 568;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
RESULT 1086  
ID ADG74258 standard; protein; 570 AA.  
DE Fruit fly frizzled protein, SEQ ID No 43.  
PN WO200292635-A2.  
PD 21-NOV-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 1.8%; Score 8; DB 7; Length 570;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
RESULT 1087  
ID ABH71745 standard; protein; 582 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 42027.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
RESULT 1088  
ID ADB85519 standard; protein; 584 AA.  
DE Human MNB modulator of the SREBP pathway protein sequence.  
PN WO2003066811-A2.  
PD 14-AUG-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 1.8%; Score 8; DB 7; Length 584;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
RESULT 1089  
ID ADQ96272 standard; protein; 584 AA.  
DE T cell activation associated protein #225.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAHI KASEI PHARMA CORP.  
Query Match 1.8%; Score 8; DB 8; Length 584;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
RESULT 1090  
ID AAG41762 standard; protein; 590 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 52001.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.8%; Score 8; DB 3; Length 590;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1091  
ID AAO20499 standard; protein; 593 AA.  
DE Protein of APP related human homologue hCP41313 #1.  
PN WO200226820-A2.  
PD 04-APR-2002.  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
Query Match 1.8%; Score 8; DB 5; Length 593;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1092  
ID AAE37144 standard; protein; 608 AA.  
DE Drosophila melanogaster salvador protein.  
PN WO2003035845-A2.  
PD 01-MAY-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 1.8%; Score 8; DB 6; Length 608;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1093  
ID AAY35161 standard; protein; 609 AA.  
DE Chlamydia pneumoniae surface exposed polypeptide.  
PN WO9927105-A2.  
PD 03-JUN-1999.  
PA (GEST ) GENSET.  
Query Match 1.8%; Score 8; DB 2; Length 609;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1094  
ID ADJ70515 standard; protein; 609 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID2321.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 1.8%; Score 8; DB 7; Length 609;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 1095  
ID AAM93441 standard; protein; 629 AA.  
DE Human polypeptide, SEQ ID NO: 3082.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 1.8%; Score 8; DB 4; Length 629;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1096  
ID ADL31049 standard; protein; 629 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 3082.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 1.8%; Score 8; DB 8; Length 629;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1097  
ID ARM82107 standard; protein; 629 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO51771, SEQ:5435.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 1.8%; Score 8; DB 8; Length 629;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1098  
ID AAM50042 standard; protein; 630 AA.  
DE N. clavipes spidroin synthetic homologue SO1 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPRP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 1.8%; Score 8; DB 5; Length 630;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1099  
ID AAB74207 standard; protein; 633 AA.

DE Protein encoded by Arabidopsis gene #2.  
 PN WO200114563-A1.  
 PD 01-MAR-2001.  
 PA (GORI/) GORING D.  
 PA (STLV/) SILVA N.  
 Query Match 1.8%; Score 8; DB 4; Length 633;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 RESULT 1100  
 ID ABB91790 standard; protein; 633 AA.  
 DE Herbicidically active polypeptide SEQ ID NO 1001.  
 PN WO200210210-A2.  
 PD 07-FEB-2002.  
 PA (FARB) BAYER AG.  
 Query Match 1.8%; Score 8; DB 5; Length 633;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 RESULT 1101  
 ID ABU44612 standard; protein; 633 AA.  
 DE Protein encoded by Prokaryotic essential gene #30139.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 1.8%; Score 8; DB 6; Length 633;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 RESULT 1102  
 ID ABR82940 standard; protein; 633 AA.  
 DE Arabidopsis PERK1 receptor related protein.  
 PN WO2003072763-A1.  
 PD 04-SEP-2003.  
 PA (GORI/) GORING D.  
 PA (SILV/) SILVA N.  
 PA (HAFF/) HAFFANI Y Z.  
 Query Match 1.8%; Score 8; DB 7; Length 633;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 RESULT 1103  
 ID AAW79262 standard; protein; 635 AA.  
 DE Human protein SEQ ID NO 1924.  
 PN WO200157190-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 1.8%; Score 8; DB 4; Length 635;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 RESULT 1104  
 ID AAO20500 standard; protein; 645 AA.  
 DE Protein of APP related human homologue hCP41313 #2.  
 PN WO200226820-A2.  
 PD 04-APR-2002.  
 PA (NOVS) NOVARTIS AG.  
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 Query Match 1.8%; Score 8; DB 5; Length 645;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 RESULT 1105  
 ID ADJ49033 standard; protein; 645 AA.  
 DE O11-associated gene related protein #533.  
 PN US2004025202-A1.  
 PD 05-FEB-2004.  
 PA (LAUR/) LAURIE C C.  
 PA (RAVA/) RAVANELLO M.  
 PA (SAVA/) SAVAGE T.  
 PA (LEDE/) LEDEAUX J R.  
 PA (ROGE/) ROGERS J A.  
 Query Match 1.8%; Score 8; DB 8; Length 645;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 RESULT 1106  
 ID AAW27178 standard; protein; 646 AA.  
 DE Nephila clavipes spider silk protein.  
 PN WO9708315-A1.  
 PD 06-MAR-1997.  
 PA (BASE/) BASEL R M.  
 PA (ELIO/) ELION G R.  
 Query Match 1.8%; Score 8; DB 2; Length 646;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 RESULT 1107  
 ID AAO20518 standard; protein; 646 AA.

DE Protein of APP related human homologue hCP41313 #3.  
 PN WO200226820-A2.  
 PD 04-APR-2002.  
 PA (NOVS) NOVARTIS AG.  
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 Query Match 1.8%; Score 8; DB 5; Length 646;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 RESULT 1108  
 ID ADB61321 standard; protein; 646 AA.  
 DE Spider silk related Maspi protein.  
 PN WO2003060099-A2.  
 PD 24-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 PA (ALWA/) ALWATTARI A.  
 Query Match 1.8%; Score 8; DB 7; Length 646;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 RESULT 1109  
 ID ADC35240 standard; protein; 646 AA.  
 DE Maspi silk protein, SEQ ID 1.  
 PN WO2003057727-A1.  
 PD 17-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 Query Match 1.8%; Score 8; DB 7; Length 646;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 RESULT 1110  
 ID ADM46149 standard; protein; 646 AA.  
 DE Nephila clavipes spidroin 1 (Maspi) protein.  
 PN WO2003057720-A2.  
 PD 17-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 Query Match 1.8%; Score 8; DB 7; Length 646;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 RESULT 1111  
 ID AAW81977 standard; protein; 649 AA.  
 DE Ehrlichia sp. B3 protein.  
 PN WO9849312-A2.  
 PD 05-NOV-1998.  
 PA (AQUI-) AQUILA BIOPHARMACEUTICALS INC.  
 Query Match 1.8%; Score 8; DB 2; Length 649;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 RESULT 1112  
 ID AAY40097 standard; protein; 651 AA.  
 DE Spider silk protein spidroine major 1.  
 PN FR2774588-A1.  
 PD 13-AUG-1999.  
 PA (OREA) L'OREAL SA.  
 Query Match 1.8%; Score 8; DB 2; Length 651;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 RESULT 1113  
 ID AAU11781 standard; protein; 651 AA.  
 DE Spider natural silk protein spidroin 1.  
 PN WO200190389-A2.  
 PD 29-NOV-2001.  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 Query Match 1.8%; Score 8; DB 5; Length 651;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 RESULT 1114  
 ID ARG74687 standard; protein; 651 AA.  
 DE Human CGPD protein 914113CD1 SEQ ID 13.  
 PN WO200304322-A2.  
 PD 20-FEB-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 1.8%; Score 8; DB 6; Length 651;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 RESULT 1115  
 ID ABE62608 standard; protein; 663 AA.  
 DE Human P-TEFB protein, Cyclin T2A.  
 PN US2003039658-A1.  
 PD 27-FEB-2003.  
 PA (ESTA/) ESTABLE M.  
 PA (ROED/) ROEDER R A.  
 Query Match 1.8%; Score 8; DB 6; Length 663;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;

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RESULT 1116
ID AAM80246 standard; protein; 676 AA.
DE Human protein SEQ ID NO 3892.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSS-) HYSEQ INC.
Query Match 1.8%; Score 8; DB 4; Length 676;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1117
ID RAM50047 standard; protein; 676 AA.
DE N. clavipes spidroin synthetic homologue S01 protein #2.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKF-) IPK INST PFLANZENGENTIK & KULTURPLANZE.
Query Match 1.8%; Score 8; DB 5; Length 676;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1118
ID ADR09462 standard; protein; 676 AA.
DE Human protein useful for treating neurological disease Seq 2968.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.8%; Score 8; DB 8; Length 676;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1119
ID ABB61419 standard; protein; 677 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11049.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 677;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1120
ID ADI40843 standard; protein; 677 AA.
DE Human kinase and phosphatase KPP-9 protein SEQ ID NO:9.
PN WO2004009778-A2.
PD 29-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 1.8%; Score 8; DB 8; Length 677;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1121
ID AAO16797 standard; protein; 682 AA.
DE Human secreted protein related to the EGF subfamily.
PN WO2003006483-A2.
PD 23-JAN-2003.
PA (APPL-) APPLERA CORP.
Query Match 1.8%; Score 8; DB 6; Length 682;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1122
ID ADS10604 standard; protein; 691 AA.
DE Human therapeutic protein - SEQ ID 841.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 1.8%; Score 8; DB 8; Length 691;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1123
ID AAB65619 standard; protein; 692 AA.
DE Novel protein kinase, SEQ ID NO: 145.
PN WO200073469-A2.
PD 07-DEC-2000.
PA (SUGE-) SUGEN INC.
Query Match 1.8%; Score 8; DB 4; Length 692;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1124
ID ADN38946 standard; protein; 692 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:264.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.8%; Score 8; DB 7; Length 692;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1125
ID ADI29225 standard; protein; 692 AA.
DE Human MARK3-associated protein #19.
PN US2003232771-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 1.8%; Score 8; DB 8; Length 692;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1126
ID AAW31267 standard; protein; 694 AA.
DE Drosophila frizzled-2 protein (wnt receptor).
PN WO9739357-A1.
PD 23-OCT-1997.
PA (STRD-) UNIV LELAND STANFORD JUNIOR.
PA (UYJO-) UNIV JOHNS HOPKINS.
Query Match 1.8%; Score 8; DB 2; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
RESULT 1127
ID ABB71797 standard; protein; 694 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42183.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
RESULT 1128
ID ABR58650 standard; protein; 695 AA.
DE Human cancer related protein SEQ ID NO:307.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.8%; Score 8; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
RESULT 1129
ID AAR14308 standard; protein; 718 AA.
DE N. clavipes dragline silk protein-1.
PN EP452925-A.
PD 23-OCT-1991.
PA (UYWY-) UNIV OF WYOMING.
Query Match 1.8%; Score 8; DB 2; Length 718;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1130
ID AAW53346 standard; protein; 718 AA.
DE Nephila clavipes spider silk protein.
PN US5728810-A.
PD 17-MAR-1998.
PA (UYWY-) UNIV WYOMING.
Query Match 1.8%; Score 8; DB 2; Length 718;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1131
ID RAY59070 standard; protein; 718 AA.
DE N. clavipes spider silk protein 1.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match 1.8%; Score 8; DB 3; Length 718;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1132
ID ABB65778 standard; protein; 724 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24126.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 724;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
RESULT 1133
ID ADM04578 standard; protein; 724 AA.
DE Human protein of the invention SEQ ID NO:3263.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.8%; Score 8; DB 7; Length 724;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
RESULT 1134
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ID ABU62609 standard; protein; 730 AA.  
DE Human P-TEFB protein, Cyclin T2B.  
PN US2003039658-A1.  
PD 27-FEB-2003.  
PA (ESTA/) ESTABLE M.  
PA (ROED/) ROEDER R A.  
Query Match 1.8%; Score 8; DB 6; Length 730;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
RESULT 1135  
ID ADJ69158 standard; protein; 730 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID564.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 1.8%; Score 8; DB 7; Length 730;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
RESULT 1136  
ID ABB60124 standard; protein; 752 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7164.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 752;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
RESULT 1137  
ID AA41734 standard; protein; 763 AA.  
DE Human TRAP-2 kinase.  
PN WO9801541-A1.  
PD 15-JAN-1998.  
PA (TULA-) TULARIK INC.  
Query Match 1.8%; Score 8; DB 2; Length 763;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1138  
ID AAU02222 standard; protein; 763 AA.  
DE Rat Dyrrk, a homologue of Drosophila minibrain mnb.  
PN US6251664-B1.  
PD 26-JUN-2001.  
PA (PALL/) ESTIVILL PALLEJA X.  
Query Match 1.8%; Score 8; DB 4; Length 763;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1139  
ID AAU02221 standard; protein; 763 AA.  
DE Human MNB, homologue of Drosophila minibrain mnb.  
PN US6251664-B1.  
PD 26-JUN-2001.  
PA (PALL/) ESTIVILL PALLEJA X.  
Query Match 1.8%; Score 8; DB 4; Length 763;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1140  
ID ABB57155 standard; protein; 763 AA.  
DE Mouse ischaemic condition related protein sequence SEQ ID NO:377.  
PN WO200188188-A2.  
PD 22-NOV-2001.  
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Query Match 1.8%; Score 8; DB 5; Length 763;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1141  
ID ABR54250 standard; protein; 763 AA.  
DE Human NOV39a protein SEQ ID NO:168.  
PN WO2003023001-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.8%; Score 8; DB 6; Length 763;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1142  
ID AAU99562 standard; protein; 765 AA.  
DE Novel human protein (NHP), kinase #2.  
PN WO200231129-A2.  
PD 18-APR-2002.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 1.8%; Score 8; DB 5; Length 765;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;

RESULT 1143  
ID ADJ96623 standard; protein; 765 AA.  
DE Human calcium/calmodulin-dependent protein kinase DCAMKL2 protein Seq 80.  
PN WO2004006838-A2.  
PD 22-JAN-2004.  
PA (SUGE-) SUGEN INC.  
Query Match 1.8%; Score 8; DB 8; Length 765;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1144  
ID AAG66161 standard; protein; 766 AA.  
DE Human serine/threonine protein kinase, 15985.  
PN WO200216588-A2.  
PD 28-FEB-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.8%; Score 8; DB 5; Length 766;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1145  
ID AAE21719 standard; protein; 766 AA.  
DE Human PKIN-14 protein.  
PN WO200218557-A2.  
PD 07-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.8%; Score 8; DB 5; Length 766;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1146  
ID AAU99561 standard; protein; 766 AA.  
DE Novel human protein (NHP), kinase #1.  
PN WO200231129-A2.  
PD 18-APR-2002.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 1.8%; Score 8; DB 5; Length 766;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1147  
ID ADC77671 standard; protein; 766 AA.  
DE Human 15985 protein SEQ ID NO:34.  
PN WO2003073983-A2.  
PD 12-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.8%; Score 8; DB 7; Length 766;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1148  
ID ADQ9118 standard; protein; 766 AA.  
DE Human urological disorder related protein 15985 SEQ:70.  
PN WO2004065576-A2.  
PD 05-AUG-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.8%; Score 8; DB 8; Length 766;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1149  
ID ADN23352 standard; protein; 772 AA.  
DE Bacterial polypeptide #6005.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.8%; Score 8; DB 8; Length 772;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1150  
ID AAM50045 standard; protein; 773 AA.  
DE N. clavipes spidroin homologue SM12-70xELP for plant expression.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 1.8%; Score 8; DB 5; Length 773;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1151  
ID ADN23353 standard; protein; 775 AA.  
DE Bacterial polypeptide #6006.  
PN US2003233675-A1.  
PD 18-DEC-2003.

PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.8%; Score 8; DB 8; Length 775;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 1152  
ID AAM50046 standard; protein; 777 AA.  
DE N. clavipes spidroin homologue SM12-70xELP for E. coli expression.  
PN DB10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 1.8%; Score 8; DB 5; Length 777;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1153  
ID ABU36827 standard; protein; 778 AA.  
DE Protein encoded by Prokaryotic essential gene #22354.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 8; DB 6; Length 778;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1154  
ID ADI40872 standard; protein; 783 AA.  
DE Human kinase and phosphatase KPP-38 protein SEQ ID NO:38.  
PN WO2004009778-A2.  
PD 29-JAN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 1.8%; Score 8; DB 8; Length 783;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1155  
ID ABB62304 standard; protein; 805 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 13704.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 805;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
RESULT 1156  
ID ABB60866 standard; protein; 806 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 9390.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 806;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
RESULT 1157  
ID AAW37501 standard; protein; 816 AA.  
DE Human nel-related protein type 2.  
PN EP796913-A2.  
PD 24-SEP-1997.  
PA (SAKA ) OTSUKA PHARM CO LTD.  
Query Match 1.8%; Score 8; DB 2; Length 816;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
RESULT 1158  
ID ABR56522 standard; protein; 816 AA.  
DE Human nel-related protein type 2 SEQ ID:37.  
PN EP1295944-A2.  
PD 26-MAR-2003.  
PA (SAKA ) OTSUKA PHARM CO LTD.  
Query Match 1.8%; Score 8; DB 6; Length 816;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
RESULT 1159  
ID ADQ18201 standard; protein; 816 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1018.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.8%; Score 8; DB 8; Length 816;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
RESULT 1160  
ID ADQ76516 standard; protein; 816 AA.  
DE Amino acid sequence of human NRP2.  
PN EP1439230-A2.  
PD 21-JUL-2004.  
PA (SAKA ) OTSUKA PHARM CO LTD.  
PA (PROT-) PROTEIN DESIGN LAB INC.  
Query Match 1.8%; Score 8; DB 8; Length 816;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
RESULT 1161  
ID ADP56112 standard; protein; 816 AA.  
DE Human PRO protein sequence SEQ ID NO:2088.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 1.8%; Score 8; DB 8; Length 816;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
RESULT 1162  
ID ADR32029 standard; protein; 816 AA.  
DE Human NELL2, SEQ ID 8.  
PN WO2004072100-A2.  
PD 26-AUG-2004.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 1.8%; Score 8; DB 8; Length 816;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
RESULT 1163  
ID ABB64699 standard; protein; 821 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 20889.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 821;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
RESULT 1164  
ID ABP97380 standard; protein; 825 AA.  
DE Human DCAMKLI-like serine/threonine kinase, SEQ ID NO:2.  
PN WO2003018816-A1.  
PD 06-MAR-2003.  
PA (FARB ) BAYER AG.  
Query Match 1.8%; Score 8; DB 6; Length 825;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
RESULT 1165  
ID ADA54824 standard; protein; 846 AA.  
DE Human protein, SEQ ID 2392.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 1.8%; Score 8; DB 6; Length 846;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 1166  
ID ADG39856 standard; protein; 847 AA.  
DE Protein similar to human NOV12 #2.  
PN US2003203843-A1.  
PD 30-OCT-2003.  
PA (PENA/) PENA C E A.  
PA (GUOX/) GUO X.  
PA (SHIM/) SHIMKETS R A.  
PA (PADI/) PADIGARU M.  
PA (KEKU/) KEKUDA R.  
PA (SPYT/) SPYTEK K A.  
PA (MEHR/) MEHRABAN F.  
PA (TOPE/) TOPPER J N.  
PA (MALY/) MALYANKAR U M.  
PA (WASS/) WASSERMAN S M.  
PA (EDIN/) EDINGER S R.  
PA (SMIT/) SMITHSON G.  
PA (GUNT/) GUNTHER E.  
PA (KOMU/) KOMUVES L.  
Query Match 1.8%; Score 8; DB 7; Length 847;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 1167  
ID ABB60212 standard; protein; 869 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7428.  
PN WO200171042-A2.

PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 869;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1168  
ID ADJ69388 standard; protein; 877 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1194.  
PN W02003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 1.8%; Score 8; DB 7; Length 877;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1169  
ID ADM29420 standard; protein; 917 AA.  
DE Mouse macrophage colony stimulating factor 1 receptor.  
PN W02003064628-A2.  
PD 07-AUG-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.8%; Score 8; DB 7; Length 917;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1170  
ID ADM29419 standard; protein; 917 AA.  
DE Rat macrophage colony stimulating factor 1 receptor.  
PN W02003064628-A2.  
PD 07-AUG-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.8%; Score 8; DB 7; Length 917;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1171  
ID ABR61376 standard; protein; 928 AA.  
DE Human GlcNAC-phosphotransferase alpha-subunit.  
PN US6537785-B1.  
PD 25-MAR-2003.  
PA (GENZ-) GENZYME GLYCOBIOLOGY RES INST INC.  
Query Match 1.8%; Score 8; DB 4; Length 928;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1172  
ID ADD27812 standard; protein; 928 AA.  
DE Human GlcNAC-phosphotransferase alpha subunit.  
PN US2003119088-A1.  
PD 26-JUN-2003.  
PA (NOVA-) NOVAZYME PHARM INC.  
Query Match 1.8%; Score 8; DB 7; Length 928;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1173  
ID ABR01488 standard; protein; 928 AA.  
DE Human GlcNAC-phosphotransferase alpha subunit precursor protein.  
PN US2003124652-A1.  
PD 03-JUL-2003.  
PA (NOVA-) NOVAZYME PHARM INC.  
Query Match 1.8%; Score 8; DB 7; Length 928;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1174  
ID ABR01537 standard; protein; 928 AA.  
DE Human GlcNAC-phosphotransferase alpha subunit precursor protein.  
PN US2003124653-A1.  
PD 03-JUL-2003.  
PA (NOVA-) NOVAZYME PHARM INC.  
Query Match 1.8%; Score 8; DB 7; Length 928;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1175  
ID ADO01020 standard; protein; 968 AA.  
DE Fruit fly AD-related protein CG14918.  
PN US2004067535-A1.  
PD 08-APR-2004.  
PA (LIFE-) LIFE SCI DEV CORP.  
Query Match 1.8%; Score 8; DB 8; Length 968;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
RESULT 1176  
ID AAM50038 standard; protein; 989 AA.  
DE N. clavipes spideroin synthetic homologue S01SM12 protein.  
PN DE10113781-A1.

PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 1.8%; Score 8; DB 5; Length 989;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1177  
ID ABG14604 standard; protein; 994 AA.  
DE Novel human diagnostic protein #14595.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.8%; Score 8; DB 4; Length 994;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1178  
ID ABG07468 standard; protein; 994 AA.  
DE Novel human diagnostic protein #7459.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.8%; Score 8; DB 4; Length 994;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1179  
ID ABG19901 standard; protein; 994 AA.  
DE Novel human diagnostic protein #19892.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.8%; Score 8; DB 4; Length 994;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1180  
ID ABG14924 standard; protein; 994 AA.  
DE Novel human diagnostic protein #14915.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.8%; Score 8; DB 4; Length 994;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1181  
ID ADJ69375 standard; protein; 1027 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1181.  
PN W02003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 1.8%; Score 8; DB 7; Length 1027;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
RESULT 1182  
ID ABB63413 standard; protein; 1108 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 17031.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 1108;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1183  
ID ADN21459 standard; protein; 1133 AA.  
DE Bacterial polypeptide #4112.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY-) CAO Y.  
PA (HINK-) HINKLE G J.  
PA (SLAT-) SLATER S C.  
PA (CHEN-) CHEN X.  
PA (GOLD-) GOLDMAN B S.  
Query Match 1.8%; Score 8; DB 8; Length 1133;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 1184  
ID AAY68784 standard; protein; 1135 AA.  
DE Amino acid sequence of a human phosphorylation effector PHSP-16.  
PN W0200006728-A2.  
PD 10-FEB-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 1.8%; Score 8; DB 3; Length 1135;  
Best Local Similarity 100.0%; Pred. No. 9e+02;

RESULT 1185  
ID AAR6391 standard; protein; 1141 AA.  
DE Human SREBP-2.  
PN WO9426922-A2.  
PD 24-NOV-1994.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 1.8%; Score 8; DB 2; Length 1141;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 1186  
ID AAY50700 standard; protein; 1141 AA.  
DE Human SREBP-2 protein.  
PN DE19816902-A1.  
PD 28-OCT-1999.  
PA (KRON/) KRONE W.  
PA (MUEL/) MUELLER-WIELAND D.  
Query Match 1.8%; Score 8; DB 2; Length 1141;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 1187  
ID ADK60415 standard; protein; 1141 AA.  
DE Angiogenesis differentially expressed protein #55.  
PN FR2836687-A1.  
PD 05-SEP-2003.  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
Query Match 1.8%; Score 8; DB 8; Length 1141;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 1188  
ID ADK60716 standard; protein; 1141 AA.  
DE Angiogenesis differentially expressed protein #55.  
PN FR2836686-A1.  
PD 05-SEP-2003.  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
Query Match 1.8%; Score 8; DB 8; Length 1141;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 1189  
ID ADP73339 standard; protein; 1141 AA.  
DE Human mitogen-activated protein kinase kinase kinase 4 (MAP4K4).  
PN FR2843753-A1.  
PD 27-FEB-2004.  
PA (GENE/) GENE S.  
PA (ALMS/) AL M S.  
Query Match 1.8%; Score 8; DB 8; Length 1141;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 1190  
ID AEM82371 standard; protein; 1141 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO83293, SEQ:6086.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 1.8%; Score 8; DB 8; Length 1141;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 1191  
ID ADQ39979 standard; protein; 1141 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1642.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 1.8%; Score 8; DB 8; Length 1141;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 1192  
ID ADQ39980 standard; protein; 1141 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1643.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 1.8%; Score 8; DB 8; Length 1141;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 1193  
ID AAB43016 standard; protein; 1165 AA.  
DE Human ORFX ORF2780 polypeptide sequence SEQ ID NO:5560.  
PN WO200058473-A2.  
PD 05-OCT-2000.

PA (CURA-) CURAGEN CORP.  
Query Match 1.8%; Score 8; DB 3; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
RESULT 1194  
ID ABG17470 standard; protein; 1165 AA.  
DE Novel human diagnostic protein #17461.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.8%; Score 8; DB 4; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
RESULT 1195  
ID AAO18509 standard; protein; 1165 AA.  
DE Human insulin receptor signaling modifier SEQ ID NO: 40.  
PN WO200255664-A2.  
PD 18-JUL-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 1.8%; Score 8; DB 5; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
RESULT 1196  
ID ABU03499 standard; protein; 1165 AA.  
DE Angiogenesis-associated human protein sequence #44.  
PN WO200279492-A2.  
PD 10-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 1.8%; Score 8; DB 6; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
RESULT 1197  
ID ADO85778 standard; protein; 1165 AA.  
DE Rac/axin/beta-catenin pathway modulating MAPK-associated protein #2.  
PN WO2004048542-A2.  
PD 10-JUN-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 1.8%; Score 8; DB 8; Length 1166;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
RESULT 1198  
ID ABG17468 standard; protein; 1175 AA.  
DE Novel human diagnostic protein #17459.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.8%; Score 8; DB 4; Length 1175;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
RESULT 1199  
ID AAU76512 standard; protein; 1175 AA.  
DE Human HPK/GCK-like kinase.  
PN US6346416-B1.  
PD 12-FEB-2002.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 1.8%; Score 8; DB 5; Length 1175;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
RESULT 1200  
ID ADK60186 standard; protein; 1175 AA.  
DE Angiogenesis differentially expressed protein GS-P9.  
PN FR2836687-A1.  
PD 05-SEP-2003.  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
Query Match 1.8%; Score 8; DB 8; Length 1175;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
RESULT 1201  
ID ADK60487 standard; protein; 1175 AA.  
DE Angiogenesis differentially expressed protein GS-P9.  
PN FR2836686-A1.  
PD 05-SEP-2003.  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
Query Match 1.8%; Score 8; DB 8; Length 1175;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
RESULT 1202  
ID ADP73110 standard; protein; 1175 AA.  
DE Angiogenesis inhibitor human protein sequence, GS-P9.  
PN FR2843753-A1.



PD 27-FEB-2004.  
 PA (GENE/)/ GENE S.  
 PA (ALMS/)/ AL M S.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 8; Length 1175;  
 RESULT 1203  
 ID ADR40445 standard; protein; 1192 AA.  
 DE Mouse inositol 1,4,5-triphosphate 3-kinase (IP3KB) enzyme.  
 PN WO2004066926-A2.  
 PD 12-AUG-2004.  
 PA (IRMI-) IRM LLC.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 8; Length 1192;  
 RESULT 1204  
 ID ADR39772 standard; protein; 1194 AA.  
 DE Human kinase and phosphatase KPP-45 protein SEQ ID NO:45.  
 PN WO2004074453-A2.  
 PD 02-SEP-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 8; Length 1194;  
 RESULT 1205  
 ID ADD27810 standard; protein; 1199 AA.  
 DE Soluble human GlnAc-phosphotransferase.  
 PN US2003119088-A1.  
 PD 26-JUN-2003.  
 PA (NOVA-) NOVAZYME PHARM INC.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 7; Length 1199;  
 RESULT 1206  
 ID ABW01487 standard; protein; 1199 AA.  
 DE N-acetylglucosamine-1(GlcNAc)-phosphotransferase.  
 PN US2003124652-A1.  
 PD 03-JUL-2003.  
 PA (NOVA-) NOVAZYME PHARM INC.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 7; Length 1199;  
 RESULT 1207  
 ID ABW01536 standard; protein; 1199 AA.  
 DE N-acetylglucosamine-1(GlcNAc)-phosphotransferase protein.  
 PN US2003124653-A1.  
 PD 03-JUL-2003.  
 PA (NOVA-) NOVAZYME PHARM INC.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 7; Length 1199;  
 RESULT 1208  
 ID AAE04368 standard; protein; 1212 AA.  
 DE Human kinase (PKIN)-9.  
 PN WO200146397-A2.  
 PD 28-JUN-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 4; Length 1212;  
 RESULT 1209  
 ID ADE25753 standard; protein; 1212 AA.  
 DE Human protein differentially expressed in foam cells #30.  
 PN US2003194721-A1.  
 PD 16-OCT-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 7; Length 1212;  
 RESULT 1210  
 ID ABG17469 standard; protein; 1219 AA.  
 DE Novel human diagnostic protein #17460.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 4; Length 1219;  
 RESULT 1211  
 ID ADR39771 standard; protein; 1222 AA.  
 DE Human kinase and phosphatase KPP-44 protein SEQ ID NO:44.  
 PN WO2004074453-A2.

PD 02-SEP-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 8; Length 1222;  
 RESULT 1212  
 ID AA48895 standard; protein; 1230 AA.  
 DE Candida albicans CST20 protein.  
 PN WO9818927-A1.  
 PD 07-MAY-1998.  
 PA (CANA ) NAT RES COUNCIL CANADA.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 2; Length 1230;  
 RESULT 1213  
 ID ADN61483 standard; protein; 1230 AA.  
 DE Human KPP-49 protein SEQ ID NO:49.  
 PN WO2004042022-A2.  
 PD 21-MAY-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 8; Length 1233;  
 RESULT 1214  
 ID AAY55954 standard; protein; 1233 AA.  
 DE Mouse STE20-related protein kinase NIK\_m.  
 PN WO9953036-A2.  
 PD 21-OCT-1999.  
 PA (SUGB-) SUGEN INC.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 2; Length 1233;  
 RESULT 1215  
 ID AAY55931 standard; protein; 1239 AA.  
 DE Human ZC1 protein.  
 PN WO9953036-A2.  
 PD 21-OCT-1999.  
 PA (SUGB-) SUGEN INC.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 2; Length 1239;  
 RESULT 1216  
 ID AAM50037 standard; protein; 1255 AA.  
 DE N. clavipes spidroin synthetic homologue SO1S01 protein.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 5; Length 1255;  
 RESULT 1217  
 ID AAE25290 standard; protein; 1256 AA.  
 DE Human nucleic acid-associated protein (NAAP-9).  
 PN WO200250279-A2.  
 PD 27-JUN-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 5; Length 1256;  
 RESULT 1218  
 ID ABB78296 standard; protein; 1294 AA.  
 DE Amino acid sequence of lipid-associated molecule (LIPAM)-7.  
 PN WO200263005-A2.  
 PD 15-AUG-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 5; Length 1294;  
 RESULT 1219  
 ID ABB71827 standard; protein; 1333 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 42273.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match  
 Best Local Similarity 1.8%; Score 8; DB 4; Length 1333;  
 RESULT 1220  
 ID AAW59359 standard; protein; 1349 AA.  
 DE Human retinal degeneration B3 polypeptide (hrdgB3).  
 PN WO9816639-A1.  
 PD 23-APR-1998.

PA (SUGS-) SUGEN INC.  
PA (UYNT-) UNIV NEW YORK MEDICAL CENT.  
Query Match 1.8%; Score 8; DB 2; Length 1349;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1221  
ID ADN00366 standard; protein; 1359 AA.  
DE Novel human protein #7.  
PN JF2004073126-A.  
PD 11-MAR-2004.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
Query Match 1.8%; Score 8; DB 8; Length 1359;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1222  
ID ADN61482 standard; protein; 1384 AA.  
DE Human KPP-48 protein SEQ ID NO:48.  
PN W02004042022-A2.  
PD 21-MAY-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 1.8%; Score 8; DB 8; Length 1384;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1223  
ID ADJ96675 standard; protein; 1392 AA.  
DE Human protein kinase ZC1 protein SeqID 132.  
PN W02004006838-A2.  
PD 22-JAN-2004.  
PA (SUGS-) SUGEN INC.  
Query Match 1.8%; Score 8; DB 8; Length 1392;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1224  
ID AAM78991 standard; protein; 1393 AA.  
DE Human protein SEQ ID NO 1653.  
PN W0200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.8%; Score 8; DB 4; Length 1393;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1225  
ID ADH29597 standard; protein; 1431 AA.  
DE Human CRKRS-related Gene variant protein.  
PN US2003190621-A1.  
PD 09-OCT-2003.  
PA (DAIK/) DAI K.  
Query Match 1.8%; Score 8; DB 8; Length 1431;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1226  
ID ABU07381 standard; protein; 1459 AA.  
DE Human protein NOV12.  
PN W0200285922-A2.  
PD 31-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.8%; Score 8; DB 6; Length 1459;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1227  
ID ADG39794 standard; protein; 1459 AA.  
DE Human novel protein NOV12.  
PN US2003203843-A1.  
PD 30-OCT-2003.  
PA (PENA/) PENNA C E A.  
PA (GUOX/) GUO X.  
PA (SHIM/) SHIMKETS R A.  
PA (PADI/) PADIGARU M.  
PA (KEKU/) KEKUDA R.  
PA (SPYT/) SPYTEK K A.  
PA (MEHR/) MEHRABAN F.  
PA (TOPP/) TOPPER J N.  
PA (WALY/) WALYANKAR U M.  
PA (WASS/) WASSERMAN S M.  
PA (EDIN/) EDINGER S R.  
PA (SMIT/) SMITHSON G.  
PA (GUNT/) GUNTHER E.  
PA (KOMU/) KOMUVES L.  
Query Match 1.8%; Score 8; DB 7; Length 1459;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1228  
ID AAB5644 standard; protein; 1490 AA.  
DE Novel protein Kinase, SEQ ID NO: 171.  
PN W0200073469-A2.  
PD 07-DEC-2000.  
PA (SUGS-) SUGEN INC.  
Query Match 1.8%; Score 8; DB 4; Length 1490;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1229  
ID ABR47427 standard; protein; 1490 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:86.  
PN W02003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.8%; Score 8; DB 6; Length 1490;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1230  
ID ABO53039 standard; protein; 1490 AA.  
DE Human spliceosome associated protein (SAP) #80.  
PN US2003088803-A1.  
PD 10-APR-2003.  
PA (REED/) REED R.  
PA (ZHOU/) ZHOU Z.  
Query Match 1.8%; Score 8; DB 6; Length 1490;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1231  
ID ADD89963 standard; protein; 1490 AA.  
DE Human cancer-associated protein kinase CRK7.  
PN W02003083096-A2.  
PD 09-OCT-2003.  
PA (KINE-) KINETEK PHARM INC.  
Query Match 1.8%; Score 8; DB 7; Length 1490;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1232  
ID ADJ69106 standard; protein; 1490 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID912.  
PN W02003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 1.8%; Score 8; DB 7; Length 1490;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1233  
ID ADH13182 standard; protein; 1490 AA.  
DE Human malignant neoplasia-related protein SeqID31.  
PN EP1365034-A2.  
PD 26-NOV-2003.  
PA (FARB-) BAYER AG.  
Query Match 1.8%; Score 8; DB 8; Length 1490;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1234  
ID ADH09507 standard; protein; 1490 AA.  
DE Human host factor protein, SEQ ID No 35.  
PN W02003094847-A2.  
PD 20-NOV-2003.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.8%; Score 8; DB 8; Length 1490;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1235  
ID ADH09508 standard; protein; 1490 AA.  
DE Human host factor protein, SEQ ID No 36.  
PN W02003094847-A2.  
PD 20-NOV-2003.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.8%; Score 8; DB 8; Length 1490;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1236  
ID ADH09506 standard; protein; 1490 AA.  
DE Human host factor protein, SEQ ID No 34.  
PN W02003094847-A2.  
PD 20-NOV-2003.  
PA (UYEM-) UNIV EMORY.

Query Match 1.8%; Score 8; DB 8; Length 1490;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1237  
ID AD129251 standard; protein; 1490 AA.  
DE Human MARK3-associated protein #38.  
PN US2003232771-A1.  
PD 18-DEC-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 1.8%; Score 8; DB 8; Length 1490;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1238  
ID ABB64829 standard; protein; 1518 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 21279.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 1518;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1239  
ID ABG17466 standard; protein; 1655 AA.  
DE Novel human diagnostic protein #17457.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSE INC.  
Query Match 1.8%; Score 8; DB 4; Length 1655;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1240  
ID ABB94266 standard; protein; 1723 AA.  
DE Chlamydia pneumoniae protein sequence SEQ ID NO:394.  
PN WO200208267-A2.  
PD 31-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.8%; Score 8; DB 5; Length 1723;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1241  
ID ABB94267 standard; protein; 1723 AA.  
DE Chlamydia pneumoniae protein sequence SEQ ID NO:395.  
PN WO200208267-A2.  
PD 31-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.8%; Score 8; DB 5; Length 1723;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1242  
ID ABB90585 standard; protein; 1723 AA.  
DE Chlamydia pneumoniae cp6830 protein, SEQ ID NO:119.  
PN WO200202606-A2.  
PD 10-JAN-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 1.8%; Score 8; DB 5; Length 1732;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1243  
ID ABU26843 standard; protein; 1732 AA.  
DE Protein encoded by Prokaryotic essential gene #12370.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 8; DB 6; Length 1732;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1244  
ID ADN17774 standard; protein; 1797 AA.  
DE Bacterial polypeptide #427.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.8%; Score 8; DB 8; Length 1797;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1245  
ID ABO39949 standard; protein; 1823 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1612.

PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 1.8%; Score 8; DB 8; Length 1823;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1246  
ID AAR44504 standard; protein; 1830 AA.  
DE Urea amide lyase.  
PN JP05304965-A.  
PD 19-NOV-1993.  
PA (TOYM ) TOYOBO KK.  
Query Match 1.8%; Score 8; DB 2; Length 1830;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1247  
ID ADJ68314 standard; protein; 1870 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID120.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 1.8%; Score 8; DB 7; Length 1870;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1248  
ID AAM50039 standard; protein; 1880 AA.  
DE N. clavipes spidroin synthetic homologue SO1SO1SO1 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPELANZE.  
Query Match 1.8%; Score 8; DB 5; Length 1880;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1249  
ID ABU54584 standard; protein; 2017 AA.  
DE Human NOVX polypeptide #43.  
PN WO200281498-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.8%; Score 8; DB 6; Length 2017;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1250  
ID ADJ69868 standard; protein; 2060 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1674.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 1.8%; Score 8; DB 7; Length 2060;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1251  
ID AAB31516 standard; protein; 2087 AA.  
DE Amino acid sequence of the rat Shankla polypeptide.  
PN WO200078921-A2.  
PD 28-DEC-2000.  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
Query Match 1.8%; Score 8; DB 4; Length 2087;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1252  
ID AAB12000 standard; protein; 2091 AA.  
DE Rat p3103 protein.  
PN JP2000184884-A.  
PD 04-JUL-2000.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 1.8%; Score 8; DB 3; Length 2091;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1253  
ID ADO39951 standard; protein; 2102 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1614.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 1.8%; Score 8; DB 8; Length 2102;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1254

ID ADQ39950 standard; protein; 2108 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1613.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 1.8%; Score 8; DB 8; Length 2108;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1255  
ID ABB80768 standard; protein; 2145 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO81398, SEQ:1980.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 1.8%; Score 8; DB 8; Length 2145;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1256  
ID AAU33195 standard; protein; 2153 AA.  
DE Novel human secreted protein #3686.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.8%; Score 8; DB 4; Length 2153;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1257  
ID ABB80769 standard; protein; 2157 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO81399, SEQ:1982.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 1.8%; Score 8; DB 8; Length 2157;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1258  
ID ADQ39952 standard; protein; 2157 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1615.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 1.8%; Score 8; DB 8; Length 2157;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1259  
ID ADQ89666 standard; protein; 2228 AA.  
DE Antagonist of cell cycle progression polypeptide #48.  
PN WO2004063362-A2.  
PD 23-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
Query Match 1.8%; Score 8; DB 8; Length 2228;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1260  
ID ABB58139 standard; protein; 2230 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 1209.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 2230;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1261  
ID ABB63947 standard; protein; 3726 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 18633.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 1.8%; Score 8; DB 4; Length 3726;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
RESULT 1262  
ID ADO57969 standard; peptide; 8 AA.  
DE MHC multimer linker peptide SEQ ID 4.  
PN DE10247014-A1.  
PD 22-APR-2004.  
PA (ERFL/) ERFLUE V.  
Query Match 1.6%; Score 7; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1263  
ID AAY81276 standard; peptide; 10 AA.

DE Gly/Ser-rich linker peptide, SEQ ID NO:78.  
PN WO200006717-A2.  
PD 10-FEB-2000.  
PA (GETH) GENENTECH INC.  
Query Match 1.6%; Score 7; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1264  
ID RAG93434 standard; peptide; 10 AA.  
DE Disconnected protein complementary peptide 105.  
PN GB2356401-A.  
PD 23-MAY-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1265  
ID AAG97098 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 3292.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1266  
ID RAG97100 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 3294.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1267  
ID RAG95246 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 1440.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1268  
ID AAG97132 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 3326.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1269  
ID RAG97096 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 3290.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1270  
ID RAG96428 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 2622.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1271  
ID AAG97078 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 3272.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1272  
ID RAG94120 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 314.

PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1273  
ID AAG95016 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 1210.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1274  
ID AAG97102 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 3296.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1275  
ID AAG97136 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 3330.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1276  
ID AAG96426 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 2620.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1277  
ID AAG97076 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 3270.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1278  
ID AAG97118 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 3312.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1279  
ID AAG93850 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 44.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1280  
ID AAG94062 standard; peptide; 10 AA.  
DE Human complementary peptide, SEQ ID NO: 256.  
PN WO200142277-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1281  
ID AAG85129 standard; peptide; 10 AA.  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 78.  
PN WO200142276-A1.

PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1282  
ID AAG85127 standard; peptide; 10 AA.  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 76.  
PN WO200142276-A1.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1283  
ID AAG85329 standard; peptide; 10 AA.  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 278.  
PN WO200142276-A1.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1284  
ID AAG85131 standard; peptide; 10 AA.  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 80.  
PN WO200142276-A1.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1285  
ID AAM43046 standard; peptide; 10 AA.  
DE Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 355.  
PN WO200142278-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1286  
ID AAM43044 standard; peptide; 10 AA.  
DE Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 353.  
PN WO200142278-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 1.6%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1287  
ID ADC34710 standard; peptide; 10 AA.  
DE (Ser4Gly)2 protease substrate, PFPS11.  
PN US6503886-B1.  
PD 07-JAN-2003.  
PA (SELE-) SELECTIVE GENETICS INC.  
Query Match 1.6%; Score 7; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 1288  
ID ADA38153 standard; peptide; 12 AA.  
DE Peptide amphiphile composition 8 containing an RGD cell adhesion motif.  
PN WO2003054146-A2.  
PD 03-JUL-2003.  
PA (NOUN) UNIV NORTHWESTERN.  
Query Match 1.6%; Score 7; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
RESULT 1289  
ID ADR39905 standard; peptide; 12 AA.  
DE Surgical implant-related peptide amphiphile 9.  
PN WO2004072104-A2.  
PD 26-AUG-2004.  
PA (NOUN) UNIV NORTHWESTERN.  
Query Match 1.6%; Score 7; DB 8; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
RESULT 1290  
ID AAR27243 standard; peptide; 13 AA.  
DE Sequence of serine-rich peptide linker.  
PN WO9215682-A1.  
PD 17-SEP-1992.

PA (CREA-) CREATIVE BIOMOLECULES INC.  
Query Match 1.6%; Score 7; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
RESULT 1291  
ID AAR92865 standard; peptide; 13 AA.  
DE Cell adhesion modulatory peptide APB.  
PN DB4430601-A1.  
PD 23-FEB-1996.  
PA (BEIE-) BEIERSDORF AG.  
Query Match 1.6%; Score 7; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
RESULT 1292  
ID AAY59102 standard; peptide; 13 AA.  
DE N. clavipes spider silk protein 1 repeat fragment.  
PN US598984-A.  
PD 23-NOV-1999.  
PA (UYWY-) UNIV WYOMING.  
Query Match 1.6%; Score 7; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
RESULT 1293  
ID AAM98057 standard; peptide; 13 AA.  
DE Human peptide #1332 encoded by a SNP oligonucleotide.  
PN WO200147944-A2.  
PD 05-JUL-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.6%; Score 7; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
RESULT 1294  
ID AAM98358 standard; peptide; 14 AA.  
DE Human peptide #1633 encoded by a SNP oligonucleotide.  
PN WO200147944-A2.  
PD 05-JUL-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.6%; Score 7; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
RESULT 1295  
ID AAR39572 standard; protein; 15 AA.  
DE Sequence of a new linker.  
PN WO9316185-A2.  
PD 19-AUG-1993.  
PA (CREA-) CREATIVE BIOMOLECULES INC.  
PA (CETU-) CETUS ONCOLOGY CORP.  
Query Match 1.6%; Score 7; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1296  
ID AAW53355 standard; peptide; 15 AA.  
DE Nephila clavipes spider silk protein tandem repeat unit SEQ ID NO:13.  
PN US5728810-A.  
PD 17-MAR-1998.  
PA (UYWY-) UNIV WYOMING.  
Query Match 1.6%; Score 7; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1297  
ID AAY90828 standard; peptide; 15 AA.  
DE Linker amino acid sequence SEQ ID NO:31.  
PN US6054561-A.  
PD 25-APR-2000.  
PA (CHIR-) CHIRON CORP.  
Query Match 1.6%; Score 7; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1298  
ID ABB55909 standard; peptide; 15 AA.  
DE Vascular dementia-associated protein isoform (VPI) 109.  
PN WO200169261-A2.  
PD 20-SEP-2001.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Query Match 1.6%; Score 7; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1299  
ID AAU08688 standard; peptide; 15 AA.  
DE Antibody L19-Fibronectin-2 (IL-2) fusion protein amino acid linker.  
PN WO200162298-A2.  
PD 30-AUG-2001.

PA (PHIL-) PHILOGEN SRL.  
Query Match 1.6%; Score 7; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1300  
ID RAU04949 standard; peptide; 15 AA.  
DE Humanised anti-p185 antibody/IL-2 fusion protein, linker peptide #2.  
PN WO200153354-A2.  
PD 26-JUL-2001.  
PA (CHIR-) CHIRON CORP.  
PA (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.  
PA (HAMI-) HAMILTON REGIONAL CANCER CENT.  
Query Match 1.6%; Score 7; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1301  
ID AAG80185 standard; peptide; 15 AA.  
DE Fusion construct human STAT3/CD4 linker peptide.  
PN WO200178785-A2.  
PD 25-OCT-2001.  
PA (BIOT-) BIOTECHTID GMBH.  
Query Match 1.6%; Score 7; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1302  
ID RAU99372 standard; peptide; 15 AA.  
DE Peptide linker, GLG, used to construct IFN beta single chain dimers.  
PN WO200236628-A2.  
PD 10-MAY-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 1.6%; Score 7; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1303  
ID ABG97612 standard; peptide; 15 AA.  
DE Apolipoprotein analogue 1 (Apo A1) associated spacer peptide #6.  
PN WO200236609-A2.  
PD 16-MAY-2002.  
PA (PROT-) PROTEOPHARMA APS.  
Query Match 1.6%; Score 7; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1304  
ID AAU11789 standard; peptide; 15 AA.  
DE Silk fibre forming region repeat unit.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO-) DU PONT DE NEMOURS & CO E I.  
Query Match 1.6%; Score 7; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1305  
ID ABU08677 standard; peptide; 15 AA.  
DE Human single chain MHC class I polypeptide associated linker #1.  
PN US2003003535-A1.  
PD 02-JAN-2003.  
PA (TECR-) TECHNION RES & DEV FOUND LTD.  
Query Match 1.6%; Score 7; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1306  
ID ABW00718 standard; peptide; 15 AA.  
DE Linker #2, peptide used in the invention.  
PN US2002168375-A1.  
PD 14-NOV-2002.  
PA (CHIR-) CHIRON CORP.  
Query Match 1.6%; Score 7; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1307  
ID ADN60232 standard; protein; 15 AA.  
DE Linker peptide.  
PN US6723517-B1.  
PD 20-APR-2004.  
PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.  
Query Match 1.6%; Score 7; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1308  
ID ADR40520 standard; protein; 15 AA.  
DE Spider silk dragline peptide formula #2.  
PN WO2004073644-A2.

PD 02-SEP-2004.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1309  
ID AUR38601 standard; peptide; 15 AA.  
DE Anti-botulinum neurotoxin antibody associated linker #3.  
PN US2004175385-A1.  
PD 09-SEP-2004.  
PA (REGC) UNIV CALIFORNIA.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 1310  
ID AAP50321 standard; protein; 17 AA.  
DE Spacer peptide between cytotoxic and target cell binding regions.  
PN WO8503508-A.  
PD 15-AUG-1985.  
PA (CETU) CETUS CORP.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1311  
ID AAP91928 standard; peptide; 17 AA.  
DE Spacer fragment.  
PN EP335476-A.  
PD 04-OCT-1989.  
PA (CETU) CETUS CORP.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1312  
ID AAY67939 standard; peptide; 17 AA.  
DE EPOA-hSA fusion protein peptide linker #2.  
PN WO9966054-A2.  
PD 23-DEC-1999.  
PA (GENZ) GENZYME TRANSGENICS CORP.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1313  
ID AAU68114 standard; peptide; 17 AA.  
DE Human Breast cancer-associated protein isoform, BPI-317 peptide #2.  
PN WO200171357-A2.  
PD 27-SEP-2001.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1314  
ID AAU68434 standard; peptide; 17 AA.  
DE Human Breast cancer-associated protein isoform, BPI-362 peptide #1.  
PN WO200171357-A2.  
PD 27-SEP-2001.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1315  
ID AAU68143 standard; peptide; 17 AA.  
DE Human Breast cancer-associated protein isoform, BPI-25 peptide #1.  
PN WO200171357-A2.  
PD 27-SEP-2001.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1316  
ID AAU68451 standard; peptide; 17 AA.  
DE Human Breast cancer-associated protein isoform, BPI-367 peptide #1.  
PN WO200171357-A2.  
PD 27-SEP-2001.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1317  
ID AAU68344 standard; peptide; 17 AA.  
DE Human Breast cancer-associated protein isoform, BPI-343 peptide #1.  
PN WO200171357-A2.  
PD 27-SEP-2001.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1318  
ID AAO17004 standard; peptide; 17 AA.  
DE Linker peptide used to construct alpha-MSH concatamer SEQ ID NO: 68.  
PN WO200206316-A2.  
PD 24-JAN-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1319  
ID ADB24918 standard; peptide; 17 AA.  
DE Peptide linker #4.  
PN US2003049801-A1.  
PD 13-MAR-2003.  
PA (WUCC) WU C.  
PA (LINR) LIN R.  
PA (HSUP) HSU P.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1320  
ID ADB24915 standard; peptide; 17 AA.  
DE Peptide linker #4.  
PN US2003049694-A1.  
PD 13-MAR-2003.  
PA (WUCC) WU C.  
PA (LINR) LIN R.  
PA (HSUP) HSU P.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1321  
ID ABU10017 standard; peptide; 17 AA.  
DE Alpha-MSH concatamer related linker peptide #5.  
PN US2002193332-A1.  
PD 13-DEC-2002.  
PA (HEDL) HEDLEY M L.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1322  
ID ADQ28276 standard; peptide; 17 AA.  
DE Peptide linker #4.  
PN US2004117863-A1.  
PD 17-JUN-2004.  
PA (EDGE) EDGE M D.  
PA (POLL) POLLOCK D.  
PA (SCHE) ECHELARD Y.  
PA (NEAD) MEADE H M.  
PA (RYBA) RYBAK S M.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 1323  
ID AAY71888 standard; peptide; 18 AA.  
DE Linker peptide #7, to construct human OPG-Fc fragment fusion protein.  
PN WO200118203-A1.  
PD 15-MAR-2001.  
PA (AMGE-) AMGEN INC.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
RESULT 1324  
ID AAW49208 standard; peptide; 19 AA.  
DE Human leucocyte antigen DQ4 binding peptide #99.  
PN JP08151396-A.  
PD 11-JUN-1996.  
PA (TEIJ) TEIJIN LTD.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
RESULT 1325  
ID ADH47607 standard; peptide; 20 AA.  
DE Human lung tumour clone peptide, SEQ ID NO 2088.  
PN WO2003037267-A2.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.

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Query Match      1.6%; Score 7; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
RESULT 1326
ID ADH47608 standard; peptide; 20 AA.
DE Human lung tumour clone peptide, SEQ ID NO 2089.
PN WO2003037267-A2.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match      1.6%; Score 7; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
RESULT 1327
ID ADJ21527 standard; peptide; 20 AA.
DE Human lung cancer-related L978P peptide fragment - SEQ ID 2089.
PN US2003211510-A1.
PD 13-NOV-2003.
PA (CORI-) CORIXA CORP.
Query Match      1.6%; Score 7; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
RESULT 1328
ID ADJ21526 standard; peptide; 20 AA.
DE Human lung cancer-related L978P peptide fragment - SEQ ID 2088.
PN US2003211510-A1.
PD 13-NOV-2003.
PA (CORI-) CORIXA CORP.
Query Match      1.6%; Score 7; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
RESULT 1329
ID AAW53348 standard; peptide; 21 AA.
DE Nephila clavipes spider silk protein tandem repeat unit SEQ ID NO:5.
PN US5728810-A.
PD 17-MAR-1998.
PA (UYWY-) UNIV WYOMING.
Query Match      1.6%; Score 7; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
RESULT 1330
ID AAY59072 standard; peptide; 21 AA.
DE N. clavipes spider silk protein repeat unit.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match      1.6%; Score 7; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
RESULT 1331
ID ADN37739 standard; peptide; 22 AA.
DE Soft segment found in a monomer unit of DP-1B SEQ ID NO:8.
PN WO2004035750-A2.
PD 29-APR-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match      1.6%; Score 7; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
RESULT 1332
ID AAY79554 standard; peptide; 23 AA.
DE Linker peptide used in single chain polypeptide binding molecule.
PN WO200023087-A1.
PD 27-APR-2000.
PA (SUNO-) SUNOL MOLECULAR CORP.
Query Match      1.6%; Score 7; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 1333
ID AAE36907 standard; peptide; 23 AA.
DE N. senegalensis major ampullate spidroin 1 (MaSp1) consensus peptide.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match      1.6%; Score 7; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 1334
ID AAY59101 standard; peptide; 25 AA.
DE N. clavipes spider silk protein 1 repeat fragment.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match      1.6%; Score 7; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1335
ID AAU8959 standard; peptide; 26 AA.
DE Insulin/insulin-like growth factor receptor-binding peptide #915.
PN WO200172771-A2.
PD 04-OCT-2001.
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA (NOVO) NOVO NORDISK AS.
Query Match      1.6%; Score 7; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1336
ID ADA03793 standard; peptide; 26 AA.
DE Insulin receptor (IR) related Formula 1 motif peptide SEQ ID NO:424.
PN WO2003027246-A2.
PD 03-APR-2003.
PA (NOVO) NOVO NORDISK AS.
PA (DGIB-) DGI BIOTECHNOLOGIES.
Query Match      1.6%; Score 7; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1337
ID ADH95006 standard; protein; 26 AA.
DE Insulin receptor motif polypeptide, SEQ ID NO 424.
PN WO2003070747-A2.
PD 28-AUG-2003.
PA (NOVO) NOVO NORDISK AS.
PA (DGIB-) DGI BIOTECHNOLOGIES.
Query Match      1.6%; Score 7; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1338
ID ADL67697 standard; peptide; 26 AA.
DE IGF-1R/IR binding peptide seq id 424.
PN US2004023887-A1.
PD 05-FEB-2004.
PA (PILL/) PILLUTLA R.
PA (DEDO/) DEDOVA O.
PA (BLUM/) BLUME A J.
PA (GOLD/) GOLDSTEIN N I.
PA (BRIS/) BRISSETTE R.
PA (WANG/) WANG P.
PA (LIUH/) LIU H.
PA (HSIA/) HSIAO K.
PA (LENN/) LENNICK M.
PA (FLET/) FLETCHER P.
Query Match      1.6%; Score 7; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1339
ID ADM37542 standard; peptide; 26 AA.
DE Anti-IR formula 1 motif peptide #280.
PN US2003236190-A1.
PD 25-DEC-2003.
PA (PILL/) PILLUTLA R.
PA (BRIS/) BRISSETTE R.
PA (BLUM/) BLUME A J.
PA (SCHA/) SCHAFFER L.
PA (BRAN/) BRANDT J.
PA (GOLD/) GOLDSTEIN N I.
PA (SPET/) SPETZLER J.
PA (OSTE/) OSTERGAARD S.
PA (HANS/) HANSEN P H.
Query Match      1.6%; Score 7; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1340
ID ADJ81392 standard; peptide; 27 AA.
DE Self-assembling polymer peptide #247.
PN WO2003056297-A2.
PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match      1.6%; Score 7; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 1341
ID ADJ81262 standard; peptide; 27 AA.
DE Self-assembling polymer peptide #117.
PN WO2003056297-A2.
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PD 10-JUL-2003.  
 PA (TUFT ) TUFTS COLLEGE.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 7; Length 27;  
 RESULT 1342  
 ID A0J81306 standard; peptide; 27 AA.  
 DE Self-assembling polymer peptide #161.  
 PN WO2003056297-A2.  
 PD 10-JUL-2003.  
 PA (TUFT ) TUFTS COLLEGE.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 7; Length 27;  
 RESULT 1343  
 ID A0J81168 standard; peptide; 27 AA.  
 DE Self-assembling polymer peptide #23.  
 PN WO2003056297-A2.  
 PD 10-JUL-2003.  
 PA (TUFT ) TUFTS COLLEGE.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 7; Length 27;  
 RESULT 1344  
 ID A0I15297 standard; peptide; 28 AA.  
 DE N clavipes spider silk consensus peptide #1.  
 PN WO2004044172-A2.  
 PD 27-MAY-2004.  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 8; Length 28;  
 RESULT 1345  
 ID ADR40519 standard; protein; 28 AA.  
 DE Spider silk dragline peptide formula #1.  
 PN WO2004073644-A2.  
 PD 02-SEP-2004.  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 8; Length 28;  
 RESULT 1346  
 ID AAU11792 standard; peptide; 29 AA.  
 DE Silk fibre forming region repeat monomer.  
 PN WO200190389-A2.  
 PD 29-NOV-2001.  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 5; Length 29;  
 RESULT 1347  
 ID AAY59111 standard; peptide; 30 AA.  
 DE N clavipes spider silk protein 1 repeat fragment.  
 PN US5989894-A.  
 PD 23-NOV-1999.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 3; Length 30;  
 RESULT 1348  
 ID AAY59124 standard; peptide; 30 AA.  
 DE N clavipes spider silk protein 1 repeat fragment.  
 PN US5989894-A.  
 PD 23-NOV-1999.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 3; Length 30;  
 RESULT 1349  
 ID AAY59123 standard; peptide; 30 AA.  
 DE N clavipes spider silk protein 1 repeat fragment.  
 PN US5989894-A.  
 PD 23-NOV-1999.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 3; Length 30;  
 RESULT 1350  
 ID AAB15670 standard; peptide; 31 AA.  
 DE Alpha.v beta 3 receptor-specific peptide.  
 PN WO200403783-A2.  
 PD 27-JUL-2000.

PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 3; Length 31;  
 RESULT 1351  
 ID AAO22543 standard; peptide; 31 AA.  
 DE GRGDS-containing peptide.  
 PN WO200239999-A2.  
 PD 23-MAY-2002.  
 PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 5; Length 31;  
 RESULT 1352  
 ID ABP97039 standard; peptide; 31 AA.  
 DE Vitronectin derived GRGDS motif peptide #2.  
 PN WO2003020280-A2.  
 PD 13-MAR-2003.  
 PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 6; Length 31;  
 RESULT 1353  
 ID ADN60233 standard; protein; 31 AA.  
 DE Minimal activation motif-1X-Linker-1X peptide.  
 PN US6723517-B1.  
 PD 20-APR-2004.  
 PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 8; Length 31;  
 RESULT 1354  
 ID ADO57972 standard; peptide; 31 AA.  
 DE MHC multimer linker peptide SEQ ID 7.  
 PN DE10247014-A1.  
 PD 22-APR-2004.  
 PA (ERFL/) ERFLE V.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 8; Length 31;  
 RESULT 1355  
 ID AAY59107 standard; peptide; 32 AA.  
 DE N clavipes spider silk protein 1 repeat fragment.  
 PN US5989894-A.  
 PD 23-NOV-1999.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 3; Length 32;  
 RESULT 1356  
 ID AAW53350 standard; peptide; 33 AA.  
 DE Nephila clavipes spider silk protein tandem repeat unit SEQ ID NO.7.  
 PN US5728810-A.  
 PD 17-MAR-1998.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 2; Length 33;  
 RESULT 1357  
 ID AAY59074 standard; peptide; 33 AA.  
 DE N clavipes spider silk protein repeat unit.  
 PN US5989894-A.  
 PD 23-NOV-1999.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 3; Length 33;  
 RESULT 1358  
 ID AAE18322 standard; peptide; 33 AA.  
 DE Spider silk protein monomer sequence used to construct NcDS.24.  
 PN WO200200016-A1.  
 PD 03-JAN-2002.  
 PA (LUMI-) LUMINIS PTY LTD.  
 Query Match  
 Best Local Similarity 1.6%; Score 7; DB 5; Length 33;  
 RESULT 1359  
 ID AAE36905 standard; peptide; 33 AA.  
 DE Nephila clavipes major ampullate spidroin 1 (Maspl) consensus peptide.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.

Query Match 1.6%; Score 7; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
RESULT 1369  
ID AAU09054 standard; peptide; 34 AA.  
DE Silk spider spidroin 1 34 amino acid long repeat motif.  
PN WO200156626-A1.  
PD 09-AUG-2001.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 1.6%; Score 7; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
RESULT 1370  
ID ABP56042 standard; peptide; 34 AA.  
DE Proopiomelanocortin related sequence SEQ ID NO:12.  
PN WO200256022-A2.  
PD 18-JUL-2002.  
PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.  
Query Match 1.6%; Score 7; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
RESULT 1371  
ID AAU11788 standard; peptide; 34 AA.  
DE Silk fibre forming region repeat consensus sequence.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO-) DU PONT DE NEMOURS & CO E I.  
Query Match 1.6%; Score 7; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
RESULT 1372  
ID ADB61295 standard; peptide; 34 AA.  
DE Dragline silk protein, Nephila spidroin I (MaSp 1) peptide region  
PN WO2003060099-A2.  
PD 24-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
PA (ALWA-) ALWATTARI A.  
Query Match 1.6%; Score 7; DB 7; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
RESULT 1373  
ID ADC35267 standard; peptide; 34 AA.  
DE Silk protein motif, SEQ ID 28.  
PN WO2003057727-A1.  
PD 17-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 1.6%; Score 7; DB 7; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
RESULT 1374  
ID ADJ81402 standard; peptide; 34 AA.  
DE Self-assembling polymer peptide #257.  
PN WO2003056297-A2.  
PD 10-JUL-2003.  
PA (TUFT-) TUFTS COLLEGE.  
Query Match 1.6%; Score 7; DB 7; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
RESULT 1375  
ID ADJ81272 standard; peptide; 34 AA.  
DE Self-assembling polymer peptide #127.  
PN WO2003056297-A2.  
PD 10-JUL-2003.  
PA (TUFT-) TUFTS COLLEGE.  
Query Match 1.6%; Score 7; DB 7; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
RESULT 1376  
ID ADM46123 standard; peptide; 34 AA.  
DE Nephila clavipes spidroin 1 (MaSp1) repeat motif peptide.  
PN WO2003057720-A2.  
PD 17-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 1.6%; Score 7; DB 7; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
RESULT 1377  
ID ADN37738 standard; peptide; 34 AA.  
DE Monomer unit of DP-1B conserved consensus motif SEQ ID NO:7.  
PN WO2004035750-A2.  
PD 29-APR-2004.  
PA (DUPO-) DU PONT DE NEMOURS & CO E I.

Query Match 1.6%; Score 7; DB 8; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
RESULT 1378  
ID AAR10318 standard; protein; 36 AA.  
DE Bovine BMP - exon 4.  
PN EP409472-A.  
PD 23-JAN-1991.  
PA (CHIR-) CHIRON CORP.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
RESULT 1379  
ID AAU79502 standard; peptide; 38 AA.  
DE Fragment for resistance against dehydration stress, peptide #1.  
PN WO200226800-A1.  
PD 04-APR-2002.  
PA (SEIR-) SEIREN CO LTD.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 5; Length 38;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 1380  
ID ABP60376 standard; peptide; 38 AA.  
DE Sericin derived peptide SEQ ID NO 1.  
PN WO200286133-A1.  
PD 31-OCT-2002.  
PA (SEIR-) SEIREN CO LTD.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 6; Length 38;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 1381  
ID AAM20105 standard; protein; 42 AA.  
DE Peptide #6539 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1382  
ID ABB40301 standard; peptide; 42 AA.  
DE Peptide #7807 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1383  
ID AAM33987 standard; protein; 42 AA.  
DE Peptide #8024 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1384  
ID AAB67213 standard; peptide; 42 AA.  
DE HER2 peptide ligand #2.  
PN WO200102440-A1.  
PD 11-JAN-2001.  
PA (GETH-) GENENTECH INC.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1385  
ID ABB24705 standard; protein; 42 AA.  
DE Protein #6704 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1386  
ID AAM73800 standard; protein; 42 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34106.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1387  
ID AAM61095 standard; protein; 42 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33200.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1388  
ID AAG55548 standard; peptide; 42 AA.  
DE Human liver peptide, SEQ ID NO 34196.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1389  
ID ABG43687 standard; peptide; 42 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 33352.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 5; Length 42;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1390  
ID AAM86005 standard; protein; 43 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:13598.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 43;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
RESULT 1391  
ID ABB70984 standard; protein; 44 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39744.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 4; Length 44;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 1392  
ID ABO57991 standard; protein; 47 AA.  
DE Human genome derived single exon protein #4225.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 8; Length 47;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
RESULT 1393  
ID AAR65749 standard; peptide; 49 AA.  
DE Linker sequence used in IL-3 containing fusion protein.  
PN WO9521254-A1.  
PD 10-AUG-1995.  
PA (SEAR-) SEARLE & CO G D.  
Query Match  
Best Local Similarity 1.6%; Score 7; DB 2; Length 49;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 1394  
ID AAE14027 standard; protein; 49 AA.  
DE Chemically modified myelopietin (MPO) conjugate related protein #16.  
PN WO200176639-A2.  
PD 18-OCT-2001.  
PA (PHAA-) PHARMACIA CORP.  
PA (FINN/) FINN R.  
PA (GOKA/) GOKARN Y.  
PA (HILL/) HILLS R.  
PA (NICA/) NICASTRO P.  
PA (QIHH/) QI H.  
PA (SEDO/) SEDO K.  
PA (SIEG/) SIEGEL N.  
PA (WALT/) WALTER S.

Query Match 1.6%; Score 7; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 1395  
ID ABG97800 standard; peptide; 49 AA.  
DE Human interleukin-3 associated protein #11.  
PN US6436387-B1.  
PD 20-AUG-2002.  
PA (SEAR) SEARLE & CO G D.  
Query Match 1.6%; Score 7; DB 5; Length 49;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 1396  
ID ADJ14406 standard; protein; 49 AA.  
DE Protein related to human interleukin-3 (IL-3) mutant protein SEQ ID 169.  
PN US2003185790-A1.  
PD 02-OCT-2003.  
PA (BAUE) BAUER S C.  
PA (ABRA) ABRAMS M A.  
PA (BRA) BRAFORD-GOLDBERG S R.  
PA (CAPA) CAPARON M H.  
PA (EAST) EASTON A M.  
PA (KLEI) KLEIN B K.  
PA (MCKE) MCKEARN J P.  
PA (OLIN) OLINS P O.  
PA (PAIK) PAIK K.  
PA (THOM) THOMAS J W.  
Query Match 1.6%; Score 7; DB 8; Length 49;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 1397  
ID ABB23488 standard; protein; 50 AA.  
DE Protein #5487 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 03-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
RESULT 1398  
ID AAM58929 standard; protein; 50 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31034.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
RESULT 1399  
ID AAU54145 standard; protein; 54 AA.  
DE Propionibacterium acnes immunogenic protein #15041.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 7; DB 4; Length 54;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
RESULT 1400  
ID ABM50664 standard; protein; 54 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #15340.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 7; DB 6; Length 54;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
RESULT 1401  
ID AAU82104 standard; peptide; 56 AA.  
DE T-cell specific binding ligand peptide construct #38.  
PN WO200189286-A2.  
PD 29-NOV-2001.  
PA (CELS-) CEL-SCI CORP.  
Query Match 1.6%; Score 7; DB 5; Length 56;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
RESULT 1402  
ID AAU82108 standard; peptide; 58 AA.  
DE T-cell specific binding ligand peptide construct #42.  
PN WO200189286-A2.  
PD 29-NOV-2001.  
PA (CELS-) CEL-SCI CORP.

Query Match 1.6%; Score 7; DB 5; Length 58;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
RESULT 1403  
ID AAR65750 standard; peptide; 60 AA.  
DE Linker sequence used in IL-3 containing fusion protein.  
PN WO9521254-A1.  
PD 10-AUG-1995.  
PA (SEAR) SEARLE & CO G D.  
Query Match 1.6%; Score 7; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1404  
ID AAE14028 standard; protein; 60 AA.  
DE Chemically modified myelopoietin (MPO) conjugate related protein #17.  
PN WO200176639-A2.  
PD 18-OCT-2001.  
PA (PHAA) PHARMACIA CORP.  
PA (FINN) FINN R.  
PA (GOKA) GOKARN Y.  
PA (HILL) HILLS R.  
PA (NICA) NICASTRO P.  
PA (QIHH) QI H.  
PA (SEDO) SEDO K.  
PA (SIEG) SIEGEL N.  
PA (WALT) WALTER S.  
Query Match 1.6%; Score 7; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1405  
ID ABG97801 standard; peptide; 60 AA.  
DE Human interleukin-3 associated protein #12.  
PN US6436387-B1.  
PD 20-AUG-2002.  
PA (SEAR) SEARLE & CO G D.  
Query Match 1.6%; Score 7; DB 5; Length 60;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1406  
ID ADJ14407 standard; protein; 60 AA.  
DE Protein related to human interleukin-3 (IL-3) mutant protein SEQ ID 170.  
PN US2003185790-A1.  
PD 02-OCT-2003.  
PA (BAUE) BAUER S C.  
PA (ABRA) ABRAMS M A.  
PA (BRA) BRAFORD-GOLDBERG S R.  
PA (CAPA) CAPARON M H.  
PA (EAST) EASTON A M.  
PA (KLEI) KLEIN B K.  
PA (MCKE) MCKEARN J P.  
PA (OLIN) OLINS P O.  
PA (PAIK) PAIK K.  
PA (THOM) THOMAS J W.  
Query Match 1.6%; Score 7; DB 8; Length 60;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1407  
ID AAM17952 standard; protein; 61 AA.  
DE Peptide #4386 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 61;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1408  
ID ABB36983 standard; peptide; 61 AA.  
DE Peptide #4489 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 61;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1409  
ID AAM70123 standard; protein; 61 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30429.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.6%; Score 7; DB 4; Length 61;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1410  
ID AAM57714 standard; protein; 61 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29819.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 61;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1411  
ID AAM05593 standard; protein; 61 AA.  
DE Peptide #4275 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 61;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1412  
ID ABP35879 standard; protein; 65 AA.  
DE CTRB BOVIN positions predicted to confer specificity.  
PN EPI056411-A2.  
PD 02-MAY-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match 1.6%; Score 7; DB 4; Length 65;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1413  
ID ABP35882 standard; protein; 65 AA.  
DE CTRA BOVIN positions predicted to confer specificity.  
PN EPI056411-A2.  
PD 02-MAY-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match 1.6%; Score 7; DB 4; Length 65;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1414  
ID ABB71482 standard; protein; 67 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 41238.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.6%; Score 7; DB 4; Length 67;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
RESULT 1415  
ID AAM90305 standard; protein; 67 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:17898.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 7; DB 4; Length 67;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
RESULT 1416  
ID AAU49753 standard; protein; 68 AA.  
DE Propionibacterium acnes immunogenic protein #10649.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 7; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 1417  
ID ABM46272 standard; protein; 68 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #10948.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 7; DB 6; Length 68;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 1418  
ID AAM15299 standard; protein; 69 AA.  
DE Peptide #1733 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 1419  
ID ABB34296 standard; peptide; 69 AA.  
DE Peptide #1802 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 1420  
ID AAM27771 standard; protein; 69 AA.  
DE Peptide #1808 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 1421  
ID ABB29135 standard; peptide; 69 AA.  
DE Peptide #1786 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 1422  
ID ABB19723 standard; protein; 69 AA.  
DE Protein #1722 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 1423  
ID AAM67483 standard; protein; 69 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 27789.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 1424  
ID AAM5090 standard; protein; 69 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27195.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 1425  
ID ASG49131 standard; peptide; 69 AA.  
DE Human liver peptide, SEQ ID NO 27779.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 1426  
ID AAM03053 standard; protein; 69 AA.  
DE Peptide #1735 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.6%; Score 7; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 1427  
ID AAG77385 standard; protein; 71 AA.  
DE Human colon cancer antigen protein SEQ ID NO:8151.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.

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Query Match      1.6%; Score 7; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
RESULT 1428
ID AAM83108 standard; protein; 71 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:10701.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      1.6%; Score 7; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
RESULT 1429
ID RAU22890 standard; protein; 73 AA.
DE Human prostate cancer antigen, Seq ID No 409.
PN WO200155316-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      1.6%; Score 7; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1430
ID ABP08745 standard; protein; 73 AA.
DE Human ORFX protein sequence SEQ ID NO:17472.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match      1.6%; Score 7; DB 5; Length 73;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1431
ID ADJ09463 standard; protein; 73 AA.
DE Human prostate cancer associated polypeptide SegID409.
PN US2003054373-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      1.6%; Score 7; DB 7; Length 73;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1432
ID ABM81841 standard; protein; 75 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82696, SEQ:4740.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match      1.6%; Score 7; DB 8; Length 75;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1433
ID AAU79903 standard; protein; 76 AA.
DE Fragment for resistance against dehydration stress, protein #1.
PN WO200226800-A1.
PD 04-APR-2002.
PA (SEIR-) SEIREN CO LTD.
Query Match      1.6%; Score 7; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1434
ID ABP60378 standard; peptide; 76 AA.
DE Sericin derived peptide SEQ ID NO 4.
PN WO200286133-A1.
PD 31-OCT-2002.
PA (SEIR-) SEIREN CO LTD.
Query Match      1.6%; Score 7; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1435
ID AAG57943 standard; protein; 77 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 74738.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match      1.6%; Score 7; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 1436
ID ABT18385 standard; protein; 80 AA.
DE Breast specific related amino acid sequence SEQ ID No 194.
PN WO200277232-A2.
PD 03-OCT-2002.
PA (DIAD-) DIADEXUS INC.
Query Match      1.6%; Score 7; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Query Match      1.6%; Score 7; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 1437
ID RAU53680 standard; protein; 81 AA.
DE Propionibacterium acnes immunogenic protein #14576.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match      1.6%; Score 7; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 1438
ID ABM50199 standard; protein; 81 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14875.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match      1.6%; Score 7; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 1439
ID AAM92148 standard; protein; 82 AA.
DE Human digestive system antigen SEQ ID NO: 1497.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      1.6%; Score 7; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1440
ID ADA57125 standard; protein; 82 AA.
DE Human secreted protein #408.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      1.6%; Score 7; DB 6; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1441
ID ADA40986 standard; protein; 82 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      1.6%; Score 7; DB 6; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1442
ID ABR47868 standard; protein; 82 AA.
DE Human secreted protein, SEQ ID 759.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      1.6%; Score 7; DB 6; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1443
ID AAB38342 standard; protein; 83 AA.
DE Human secreted protein encoded by gene 22 clone, HOFNY91.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      1.6%; Score 7; DB 3; Length 83;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1444
ID AAU43383 standard; protein; 84 AA.
DE Propionibacterium acnes immunogenic protein #4279.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match      1.6%; Score 7; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
RESULT 1445
ID ABM39902 standard; protein; 84 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4578.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match      1.6%; Score 7; DB 6; Length 84;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
RESULT 1446
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ID AAU47347 standard; protein; 86 AA.  
DE Propionibacterium acnes immunogenic protein #8243.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 4; Length 86;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 1447  
ID ABM43866 standard; protein; 86 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #8542.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 6; Length 86;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 1448  
ID AAG59693 standard; protein; 87 AA.  
DE Zsa zsa protein fragment SEQ ID NO: 77238.  
PN EF1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 1449  
ID AAU42282 standard; protein; 87 AA.  
DE Propionibacterium acnes immunogenic protein #3178.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 4; Length 87;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 1450  
ID ABM38801 standard; protein; 87 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #3477.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 6; Length 87;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 1451  
ID AAU41961 standard; protein; 88 AA.  
DE Propionibacterium acnes immunogenic protein #2857.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 4; Length 88;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1452  
ID ABP04934 standard; protein; 88 AA.  
DE Human ORFX protein sequence SEQ ID NO: 9850.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP. 1.6%; Score 7; DB 5; Length 88;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1453  
ID ABM38480 standard; protein; 88 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #3156.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 6; Length 88;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1454  
ID ABP63999 standard; protein; 91 AA.  
DE Human ORF369.  
PN US2002082206-A1.  
PD 27-JUN-2002.  
PA (LEAC/) LEACH M D.  
PA (MEHR/) MEHRABAN F.  
PA (CONL/) CONLEY P B.  
PA (TOPP/) TOPPER J N.  
PA (LAWD/) LAW D.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1455  
ID AAU17791 standard; protein; 92 AA.  
DE Novel human respiratory antigen #107.  
PN WO200155448-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC. 1.6%; Score 7; DB 4; Length 92;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
RESULT 1456  
ID AAU79904 standard; protein; 92 AA.  
DE Fragment for resistance against dehydration stress, protein #2.  
PN WO200226800-A1.  
PD 04-APR-2002.  
PA (SEIR-) SEIREN CO LTD. 1.6%; Score 7; DB 5; Length 92;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
RESULT 1457  
ID ADG41171 standard; protein; 92 AA.  
DE Human respiratory system associated protein seq id 409.  
PN US2003215893-A1.  
PD 20-NOV-2003.  
PA (HUMA-) HUMAN GENOME SCI INC. 1.8%; Score 7; DB 7; Length 92;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
RESULT 1458  
ID ADI96945 standard; protein; 92 AA.  
DE Human respiratory system associated polypeptide SeqID409.  
PN US2003077704-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC. 1.6%; Score 7; DB 7; Length 92;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
RESULT 1459  
ID AAU51144 standard; protein; 94 AA.  
DE Propionibacterium acnes immunogenic protein #12040.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 4; Length 94;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1460  
ID ABP01010 standard; protein; 94 AA.  
DE Human ORFX protein sequence SEQ ID NO: 2002.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP. 1.6%; Score 7; DB 5; Length 94;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1461  
ID ABM47663 standard; protein; 94 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #12339.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 6; Length 94;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1462  
ID AAB82467 standard; protein; 96 AA.  
DE Mouse PAR-3 exodomain region of GPAR4.  
PN WO200144496-A2.  
PD 21-JUN-2001.  
PA (NOVS) NOVARTIS RES FOUND. 1.6%; Score 7; DB 4; Length 96;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
RESULT 1463  
ID AAU09714 standard; protein; 96 AA.  
DE Polymorphic variant #1 of human SCV1 protein.  
PN WO200179236-A2.  
PD 25-OCT-2001.  
PA (GENA-) GENAISANCE PHARM INC. 1.6%; Score 7; DB 5; Length 96;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;





DE Dragline protein 1 analogue DP-1A.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (HUMA-) DU PONT DE NEMOURS & CO E I.  
Query Match 1.6%; Score 7; DB 5; Length 101;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1483  
ID ADN37737 standard; protein; 101 AA.  
DE Monomer unit of DP-1B SLP amino acid sequence SEQ ID NO:6.  
PN WO2004035750-A2.  
PD 29-APR-2004.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.6%; Score 7; DB 8; Length 101;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1484  
ID ADN37734 standard; protein; 101 AA.  
DE Spider silk-like protein SEQ ID NO:3.  
PN WO2004035750-A2.  
PD 29-APR-2004.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.6%; Score 7; DB 8; Length 101;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1485  
ID ADO15295 standard; protein; 101 AA.  
DE N clavipes spider silk DP-1B6 analogue protein SeqID3.  
PN WO2004044172-A2.  
PD 27-MAY-2004.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.6%; Score 7; DB 8; Length 101;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1486  
ID ADO15294 standard; protein; 101 AA.  
DE N clavipes spider silk DP-1B9 analogue protein SeqID2.  
PN WO2004044172-A2.  
PD 27-MAY-2004.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.6%; Score 7; DB 8; Length 101;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1487  
ID ADO15293 standard; protein; 101 AA.  
DE N clavipes spider silk DP1A analogue protein SeqID1.  
PN WO2004044172-A2.  
PD 27-MAY-2004.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.6%; Score 7; DB 8; Length 101;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1488  
ID ADR40516 standard; protein; 101 AA.  
DE Monomer of spider silk DP-1B.9 analog protein.  
PN WO2004073644-A2.  
PD 02-SEP-2004.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.6%; Score 7; DB 8; Length 101;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1489  
ID ADR40515 standard; protein; 101 AA.  
DE Monomer of spider silk DP-1A analog protein.  
PN WO2004073644-A2.  
PD 02-SEP-2004.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.6%; Score 7; DB 8; Length 101;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1490  
ID ADR40517 standard; protein; 101 AA.  
DE Monomer of spider silk DP-1B.16 analog protein.  
PN WO2004073644-A2.  
PD 02-SEP-2004.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.6%; Score 7; DB 8; Length 101;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 1491  
ID AAM84388 standard; protein; 102 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:11981.

PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 7; DB 4; Length 102;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 1492  
ID AAG11758 standard; protein; 103 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10600.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
PA (HELI-) HELIX RES INST.  
Query Match 1.6%; Score 7; DB 3; Length 103;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 1493  
ID AAB94623 standard; protein; 103 AA.  
DE Human protein sequence SEQ ID NO:15479.  
PN EPI074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 1.6%; Score 7; DB 4; Length 103;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 1494  
ID ADM07515 standard; protein; 105 AA.  
DE Canine immunoglobulin lambda variable domain protein 19.  
PN WO2003060080-A2.  
PD 24-JUL-2003.  
PA (IDEX-) IDEXX LAB INC.  
Query Match 1.6%; Score 7; DB 7; Length 105;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
RESULT 1495  
ID AAM86228 standard; protein; 106 AA.  
DE Poxvirus ORF-1 truncated fragment 3.  
PN WO9849300-A2.  
PD 05-NOV-1998.  
PA (COLL-) COLLATERAL THERAPEUTICS  
Query Match 1.6%; Score 7; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
RESULT 1496  
ID ADK98991 standard; protein; 106 AA.  
DE S agalactiae SAG1473 (cell wall surface anchor family)-related protein 4.  
PN WO2004018646-A2.  
PD 04-MAR-2004.  
PA (CHIR) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 1.6%; Score 7; DB 8; Length 106;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
RESULT 1497  
ID AAM92113 standard; protein; 107 AA.  
DE Human digestive system antigen SEQ ID NO: 1462.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 7; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
RESULT 1498  
ID ABB76673 standard; protein; 107 AA.  
DE Protein related to Bombyx mori silk fibroin.  
PN WO200240528-A1.  
PD 23-MAY-2002.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match 1.6%; Score 7; DB 5; Length 107;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
RESULT 1499  
ID ADJ81412 standard; peptide; 109 AA.  
DE Self-assembling polymer peptide #267.  
PN WO2003056297-A2.  
PD 10-JUL-2003.  
PA (TUFT) TUFTS COLLEGE.  
Query Match 1.6%; Score 7; DB 7; Length 109;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
RESULT 1500  
ID ADJ81177 standard; peptide; 109 AA.  
DE Self-assembling polymer peptide #32.  
PN WO2003056297-A2.

PD 10-JUL-2003.  
PA (TUFT ) TUFTS COLLEGE.  
Query Match 1.6%; Score 7; DB 7; Length 109;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 7, 2005, 00:25:38 ; Search time 44 Seconds  
(without alignments)  
746.491 Million cell updates/sec

Title: US-10-063-561-52

Perfect score: 440

Sequence: 1 MKPQGPLACLLALCLGSGE.....KLGFINWDINKQRRSRIP 440

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
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- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	19.5	230	4	US-09-673-395A-256
2	25	5.7	72	4	US-09-513-999C-5563
3	25	5.7	72	4	US-09-513-999C-5564
4	14	3.2	250	4	US-09-248-796A-22487
5	12	2.7	80	4	US-09-248-796A-23892
6	11	2.5	663	4	US-09-949-016-7198
7	10	2.3	180	4	US-09-248-796A-22352
8	10	2.3	214	4	US-09-949-016-9109
9	10	2.3	441	4	US-09-949-016-6315
10	10	2.3	541	4	US-09-248-796A-26119
11	9	2.0	60	4	US-09-134-000C-6510
12	9	2.0	184	4	US-09-107-532A-5997
13	9	2.0	406	4	US-09-248-796A-14345
14	9	2.0	512	4	US-09-270-767-43154
15	9	2.0	529	4	US-09-381-656-1
16	9	2.0	607	4	US-09-328-352-6716
17	9	2.0	714	4	US-09-949-016-11158
18	9	2.0	1306	4	US-09-538-092-330
19	9	2.0	1712	4	US-09-949-016-9450
20	8	1.8	28	1	US-08-425-069-50
21	8	1.8	28	2	US-08-317-844B-50
22	8	1.8	30	1	US-08-425-069-58
23	8	1.8	30	2	US-08-317-844B-58
24	8	1.8	31	1	US-08-425-069-46
25	8	1.8	31	2	US-08-317-844B-46
26	8	1.8	62	3	US-09-247-155-127
27	8	1.8	67	4	US-09-583-110-3048
					Sequence 256, App
					Sequence 5563, App
					Sequence 5564, App
					Sequence 22487, A
					Sequence 23892, A
					Sequence 7198, App
					Sequence 22352, A
					Sequence 9109, App
					Sequence 6315, App
					Sequence 26119, A
					Sequence 6510, App
					Sequence 5997, App
					Sequence 14345, A
					Sequence 43154, A
					Sequence 11158, A
					Sequence 330, App
					Sequence 9450, App
					Sequence 50, Appl
					Sequence 58, Appl
					Sequence 58, Appl
					Sequence 46, Appl
					Sequence 46, Appl
					Sequence 127, App
					Sequence 3048, App

Sequence 3523, Ap  
Sequence 7096, Ap  
Sequence 7639, Ap  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 56847, A  
Sequence 61204, A  
Sequence 43682, A  
Sequence 45749, A  
Sequence 37829, A  
Sequence 53046, A  
Sequence 14281, A  
Sequence 7209, Ap  
Sequence 44311, A  
Sequence 2, Appli  
Sequence 41613, A  
Sequence 45683, A  
Sequence 937, App  
Sequence 10, Appl  
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Sequence 4282, A  
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Sequence 55, Appl  
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Sequence 25818, A  
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Sequence 37, Appl  
Sequence 37, Appl  
Sequence 17, Appl  
Sequence 37, Appl  
Sequence 37, Appl

101	8	1.8	816	4	US-09-376-165-37	Sequence 37, Appl	174	7	1.6	60	3	US-08-468-609A-195	Sequence 195, App
102	8	1.8	928	4	US-08-535-872A-1	Sequence 1, Appli	175	7	1.6	60	3	US-08-446-872A-195	Sequence 195, App
103	8	1.8	928	4	US-09-636-077A-1	Sequence 1, Appli	176	7	1.6	60	4	US-08-762-227A-195	Sequence 195, App
104	8	1.8	928	4	US-09-636-060C-1	Sequence 1, Appli	177	7	1.6	60	5	PCT-US95-01185-195	Sequence 195, App
105	8	1.8	928	4	US-09-386-552-1	Sequence 1, Appli	178	7	1.6	64	4	US-09-270-767-37216	Sequence 37216, A
106	8	1.8	928	4	US-09-636-596C-1	Sequence 1, Appli	179	7	1.6	64	4	US-09-270-767-52433	Sequence 52433, A
107	8	1.8	928	4	US-10-023-894-4	Sequence 4, Appli	180	7	1.6	79	4	US-09-270-767-37592	Sequence 37592, A
108	8	1.8	928	4	US-10-306-686-1	Sequence 1, Appli	181	7	1.6	79	4	US-09-270-767-52809	Sequence 52809, A
109	8	1.8	1141	1	US-08-131-365B-54	Sequence 54, Appl	182	7	1.6	100	4	US-09-411-067C-5	Sequence 5, Appli
110	8	1.8	1141	2	US-08-668-123-54	Sequence 54, Appl	183	7	1.6	101	3	US-08-556-978B-20	Sequence 20, Appl
111	8	1.8	1199	4	US-10-023-894-2	Sequence 2, Appli	184	7	1.6	101	3	US-08-556-978B-22	Sequence 22, Appl
112	8	1.8	1233	4	US-09-645-456A-35	Sequence 35, Appl	185	7	1.6	101	3	US-08-556-978B-62	Sequence 62, Appl
113	8	1.8	1233	4	US-09-425-324A-35	Sequence 35, Appl	186	7	1.6	101	3	US-09-247-806-3	Sequence 3, Appli
114	8	1.8	1233	4	US-08-845-791-35	Sequence 35, Appl	187	7	1.6	101	3	US-09-247-806-5	Sequence 5, Appli
115	8	1.8	1233	4	US-09-688-188B-89	Sequence 89, Appl	188	7	1.6	101	3	US-09-247-806-7	Sequence 7, Appli
116	8	1.8	1233	4	US-09-291-417D-89	Sequence 89, Appl	189	7	1.6	101	3	US-09-863-859-10	Sequence 10, Appl
117	8	1.8	1239	4	US-09-688-188B-13	Sequence 13, Appl	190	7	1.6	101	4	US-09-863-859-11	Sequence 11, Appl
118	8	1.8	1239	4	US-09-291-417D-13	Sequence 13, Appl	191	7	1.6	102	4	US-09-248-796A-27799	Sequence 27799, A
119	8	1.8	1349	3	US-08-938-291A-6	Sequence 6, Appli	192	7	1.6	118	4	US-09-513-999C-4979	Sequence 4979, Ap
120	8	1.8	1349	4	US-09-589-619-6	Sequence 6, Appli	193	7	1.6	121	4	US-09-539-333D-41	Sequence 41, Appl
121	8	1.8	1744	4	US-09-438-185A-542	Sequence 542, App	194	7	1.6	124	4	US-09-621-976-5096	Sequence 5096, Ap
122	8	1.8	2142	4	US-09-538-092-1142	Sequence 1142, Ap	195	7	1.6	126	4	US-09-621-976-4117	Sequence 4117, Ap
123	7	1.6	13	1	US-08-257-341-1	Sequence 1, Appli	196	7	1.6	127	4	US-09-621-976-5097	Sequence 5097, Ap
124	7	1.6	13	1	US-08-425-069-39	Sequence 39, Appl	197	7	1.6	133	4	US-09-431-888-2	Sequence 2, Appli
125	7	1.6	13	2	US-08-317-844B-39	Sequence 39, Appl	198	7	1.6	139	4	US-09-270-767-36667	Sequence 36667, A
126	7	1.6	15	1	US-08-133-804-8	Sequence 8, Appli	199	7	1.6	139	4	US-09-270-767-51884	Sequence 51884, A
127	7	1.6	15	1	US-08-425-069-13	Sequence 13, Appl	200	7	1.6	139	4	US-09-248-796A-15962	Sequence 15962, A
128	7	1.6	15	1	US-08-461-838-8	Sequence 8, Appli	201	7	1.6	142	4	US-09-270-767-60758	Sequence 60758, A
129	7	1.6	15	2	US-08-461-386-8	Sequence 8, Appli	202	7	1.6	145	4	US-09-621-976-4037	Sequence 4037, Ap
130	7	1.6	15	2	US-08-356-786-12	Sequence 12, Appl	203	7	1.6	149	3	US-08-808-599A-40	Sequence 40, Appl
131	7	1.6	15	2	US-08-665-202-3	Sequence 3, Appli	204	7	1.6	151	4	US-09-270-767-37869	Sequence 37869, A
132	7	1.6	15	2	US-08-317-844B-13	Sequence 13, Appl	205	7	1.6	151	4	US-09-270-767-53086	Sequence 53086, A
133	7	1.6	15	3	US-08-483-749A-31	Sequence 31, Appl	206	7	1.6	152	4	US-09-270-767-35204	Sequence 35204, A
134	7	1.6	15	3	US-08-556-978B-2	Sequence 2, Appli	207	7	1.6	152	4	US-09-270-767-50421	Sequence 50421, A
135	7	1.6	15	4	US-09-315-574-3	Sequence 3, Appli	208	7	1.6	155	3	US-09-315-794-12	Sequence 12, Appl
136	7	1.6	15	4	US-09-863-859-9	Sequence 9, Appli	209	7	1.6	155	3	US-09-389-341-12	Sequence 12, Appl
137	7	1.6	15	4	US-09-324-258-18	Sequence 18, Appl	210	7	1.6	157	4	US-09-270-767-34016	Sequence 34016, A
138	7	1.6	17	4	US-09-333-213-4	Sequence 4, Appli	211	7	1.6	157	4	US-09-270-767-49233	Sequence 49233, A
139	7	1.6	17	4	US-10-077-210-4	Sequence 4, Appli	212	7	1.6	159	3	US-09-027-449-53	Sequence 53, Appl
140	7	1.6	21	1	US-08-425-069-5	Sequence 5, Appli	213	7	1.6	159	3	US-08-804-444A-53	Sequence 53, Appl
141	7	1.6	21	2	US-08-317-844B-5	Sequence 5, Appli	214	7	1.6	159	3	US-09-026-985-53	Sequence 53, Appl
142	7	1.6	23	4	US-09-422-375-4	Sequence 4, Appli	215	7	1.6	159	4	US-09-121-952A-53	Sequence 53, Appl
143	7	1.6	25	1	US-08-425-069-38	Sequence 38, Appl	216	7	1.6	163	3	US-09-234-340A-53	Sequence 53, Appl
144	7	1.6	25	2	US-08-317-844B-38	Sequence 38, Appl	217	7	1.6	163	3	US-09-025-769B-282	Sequence 282, App
145	7	1.6	29	4	US-09-863-859-12	Sequence 12, Appl	218	7	1.6	163	4	US-09-490-070A-282	Sequence 282, App
146	7	1.6	30	1	US-08-425-069-48	Sequence 48, Appl	219	7	1.6	163	4	US-09-490-153-282	Sequence 282, App
147	7	1.6	30	1	US-08-425-069-60	Sequence 60, Appl	220	7	1.6	166	4	US-09-490-324-282	Sequence 282, App
148	7	1.6	30	1	US-08-425-069-61	Sequence 61, Appl	221	7	1.6	166	4	US-09-270-767-37190	Sequence 37190, A
149	7	1.6	30	2	US-08-317-844B-48	Sequence 48, Appl	222	7	1.6	166	4	US-09-270-767-52407	Sequence 52407, A
150	7	1.6	30	2	US-08-317-844B-60	Sequence 60, Appl	223	7	1.6	175	2	US-08-993-228-8	Sequence 8, Appli
151	7	1.6	30	2	US-08-317-844B-61	Sequence 61, Appl	224	7	1.6	175	4	US-09-252-991A-26111	Sequence 26111, A
152	7	1.6	31	3	US-08-556-978B-26	Sequence 26, Appl	225	7	1.6	186	4	US-09-502-540-14288	Sequence 14288, A
153	7	1.6	31	3	US-08-556-978B-69	Sequence 69, Appl	226	7	1.6	198	4	US-09-270-767-45033	Sequence 45033, A
154	7	1.6	31	3	US-08-556-978B-89	Sequence 89, Appl	227	7	1.6	205	4	US-09-919-039-258	Sequence 258, App
155	7	1.6	31	4	US-09-324-258-19	Sequence 19, Appl	228	7	1.6	205	4	US-09-949-016-9411	Sequence 9411, Ap
156	7	1.6	32	1	US-08-425-069-44	Sequence 44, Appl	229	7	1.6	208	4	US-09-270-767-60040	Sequence 60040, A
157	7	1.6	32	2	US-08-317-844B-44	Sequence 44, Appl	230	7	1.6	209	4	US-09-543-681A-5814	Sequence 5814, Ap
158	7	1.6	33	1	US-08-425-069-7	Sequence 7, Appli	231	7	1.6	210	4	US-09-543-681A-8215	Sequence 8215, Ap
159	7	1.6	33	2	US-08-317-844B-7	Sequence 7, Appli	232	7	1.6	211	1	US-08-276-852-34	Sequence 34, Appl
160	7	1.6	34	1	US-08-425-069-52	Sequence 42, Appl	233	7	1.6	211	1	US-08-133-011-16	Sequence 16, Appl
161	7	1.6	34	1	US-08-425-069-42	Sequence 52, Appl	234	7	1.6	211	1	US-08-322-730A-16	Sequence 16, Appl
162	7	1.6	34	1	US-08-425-069-54	Sequence 54, Appl	235	7	1.6	211	1	US-08-387-874-16	Sequence 16, Appl
163	7	1.6	34	2	US-08-317-844B-42	Sequence 42, Appl	236	7	1.6	211	1	US-08-899-575-34	Sequence 34, Appl
164	7	1.6	34	2	US-08-317-844B-52	Sequence 52, Appl	237	7	1.6	211	1	US-08-899-575-34	Sequence 34, Appl
165	7	1.6	34	2	US-08-317-844B-54	Sequence 54, Appl	238	7	1.6	211	2	US-08-383-619-16	Sequence 16, Appl
166	7	1.6	34	3	US-08-556-978B-1	Sequence 1, Appli	239	7	1.6	211	3	US-08-907-739-16	Sequence 16, Appl
167	7	1.6	34	3	US-09-863-859-8	Sequence 8, Appli	240	7	1.6	211	4	US-09-729-597-16	Sequence 16, Appl
168	7	1.6	49	3	US-08-469-318-194	Sequence 194, App	241	7	1.6	211	5	PCT-US93-08364-16	Sequence 16, Appl
169	7	1.6	49	3	US-08-468-609A-194	Sequence 194, App	242	7	1.6	211	5	PCT-US95-08743-34	Sequence 34, Appl
170	7	1.6	49	3	US-08-446-872A-194	Sequence 194, App	243	7	1.6	213	4	US-09-252-991A-28745	Sequence 28745, A
171	7	1.6	49	4	US-08-762-227A-194	Sequence 194, App	244	7	1.6	216	4	US-09-795-872-5	Sequence 5, Appli
172	7	1.6	49	5	PCT-US95-01185-194	Sequence 194, App	245	7	1.6	217	4	US-09-270-767-31877	Sequence 31877, A
173	7	1.6	60	3	US-08-469-318-195	Sequence 195, App	246	7	1.6	217	4	US-09-270-767-47094	Sequence 47094, A

247	7	1.6	217	4	US-09-248-796A-25844	Sequence 25844, A	320	7	1.6	314	4	US-09-902-540-14533	Sequence 14533, A
248	7	1.6	218	4	US-09-902-540-15127	Sequence 15127, A	321	7	1.6	316	1	US-07-828-980A-2	Sequence 2, Appl
249	7	1.6	219	4	US-09-809-517A-24	Sequence 24, Appl	322	7	1.6	326	4	US-09-252-991A-17002	Sequence 17002, A
250	7	1.6	220	4	US-09-809-517A-24	Sequence 27, Appl	323	7	1.6	329	4	US-09-248-796A-17561	Sequence 17561, A
251	7	1.6	221	4	US-09-270-767-33945	Sequence 33945, A	324	7	1.6	331	4	US-09-270-767-44610	Sequence 44610, A
252	7	1.6	222	4	US-09-270-767-49162	Sequence 49162, A	325	7	1.6	331	4	US-09-270-767-45830	Sequence 45830, A
253	7	1.6	223	4	US-09-533-029-88	Sequence 88, Appl	326	7	1.6	335	3	US-08-469-318-143	Sequence 143, App
254	7	1.6	224	3	US-09-134-001C-4694	Sequence 4694, Ap	327	7	1.6	335	3	US-08-468-609A-143	Sequence 143, App
255	7	1.6	225	3	US-09-134-001C-5495	Sequence 5495, Ap	328	7	1.6	335	3	US-08-446-872A-143	Sequence 143, App
256	7	1.6	226	3	US-09-270-767-35290	Sequence 35290, A	329	7	1.6	335	3	US-08-762-227A-143	Sequence 143, App
257	7	1.6	227	4	US-09-270-767-50507	Sequence 50507, A	330	7	1.6	335	5	PCT-US95-01185-143	Sequence 143, App
258	7	1.6	228	4	US-09-248-796A-17127	Sequence 17127, A	331	7	1.6	337	3	US-08-469-318-148	Sequence 148, App
259	7	1.6	229	2	US-08-829-876-103	Sequence 103, App	332	7	1.6	337	3	US-08-468-609A-148	Sequence 148, App
260	7	1.6	230	3	US-09-234-874A-103	Sequence 103, App	333	7	1.6	337	3	US-08-446-872A-148	Sequence 148, App
261	7	1.6	231	4	US-09-234-873A-103	Sequence 103, App	334	7	1.6	337	4	US-08-762-227A-148	Sequence 148, App
262	7	1.6	232	4	US-08-829-876-101	Sequence 101, App	335	7	1.6	337	4	US-09-270-767-46550	Sequence 46550, A
263	7	1.6	233	2	US-08-829-876-105	Sequence 105, App	336	7	1.6	337	5	PCT-US95-01185-148	Sequence 148, App
264	7	1.6	234	3	US-09-234-874A-101	Sequence 101, App	337	7	1.6	345	4	US-09-270-767-45893	Sequence 45893, A
265	7	1.6	235	3	US-09-234-874A-105	Sequence 105, App	338	7	1.6	348	4	US-09-902-540-16155	Sequence 16155, A
266	7	1.6	236	4	US-09-234-873A-101	Sequence 101, App	339	7	1.6	349	3	US-08-469-318-139	Sequence 139, App
267	7	1.6	237	4	US-09-234-873A-105	Sequence 105, App	340	7	1.6	349	3	US-08-469-318-151	Sequence 151, App
268	7	1.6	238	3	US-09-605-858-32	Sequence 32, Appl	341	7	1.6	349	3	US-08-468-609A-139	Sequence 139, App
269	7	1.6	239	4	US-09-270-767-56912	Sequence 56912, A	342	7	1.6	349	3	US-08-468-609A-151	Sequence 151, App
270	7	1.6	240	4	US-09-495-880A-42	Sequence 42, Appl	343	7	1.6	349	3	US-08-446-872A-139	Sequence 139, App
271	7	1.6	241	4	US-09-949-016-11583	Sequence 11583, A	344	7	1.6	349	3	US-08-446-872A-151	Sequence 151, App
272	7	1.6	242	4	US-09-270-767-34316	Sequence 34316, A	345	7	1.6	349	4	US-08-762-227A-139	Sequence 139, App
273	7	1.6	243	4	US-09-270-767-49533	Sequence 49533, A	346	7	1.6	349	4	US-08-762-227A-151	Sequence 151, App
274	7	1.6	244	1	US-08-133-804-6	Sequence 6, Appl	347	7	1.6	349	5	PCT-US95-01185-139	Sequence 139, App
275	7	1.6	245	1	US-08-461-838-6	Sequence 6, Appl	348	7	1.6	349	5	PCT-US95-01185-151	Sequence 151, App
276	7	1.6	246	2	US-08-461-838-6	Sequence 6, Appl	349	7	1.6	350	4	US-09-248-796A-20605	Sequence 20605, A
277	7	1.6	247	2	US-08-356-786-4	Sequence 4, Appl	350	7	1.6	361	4	US-09-252-991A-31993	Sequence 31993, A
278	7	1.6	248	4	US-09-248-796A-20707	Sequence 20707, A	351	7	1.6	361	4	US-09-902-540-16412	Sequence 16412, A
279	7	1.6	249	1	US-08-257-341-7	Sequence 7, Appl	352	7	1.6	362	2	US-08-985-090-5	Sequence 5, Appl
280	7	1.6	250	4	US-09-270-767-43642	Sequence 43642, A	353	7	1.6	362	3	US-09-165-543-32	Sequence 32, Appl
281	7	1.6	251	1	US-08-133-804-2	Sequence 2, Appl	354	7	1.6	363	4	US-09-270-767-45265	Sequence 45265, A
282	7	1.6	252	1	US-08-461-884-8	Sequence 8, Appl	355	7	1.6	367	1	US-08-257-341-5	Sequence 5, Appl
283	7	1.6	253	1	US-08-463-675-8	Sequence 8, Appl	356	7	1.6	369	4	US-09-198-452A-1001	Sequence 1001, Ap
284	7	1.6	254	1	US-08-464-589-8	Sequence 8, Appl	357	7	1.6	369	4	US-09-328-352-7459	Sequence 7459, A
285	7	1.6	255	1	US-08-461-838-2	Sequence 2, Appl	358	7	1.6	372	4	US-09-252-991A-23226	Sequence 23226, A
286	7	1.6	256	2	US-08-461-838-2	Sequence 2, Appl	359	7	1.6	372	4	US-09-438-185A-931	Sequence 931, App
287	7	1.6	257	1	US-08-133-804-4	Sequence 4, Appl	360	7	1.6	374	2	US-08-446-875-4	Sequence 4, Appl
288	7	1.6	258	1	US-08-461-838-4	Sequence 4, Appl	361	7	1.6	374	2	US-08-102-385C-4	Sequence 4, Appl
289	7	1.6	259	2	US-08-461-838-4	Sequence 4, Appl	362	7	1.6	375	2	US-08-446-875-10	Sequence 10, Appl
290	7	1.6	260	4	US-09-252-991A-30124	Sequence 30124, A	363	7	1.6	375	2	US-08-102-385C-10	Sequence 10, Appl
291	7	1.6	261	4	US-09-270-767-43580	Sequence 43580, A	364	7	1.6	376	4	US-09-248-796A-15097	Sequence 15097, A
292	7	1.6	262	4	US-09-543-681A-6390	Sequence 6390, Ap	365	7	1.6	377	4	US-09-252-991A-22016	Sequence 22016, A
293	7	1.6	263	4	US-09-495-880A-26	Sequence 26, Appl	366	7	1.6	378	4	US-09-395-017B-1	Sequence 1, Appl
294	7	1.6	264	4	US-09-906-393A-20	Sequence 20, Appl	367	7	1.6	379	4	US-09-902-540-15163	Sequence 15163, A
295	7	1.6	265	4	US-09-134-000C-3441	Sequence 3441, Ap	368	7	1.6	391	4	US-09-395-017B-2	Sequence 2, Appl
296	7	1.6	266	4	US-09-252-991A-31410	Sequence 31410, A	369	7	1.6	395	4	US-09-270-767-61223	Sequence 61223, A
297	7	1.6	267	4	US-09-134-000C-3432	Sequence 3432, Ap	370	7	1.6	399	1	US-08-530-950-10	Sequence 10, Appl
298	7	1.6	268	4	US-10-101-464A-799	Sequence 799, App	371	7	1.6	399	2	US-08-874-186-92	Sequence 92, Appl
299	7	1.6	269	4	US-09-490-291-2	Sequence 2, Appl	372	7	1.6	399	3	US-08-888-429A-10	Sequence 10, Appl
300	7	1.6	270	4	US-09-949-016-11416	Sequence 11416, A	373	7	1.6	399	3	US-09-149-879-10	Sequence 10, Appl
301	7	1.6	271	6	5194600-2	Patent No. 5194600	374	7	1.6	399	4	US-09-057-009-10	Sequence 10, Appl
302	7	1.6	272	6	5194600-2	Patent No. 5194600	375	7	1.6	399	4	US-09-593-653-10	Sequence 10, Appl
303	7	1.6	273	2	US-08-353-476-111	Sequence 111, App	376	7	1.6	399	4	US-09-538-092-1129	Sequence 1129, Ap
304	7	1.6	274	4	US-09-134-000C-4591	Sequence 4591, Ap	377	7	1.6	405	4	US-09-949-016-10726	Sequence 10726, A
305	7	1.6	275	3	US-08-438-745-4	Sequence 4, Appl	378	7	1.6	406	4	US-09-252-991A-22163	Sequence 22163, A
306	7	1.6	276	3	US-08-438-745-6	Sequence 6, Appl	379	7	1.6	410	4	US-09-270-767-44592	Sequence 44592, A
307	7	1.6	277	3	US-09-219-019-4	Sequence 4, Appl	380	7	1.6	415	3	US-09-025-769B-280	Sequence 280, App
308	7	1.6	278	3	US-09-219-019-6	Sequence 6, Appl	381	7	1.6	415	4	US-09-490-153-280	Sequence 280, App
309	7	1.6	279	4	US-09-252-991A-20791	Sequence 20791, A	382	7	1.6	415	4	US-09-490-324-280	Sequence 280, App
310	7	1.6	280	5	PCT-US94-05669A-4	Sequence 4, Appl	383	7	1.6	415	4	US-09-490-324-280	Sequence 280, App
311	7	1.6	281	5	PCT-US94-05669A-6	Sequence 6, Appl	384	7	1.6	428	4	US-09-134-000C-3817	Sequence 3817, Ap
312	7	1.6	282	4	US-09-583-110-4607	Sequence 4607, Ap	385	7	1.6	429	4	US-09-252-991A-32661	Sequence 32661, A
313	7	1.6	283	4	US-09-107-433-2774	Sequence 2774, Ap	386	7	1.6	430	4	US-09-583-110-4297	Sequence 4297, Ap
314	7	1.6	284	3	US-08-469-318-142	Sequence 142, App	387	7	1.6	430	4	US-09-306-595C-8	Sequence 8, Appl
315	7	1.6	285	3	US-08-468-609A-142	Sequence 142, App	388	7	1.6	432	3	US-09-403-089A-1	Sequence 1, Appl
316	7	1.6	286	3	US-08-446-872A-142	Sequence 142, App	389	7	1.6	432	4	US-09-925-388-8	Sequence 8, Appl
317	7	1.6	287	4	US-08-762-227A-142	Sequence 142, App	390	7	1.6	432	4	US-09-807-258-32	Sequence 32, Appl
318	7	1.6	288	5	PCT-US95-01185-142	Sequence 142, App	391	7	1.6	433	4	US-09-807-258-32	Sequence 32, Appl
319	7	1.6	289	4	US-09-248-796A-21212	Sequence 21212, A	392	7	1.6	433	4	US-09-807-258-32	Sequence 32, Appl

393	7	1.6	433	4	US-09-524-101D-20	Sequence 20, Appl	466	7	1.6	494	4	US-09-198-452A-13	Sequence 13, Appl
394	7	1.6	434	4	US-09-809-517A-23	Sequence 23, Appl	467	7	1.6	494	4	US-09-438-185A-4	Sequence 4, Appl
395	7	1.6	435	4	US-09-809-517A-26	Sequence 26, Appl	468	7	1.6	496	4	US-09-540-236-3821	Sequence 3821, Ap
396	7	1.6	435	4	US-09-794-422-2	Sequence 2, Appl	469	7	1.6	503	1	US-07-612-673-2	Sequence 2, Appl
397	7	1.6	436	4	US-09-107-433-4475	Sequence 4475, Ap	470	7	1.6	506	2	US-08-820-170A-19	Sequence 19, Appl
398	7	1.6	441	4	US-09-370-767-60990	Sequence 60990, A	471	7	1.6	506	3	US-09-055-699-19	Sequence 19, Appl
399	7	1.6	441	4	US-09-794-422-4	Sequence 4, Appl	472	7	1.6	506	3	US-09-273-565-19	Sequence 19, Appl
400	7	1.6	442	4	US-09-248-796A-21400	Sequence 21400, A	473	7	1.6	506	3	US-09-565-538-19	Sequence 19, Appl
401	7	1.6	445	2	US-08-985-090-2	Sequence 2, Appl	474	7	1.6	506	3	US-09-661-468-19	Sequence 19, Appl
402	7	1.6	445	3	US-09-165-543-2	Sequence 2, Appl	475	7	1.6	506	4	US-09-976-165-19	Sequence 19, Appl
403	7	1.6	445	3	US-09-165-543-5	Sequence 5, Appl	476	7	1.6	506	4	US-09-538-092-11381	Sequence 1381, Ap
404	7	1.6	445	3	US-09-167-354-7	Sequence 7, Appl	477	7	1.6	506	4	US-09-949-016-11518	Sequence 11518, A
405	7	1.6	445	4	US-09-642-855-7	Sequence 7, Appl	478	7	1.6	507	4	US-09-248-796A-19012	Sequence 19012, A
406	7	1.6	445	4	US-09-642-514-7	Sequence 7, Appl	479	7	1.6	507	4	US-09-107-433-4015	Sequence 4015, Ap
407	7	1.6	445	4	US-09-891-053-25	Sequence 25, Appl	480	7	1.6	511	4	US-09-328-352-5220	Sequence 5220, Ap
408	7	1.6	446	4	US-09-252-991A-27110	Sequence 27110, A	481	7	1.6	513	4	US-09-248-796A-25078	Sequence 25078, A
409	7	1.6	448	4	US-09-107-532A-3962	Sequence 3962, Ap	482	7	1.6	515	4	US-09-134-000C-3767	Sequence 3767, Ap
410	7	1.6	449	4	US-09-949-016-10930	Sequence 10930, A	483	7	1.6	516	3	US-08-746-559A-4	Sequence 4, Appl
411	7	1.6	453	4	US-09-891-053-20	Sequence 20, Appl	484	7	1.6	521	1	US-07-796-361A-11	Sequence 11, Appl
412	7	1.6	455	4	US-09-370-767-45531	Sequence 45531, A	485	7	1.6	521	1	US-08-539-666-2	Sequence 2, Appl
413	7	1.6	455	4	US-09-248-796A-17535	Sequence 17535, A	486	7	1.6	522	4	US-09-252-991A-30451	Sequence 30451, A
414	7	1.6	458	4	US-09-248-796A-18424	Sequence 18424, A	487	7	1.6	522	4	US-09-949-016-7190-	Sequence 7190, Ap
415	7	1.6	461	2	US-08-463-587A-26	Sequence 26, Appl	488	7	1.6	523	2	US-08-482-728A-19	Sequence 19, Appl
416	7	1.6	461	2	US-08-463-667A-4	Sequence 4, Appl	489	7	1.6	523	3	US-09-028-366-4	Sequence 4, Appl
417	7	1.6	461	3	US-08-923-854-26	Sequence 26, Appl	490	7	1.6	523	3	US-09-715-285-4	Sequence 4, Appl
418	7	1.6	461	5	PCT-US91-09133-27	Sequence 27, Appl	491	7	1.6	524	4	US-09-242-913B-15	Sequence 15, Appl
419	7	1.6	462	4	US-09-270-767-43057	Sequence 43057, A	492	7	1.6	528	4	US-09-270-767-43914	Sequence 42914, A
420	7	1.6	464	4	US-09-949-016-10505	Sequence 10505, A	493	7	1.6	536	4	US-09-270-767-43766	Sequence 43766, A
421	7	1.6	465	4	US-09-370-767-46340	Sequence 46340, A	494	7	1.6	539	2	US-08-818-024-4	Sequence 4, Appl
422	7	1.6	466	2	US-08-726-136-28	Sequence 28, Appl	495	7	1.6	539	3	US-09-334-775A-4	Sequence 4, Appl
423	7	1.6	466	3	US-09-103-434-28	Sequence 28, Appl	496	7	1.6	539	3	US-08-789-275-6	Sequence 6, Appl
424	7	1.6	466	3	US-09-687-594-28	Sequence 28, Appl	497	7	1.6	545	4	US-09-949-016-10504	Sequence 10504, A
425	7	1.6	466	4	US-09-489-039A-9530	Sequence 9530, Ap	498	7	1.6	550	4	US-09-242-913B-14	Sequence 14, Appl
426	7	1.6	468	4	US-09-248-796A-19502	Sequence 19502, A	499	7	1.6	551	4	US-09-252-991A-18403	Sequence 18403, A
427	7	1.6	471	1	US-08-257-341-9	Sequence 9, Appl	500	7	1.6	551	4	US-09-252-991A-27787	Sequence 27787, A
428	7	1.6	472	1	US-08-278-091-5	Sequence 5, Appl	501	7	1.6	552	4	US-09-242-913B-19	Sequence 19, Appl
429	7	1.6	472	1	US-08-483-859-5	Sequence 5, Appl	502	7	1.6	554	4	US-08-809-802-8	Sequence 8, Appl
430	7	1.6	472	1	US-08-472-173-5	Sequence 5, Appl	503	7	1.6	556	4	US-09-275-252A-8	Sequence 8, Appl
431	7	1.6	472	2	US-08-487-167-5	Sequence 5, Appl	504	7	1.6	556	4	US-09-270-767-41922	Sequence 41922, A
432	7	1.6	472	2	US-08-482-816-5	Sequence 5, Appl	505	7	1.6	558	4	US-09-252-991A-24047	Sequence 24047, A
433	7	1.6	472	2	US-08-296-149-5	Sequence 5, Appl	506	7	1.6	560	4	US-09-252-991A-23548	Sequence 23548, A
434	7	1.6	472	2	US-08-801-499-5	Sequence 5, Appl	507	7	1.6	560	4	US-09-252-991A-28159	Sequence 28159, A
435	7	1.6	472	2	US-08-615-271-5	Sequence 5, Appl	508	7	1.6	561	4	US-09-134-000C-4759	Sequence 4759, Ap
436	7	1.6	472	3	US-09-074-660-5	Sequence 5, Appl	509	7	1.6	572	4	US-09-252-991A-16924	Sequence 16924, A
437	7	1.6	472	3	US-09-074-659-5	Sequence 5, Appl	510	7	1.6	587	4	US-09-270-767-45702	Sequence 45702, A
438	7	1.6	472	3	US-09-106-468-5	Sequence 5, Appl	511	7	1.6	604	3	US-08-556-978B-21	Sequence 21, Appl
439	7	1.6	472	3	US-09-106-466A-5	Sequence 5, Appl	512	7	1.6	606	3	US-08-556-978B-21	Sequence 21, Appl
440	7	1.6	472	3	US-09-106-467-5	Sequence 5, Appl	513	7	1.6	606	3	US-08-556-978B-23	Sequence 23, Appl
441	7	1.6	474	4	US-09-702-705-1812	Sequence 1812, Ap	514	7	1.6	606	3	US-09-247-806-4	Sequence 4, Appl
442	7	1.6	474	4	US-09-736-457-1812	Sequence 1812, Ap	515	7	1.6	606	3	US-09-247-806-6	Sequence 6, Appl
443	7	1.6	474	4	US-09-671-325-1812	Sequence 1279, Ap	516	7	1.6	606	3	US-09-247-806-8	Sequence 8, Appl
444	7	1.6	474	4	US-09-538-092-1279	Sequence 1279, Ap	517	7	1.6	606	3	US-09-247-806-8	Sequence 8, Appl
445	7	1.6	480	4	US-09-538-092-1001	Sequence 1001, Ap	518	7	1.6	609	4	US-09-949-016-6846	Sequence 6846, Ap
446	7	1.6	482	1	US-08-358-160-5	Sequence 5, Appl	519	7	1.6	618	4	US-09-252-991A-25459	Sequence 25459, A
447	7	1.6	484	1	US-08-358-160-7	Sequence 7, Appl	520	7	1.6	622	2	US-08-356-786-16	Sequence 16, Appl
448	7	1.6	484	4	US-09-302-540-13700	Sequence 13700, A	521	7	1.6	622	4	US-09-252-991A-19802	Sequence 19802, A
449	7	1.6	485	3	US-09-009-494-2	Sequence 2, Appl	522	7	1.6	625	4	US-09-270-767-42376	Sequence 42376, A
450	7	1.6	485	3	US-09-010-233-8	Sequence 8, Appl	523	7	1.6	632	4	US-09-270-767-42178	Sequence 42178, A
451	7	1.6	485	3	US-09-010-232-4	Sequence 4, Appl	524	7	1.6	633	4	US-09-270-767-6	Sequence 6, Appl
452	7	1.6	485	4	US-10-138-701-28	Sequence 1346, Ap	525	7	1.6	637	4	US-09-569-611C-35	Sequence 35, Appl
453	7	1.6	485	4	US-09-710-279-1346	Sequence 28, Appl	526	7	1.6	637	4	US-09-949-016-8152	Sequence 8152, Ap
454	7	1.6	486	4	US-09-302-540-16779	Sequence 16779, A	527	7	1.6	643	3	US-09-538-092-844	Sequence 844, App
455	7	1.6	487	3	US-08-961-083-42	Sequence 42, Appl	528	7	1.6	647	3	US-08-753-007A-32	Sequence 32, Appl
456	7	1.6	487	4	US-09-536-784-42	Sequence 42, Appl	529	7	1.6	647	3	US-09-398-496-32	Sequence 32, Appl
457	7	1.6	488	4	US-09-252-991A-26323	Sequence 26323, A	530	7	1.6	656	4	US-09-252-991A-25135	Sequence 25135, A
458	7	1.6	488	4	US-09-328-352-7203	Sequence 7203, Ap	531	7	1.6	666	2	US-08-737-716-14	Sequence 14, Appl
459	7	1.6	488	4	US-09-583-110-3891	Sequence 3891, Ap	532	7	1.6	666	4	US-09-270-767-46736	Sequence 46736, A
460	7	1.6	490	3	US-08-896-346-2	Sequence 2, Appl	533	7	1.6	673	4	US-09-107-532A-5134	Sequence 5134, Ap
461	7	1.6	491	3	US-08-923-454A-14	Sequence 14, Appl	534	7	1.6	674	3	US-08-653-648A-14	Sequence 14, Appl
462	7	1.6	491	3	US-09-134-001C-4677	Sequence 4677, Ap	535	7	1.6	675	4	US-09-564-418-12	Sequence 12, Appl
463	7	1.6	492	1	US-08-350-741-3	Sequence 3, Appl	536	7	1.6	676	1	US-08-282-141-4	Sequence 4, Appl
464	7	1.6	492	2	US-08-463-875A-3	Sequence 3, Appl	537	7	1.6	681	4	US-09-490-291-4	Sequence 4, Appl
465	7	1.6	492	3	US-09-413-814-72	Sequence 72, Appl	538	7	1.6	691	4	US-09-490-291-6	Sequence 6, Appl

539	7	1.6	701	4	US-09-248-796A-16628	Sequence 16628, A	612	7	1.6	1367	3	US-08-864-641B-18	Sequence 18, Appl
540	7	1.6	703	3	US-08-910-925-4	Sequence 4, Appl	613	7	1.6	1367	4	US-09-343-551-2	Sequence 2, Appl
541	7	1.6	706	4	US-09-270-767-40994	Sequence 40994, A	614	7	1.6	1367	4	US-09-949-001-18	Sequence 18, Appl
542	7	1.6	706	4	US-09-270-767-56210	Sequence 56210, A	615	7	1.6	1377	4	US-09-949-001-21	Sequence 21, Appl
543	7	1.6	716	4	US-09-270-767-41668	Sequence 41668, A	616	7	1.6	1402	4	US-09-248-796A-14503	Sequence 14503, A
544	7	1.6	717	3	US-08-910-925-1	Sequence 1, Appl	617	7	1.6	1492	4	US-09-697-898-5	Sequence 5, Appl
545	7	1.6	726	4	US-09-392-714-21	Sequence 21, Appl	618	7	1.6	1493	3	US-09-423-890-8	Sequence 8, Appl
546	7	1.6	731	4	US-09-949-016-9763	Sequence 9763, A	619	7	1.6	1584	3	US-09-457-040B-27	Sequence 27, Appl
547	7	1.6	732	3	US-08-914-999-8	Sequence 8, Appl	620	7	1.6	1593	3	US-08-628-829-4	Sequence 4, Appl
548	7	1.6	737	4	US-09-902-540-16346	Sequence 16346, A	621	7	1.6	1617	4	US-09-863-859-14	Sequence 14, Appl
549	7	1.6	739	3	US-09-022-983-2	Sequence 2, Appl	622	7	1.6	1626	4	US-09-863-859-24	Sequence 24, Appl
550	7	1.6	741	4	US-09-854-856-60	Sequence 60, Appl	623	7	1.6	1911	4	US-09-854-856-64	Sequence 64, Appl
551	7	1.6	743	3	US-08-910-925-3	Sequence 3, Appl	624	7	1.6	1912	4	US-09-949-016-10490	Sequence 10490, A
552	7	1.6	743	4	US-09-949-016-6261	Sequence 6261, A	625	7	1.6	1939	4	US-09-854-856-48	Sequence 48, Appl
553	7	1.6	745	2	US-08-674-887A-8	Sequence 8, Appl	626	7	1.6	1971	4	US-09-854-856-32	Sequence 32, Appl
554	7	1.6	745	3	US-08-951-844-8	Sequence 8, Appl	627	7	1.6	1999	4	US-09-854-856-16	Sequence 16, Appl
555	7	1.6	745	4	US-09-412-347-8	Sequence 8, Appl	628	7	1.6	2004	4	US-09-854-856-58	Sequence 58, Appl
556	7	1.6	745	4	US-09-270-767-45481	Sequence 45481, A	629	7	1.6	2032	4	US-09-854-856-42	Sequence 42, Appl
557	7	1.6	749	4	US-09-949-016-8645	Sequence 8645, A	630	7	1.6	2048	4	US-09-854-856-62	Sequence 62, Appl
558	7	1.6	749	4	US-09-949-016-8646	Sequence 8646, A	631	7	1.6	2064	4	US-09-854-856-26	Sequence 26, Appl
559	7	1.6	749	4	US-09-949-016-8647	Sequence 8647, A	632	7	1.6	2071	3	US-09-415-522-6	Sequence 6, Appl
560	7	1.6	749	4	US-09-949-016-8648	Sequence 8648, A	633	7	1.6	2076	4	US-09-854-856-46	Sequence 46, Appl
561	7	1.6	754	4	US-09-392-714-20	Sequence 20, Appl	634	7	1.6	2092	4	US-09-854-856-10	Sequence 10, Appl
562	7	1.6	766	4	US-08-311-731A-258	Sequence 258, A	635	7	1.6	2108	4	US-09-854-856-30	Sequence 30, Appl
563	7	1.6	766	4	US-09-949-016-11355	Sequence 11355, A	636	7	1.6	2110	4	US-09-270-767-46547	Sequence 46547, A
564	7	1.6	766	4	US-09-949-016-11356	Sequence 11356, A	637	7	1.6	2119	4	US-09-583-110-4893	Sequence 4893, A
565	7	1.6	766	4	US-09-949-016-11357	Sequence 11357, A	638	7	1.6	2123	4	US-09-107-433-3728	Sequence 3728, A
566	7	1.6	766	4	US-09-949-016-11358	Sequence 11358, A	639	7	1.6	2136	4	US-09-854-856-14	Sequence 14, Appl
567	7	1.6	769	4	US-09-854-856-44	Sequence 44, Appl	640	7	1.6	2141	4	US-09-854-856-56	Sequence 56, Appl
568	7	1.6	779	4	US-09-270-767-42332	Sequence 42332, A	641	7	1.6	2157	4	US-09-854-856-52	Sequence 52, Appl
569	7	1.6	785	4	US-09-538-092-872	Sequence 872, A	642	7	1.6	2169	4	US-09-854-856-40	Sequence 40, Appl
570	7	1.6	801	4	US-09-854-856-28	Sequence 28, Appl	643	7	1.6	2179	4	US-09-949-016-8129	Sequence 8129, A
571	7	1.6	801	4	US-09-949-016-6588	Sequence 6588, A	644	7	1.6	2182	2	US-08-487-826B-16	Sequence 16, Appl
572	7	1.6	809	4	US-09-863-859-13	Sequence 13, Appl	645	7	1.6	2185	4	US-09-854-856-36	Sequence 36, Appl
573	7	1.6	810	4	US-09-949-016-11152	Sequence 11152, A	646	7	1.6	2201	4	US-09-854-856-24	Sequence 24, Appl
574	7	1.6	818	4	US-09-863-859-22	Sequence 22, Appl	647	7	1.6	2217	4	US-09-854-856-20	Sequence 20, Appl
575	7	1.6	820	4	US-09-583-110-4219	Sequence 4219, A	648	7	1.6	2229	4	US-09-854-856-8	Sequence 8, Appl
576	7	1.6	821	1	US-09-377-465A-2	Sequence 2, Appl	649	7	1.6	2245	4	US-09-854-856-4	Sequence 4, Appl
577	7	1.6	827	4	US-10-101-464A-915	Sequence 915, A	650	7	1.6	2294	4	US-09-854-856-50	Sequence 50, Appl
578	7	1.6	829	4	US-09-854-856-12	Sequence 12, Appl	651	7	1.6	2322	4	US-09-854-856-34	Sequence 34, Appl
579	7	1.6	834	4	US-09-107-433-4760	Sequence 4760, A	652	7	1.6	2354	4	US-09-854-856-18	Sequence 18, Appl
580	7	1.6	846	2	US-07-728-215-33	Sequence 33, Appl	653	7	1.6	2382	4	US-09-854-856-2	Sequence 2, Appl
581	7	1.6	846	3	US-08-938-085A-33	Sequence 33, Appl	654	7	1.6	2472	4	US-09-252-991A-17052	Sequence 17052, A
582	7	1.6	846	4	US-10-072-844-33	Sequence 33, Appl	655	7	1.6	2710	2	US-08-568-459A-12	Sequence 12, Appl
583	7	1.6	846	4	US-10-072-838-33	Sequence 33, Appl	656	7	1.6	2710	2	US-08-487-826B-12	Sequence 12, Appl
584	7	1.6	846	4	US-10-072-841A-33	Sequence 33, Appl	657	7	1.6	2710	3	US-09-210-288-12	Sequence 12, Appl
585	7	1.6	846	4	US-10-219-631A-33	Sequence 33, Appl	658	7	1.6	3025	6	5223423-3	Patent No. 5223423
586	7	1.6	894	4	US-09-854-856-54	Sequence 54, Appl	659	7	1.6	3025	6	5223423-3	Patent No. 5223423
587	7	1.6	907	4	US-09-949-016-9750	Sequence 9750, A	660	7	1.6	3060	2	US-08-487-826B-14	Sequence 14, Appl
588	7	1.6	907	4	US-09-949-016-9751	Sequence 9751, A	661	6	1.4	6	2	US-08-463-667A-15	Sequence 15, Appl
589	7	1.6	922	4	US-09-854-856-38	Sequence 38, Appl	662	6	1.4	6	3	US-09-330-970-25	Sequence 25, Appl
590	7	1.6	954	4	US-09-854-856-22	Sequence 22, Appl	663	6	1.4	6	4	US-08-537-871A-62	Sequence 62, Appl
591	7	1.6	956	4	US-09-914-259-17	Sequence 17, Appl	664	6	1.4	7	1	US-08-062-024B-1	Sequence 1, Appl
592	7	1.6	966	1	US-08-571-758-2	Sequence 2, Appl	665	6	1.4	7	2	US-08-756-407-1	Sequence 1, Appl
593	7	1.6	966	1	US-08-909-984A-2	Sequence 2, Appl	666	6	1.4	7	3	US-09-020-880-35	Sequence 35, Appl
594	7	1.6	966	1	US-08-909-983-2	Sequence 2, Appl	667	6	1.4	7	3	US-09-101-544-35	Sequence 35, Appl
595	7	1.6	982	4	US-09-854-856-6	Sequence 6, Appl	668	6	1.4	7	4	US-09-755-630B-276	Sequence 276, A
596	7	1.6	1004	3	US-08-916-352-2	Sequence 2, Appl	669	6	1.4	7	4	US-09-755-274-17	Sequence 17, Appl
597	7	1.6	1004	4	US-09-949-016-6495	Sequence 6495, A	670	6	1.4	7	5	PCN-US94-05014-1	Sequence 1, Appl
598	7	1.6	1039	4	US-09-252-991A-28966	Sequence 28966, A	671	6	1.4	8	2	US-08-355-848A-38	Sequence 38, Appl
599	7	1.6	1060	3	US-08-911-393-2	Sequence 2, Appl	672	6	1.4	8	3	US-08-833-167-61	Sequence 61, Appl
600	7	1.6	1060	4	US-09-955-909-2	Sequence 2, Appl	673	6	1.4	8	3	US-08-481-968A-20	Sequence 20, Appl
601	7	1.6	1072	4	US-09-949-016-8072	Sequence 8072, A	674	6	1.4	8	3	US-08-154-712B-20	Sequence 20, Appl
602	7	1.6	1073	4	US-09-252-991A-27341	Sequence 27341, A	675	6	1.4	8	3	US-09-344-837A-61	Sequence 61, Appl
603	7	1.6	1093	4	US-09-248-796A-17108	Sequence 17108, A	676	6	1.4	8	4	US-09-947-925A-20	Sequence 20, Appl
604	7	1.6	1114	4	US-09-252-991A-24965	Sequence 24965, A	677	6	1.4	8	4	US-09-510-238A-242	Sequence 242, A
605	7	1.6	1146	3	US-08-914-999-6	Sequence 6, Appl	678	6	1.4	8	4	US-09-989-025A-17	Sequence 17, Appl
606	7	1.6	1160	3	US-08-808-599A-24	Sequence 24, Appl	679	6	1.4	8	4	US-09-770-564A-35	Sequence 35, Appl
607	7	1.6	1246	4	US-09-252-991A-23140	Sequence 23140, A	680	6	1.4	9	1	US-08-425-069-11	Sequence 11, Appl
608	7	1.6	1302	3	US-09-423-890-2	Sequence 2, Appl	681	6	1.4	9	2	US-08-317-844B-11	Sequence 11, Appl
609	7	1.6	1367	2	US-08-249-687C-2	Sequence 2, Appl	682	6	1.4	9	3	US-08-582-333A-2	Sequence 2, Appl
610	7	1.6	1367	2	US-08-625-819-2	Sequence 2, Appl	683	6	1.4	9	3	US-09-305-923A-5	Sequence 5, Appl
611	7	1.6	1367	3	US-08-746-559A-2	Sequence 2, Appl	684	6	1.4	9	4	US-09-790-317-5	Sequence 5, Appl

685	6	1.4	9	4	US-09-239-043D-379	Sequence 379, App	758	6	1.4	13	2	US-08-248-839C-32	Sequence 32, Appl
686	6	1.4	10	1	US-08-442-542-32	Sequence 32, Appl	759	6	1.4	13	2	US-08-484-905-6	Sequence 6, Appli
687	6	1.4	10	1	US-08-575-361A-35	Sequence 35, Appl	760	6	1.4	13	3	US-08-481-985B-6	Sequence 6, Appli
688	6	1.4	10	2	US-08-207-481-7	Sequence 7, Appli	761	6	1.4	13	3	US-08-370-476-6	Sequence 6, Appli
689	6	1.4	10	2	US-08-596-387B-1	Sequence 1, Appli	762	6	1.4	13	3	US-09-248-588-97	Sequence 97, Appl
690	6	1.4	10	2	US-08-647-449-29	Sequence 29, Appl	763	6	1.4	13	3	US-08-525-539A-66	Sequence 66, Appl
691	6	1.4	10	3	US-08-765-469-32	Sequence 32, Appl	764	6	1.4	13	4	US-09-554-941-13	Sequence 13, Appl
692	6	1.4	10	3	US-09-281-792B-29	Sequence 29, Appl	765	6	1.4	14	1	US-08-430-633-5	Sequence 5, Appli
693	6	1.4	10	3	US-09-067-615-1	Sequence 1, Appli	766	6	1.4	14	2	US-08-448-418-89	Sequence 89, Appl
694	6	1.4	10	4	US-09-470-191-96	Sequence 96, Appl	767	6	1.4	14	2	US-08-448-418-101	Sequence 101, App
695	6	1.4	10	4	US-08-406-824A-29	Sequence 29, Appl	768	6	1.4	14	2	US-08-373-190-3	Sequence 3, Appli
696	6	1.4	10	4	US-09-223-040-9	Sequence 9, Appli	769	6	1.4	14	2	US-08-373-190-5	Sequence 5, Appli
697	6	1.4	10	4	US-09-287-849-45	Sequence 45, Appl	770	6	1.4	14	2	US-08-620-694A-5	Sequence 5, Appli
698	6	1.4	10	4	US-08-790-317-6	Sequence 6, Appli	771	6	1.4	14	2	US-08-936-854-5	Sequence 5, Appli
699	6	1.4	10	4	US-09-239-043D-380	Sequence 380, App	772	6	1.4	14	2	US-08-438-190A-3	Sequence 3, Appli
700	6	1.4	10	4	US-09-239-043D-1433	Sequence 1433, Ap	773	6	1.4	14	2	US-08-438-190A-5	Sequence 5, Appli
701	6	1.4	10	4	US-10-077-210-1	Sequence 1, Appli	774	6	1.4	14	2	US-08-656-906-26	Sequence 26, Appl
702	6	1.4	10	4	US-09-798-689-19	Sequence 19, Appl	775	6	1.4	14	2	US-08-818-253-46	Sequence 46, Appl
703	6	1.4	10	5	PCT-US95-02689-7	Sequence 7, Appli	776	6	1.4	14	3	US-08-350-215-3	Sequence 3, Appli
704	6	1.4	10	5	PCT-US95-09818A-1	Sequence 1, Appli	777	6	1.4	14	3	US-08-350-215-5	Sequence 5, Appli
705	6	1.4	11	1	US-08-323-474-5	Sequence 5, Appli	778	6	1.4	14	3	US-09-022-255-5	Sequence 5, Appli
706	6	1.4	11	1	US-08-086-335C-13	Sequence 13, Appl	779	6	1.4	14	3	US-09-287-145A-3	Sequence 3, Appli
707	6	1.4	11	1	US-08-641-704-1	Sequence 1, Appli	780	6	1.4	14	3	US-09-022-696-5	Sequence 5, Appli
708	6	1.4	11	1	US-08-236-918A-17	Sequence 17, Appl	781	6	1.4	14	3	US-09-022-253-5	Sequence 5, Appli
709	6	1.4	11	2	US-08-385-335A-5	Sequence 5, Appli	782	6	1.4	14	3	US-09-022-260-5	Sequence 5, Appli
710	6	1.4	11	2	US-08-556-906-18	Sequence 18, Appl	783	6	1.4	14	3	US-09-046-992-6	Sequence 6, Appli
711	6	1.4	11	2	US-08-656-906-20	Sequence 20, Appl	784	6	1.4	14	3	US-09-022-259-5	Sequence 5, Appli
712	6	1.4	11	3	US-09-217-847-18	Sequence 18, Appl	785	6	1.4	14	3	US-09-022-257-5	Sequence 5, Appli
713	6	1.4	11	3	US-09-217-847-20	Sequence 20, Appl	786	6	1.4	14	3	US-08-818-252-46	Sequence 46, Appl
714	6	1.4	11	3	US-09-150-864A-17	Sequence 17, Appl	787	6	1.4	14	3	US-09-217-847-26	Sequence 26, Appl
715	6	1.4	11	4	US-08-829-558-5	Sequence 5, Appli	788	6	1.4	14	3	US-08-960-190A-29	Sequence 29, Appl
716	6	1.4	11	4	US-09-039-642B-4	Sequence 4, Appli	789	6	1.4	14	3	US-08-849-488-16	Sequence 16, Appl
717	6	1.4	11	4	US-08-406-824A-23	Sequence 23, Appl	790	6	1.4	14	3	US-09-362-808-8	Sequence 8, Appli
718	6	1.4	11	4	US-09-333-213-2	Sequence 2, Appli	791	6	1.4	14	3	US-09-173-190-8	Sequence 8, Appli
719	6	1.4	11	4	US-09-239-043D-1077	Sequence 1077, Ap	792	6	1.4	14	3	US-09-556-111-3	Sequence 3, Appli
720	6	1.4	11	4	US-09-239-043D-1545	Sequence 1545, Ap	793	6	1.4	14	3	US-09-556-111-5	Sequence 5, Appli
721	6	1.4	11	4	US-10-077-210-2	Sequence 2, Appli	794	6	1.4	14	3	US-09-316-919-62	Sequence 62, Appl
722	6	1.4	11	5	PCT-US95-08533-1	Sequence 1, Appli	795	6	1.4	14	4	US-09-146-979-89	Sequence 89, Appl
723	6	1.4	12	1	US-08-482-530-13	Sequence 13, Appl	796	6	1.4	14	4	US-09-146-979-99	Sequence 99, Appl
724	6	1.4	12	1	US-08-050-058B-13	Sequence 13, Appl	797	6	1.4	14	4	US-09-125-576B-9	Sequence 9, Appli
725	6	1.4	12	2	US-08-463-587A-12	Sequence 12, Appl	798	6	1.4	14	4	US-09-033-525-6	Sequence 6, Appli
726	6	1.4	12	2	US-08-441-871-16	Sequence 16, Appl	799	6	1.4	14	4	US-09-832-297A-8	Sequence 8, Appli
727	6	1.4	12	2	US-08-224-591-7	Sequence 7, Appli	800	6	1.4	14	4	US-09-549-679-5	Sequence 5, Appli
728	6	1.4	12	2	US-08-392-338A-1	Sequence 1, Appli	801	6	1.4	14	4	US-09-316-920A-62	Sequence 62, Appl
729	6	1.4	12	2	US-08-955-848A-39	Sequence 39, Appl	802	6	1.4	14	4	US-09-883-777-16	Sequence 16, Appl
730	6	1.4	12	2	US-08-591-196-56	Sequence 56, Appl	803	6	1.4	14	4	US-09-937-837-16	Sequence 16, Appl
731	6	1.4	12	2	US-08-926-789-7	Sequence 7, Appli	804	6	1.4	14	4	US-07-664-989B-11	Sequence 11, Appl
732	6	1.4	12	2	US-08-818-253-41	Sequence 41, Appl	805	6	1.4	15	1	US-07-664-989B-18	Sequence 18, Appl
733	6	1.4	12	3	US-09-166-750-1	Sequence 1, Appli	806	6	1.4	15	1	US-07-988-194A-43	Sequence 43, Appl
734	6	1.4	12	3	US-09-166-093-1	Sequence 1, Appli	807	6	1.4	15	1	US-07-843-125-13	Sequence 13, Appl
735	6	1.4	12	3	US-08-923-854-12	Sequence 12, Appl	808	6	1.4	15	1	US-08-346-293-15	Sequence 15, Appl
736	6	1.4	12	3	US-08-833-167-62	Sequence 62, Appl	809	6	1.4	15	1	US-08-164-151-23	Sequence 23, Appl
737	6	1.4	12	3	US-09-172-019-1	Sequence 1, Appli	810	6	1.4	15	1	US-08-133-804-7	Sequence 7, Appli
738	6	1.4	12	3	US-09-166-094-1	Sequence 1, Appli	811	6	1.4	15	1	US-08-331-398A-32	Sequence 32, Appl
739	6	1.4	12	3	US-08-818-252-41	Sequence 41, Appl	812	6	1.4	15	1	US-08-478-312-22	Sequence 22, Appl
740	6	1.4	12	3	US-09-362-805-3	Sequence 3, Appli	813	6	1.4	15	1	US-08-485-302-22	Sequence 22, Appl
741	6	1.4	12	3	US-09-173-190-3	Sequence 3, Appli	814	6	1.4	15	1	US-08-476-169-18	Sequence 18, Appl
742	6	1.4	12	3	US-09-069-821-6	Sequence 6, Appli	815	6	1.4	15	1	US-08-484-083-18	Sequence 18, Appl
743	6	1.4	12	3	US-09-344-837A-62	Sequence 62, Appl	816	6	1.4	15	1	US-08-077-252B-23	Sequence 23, Appl
744	6	1.4	12	4	US-09-316-919-57	Sequence 57, Appl	817	6	1.4	15	1	US-08-461-838-7	Sequence 7, Appli
745	6	1.4	12	4	US-09-443-213-1	Sequence 1, Appli	818	6	1.4	15	1	US-08-575-361A-27	Sequence 27, Appl
746	6	1.4	12	4	US-09-832-297A-3	Sequence 3, Appli	819	6	1.4	15	2	US-08-564-955-67	Sequence 67, Appl
747	6	1.4	12	4	US-09-316-920A-57	Sequence 57, Appl	820	6	1.4	15	2	US-08-448-418-98	Sequence 98, Appl
748	6	1.4	12	4	US-09-883-777-12	Sequence 12, Appl	821	6	1.4	15	2	US-08-461-386-7	Sequence 7, Appli
749	6	1.4	12	4	US-09-510-238A-243	Sequence 243, App	822	6	1.4	15	2	US-08-373-190-1	Sequence 1, Appli
750	6	1.4	12	4	US-09-956-086-6	Sequence 6, Appli	823	6	1.4	15	2	US-08-373-190-2	Sequence 2, Appli
751	6	1.4	12	4	US-09-956-087-6	Sequence 6, Appli	824	6	1.4	15	2	US-08-373-190-4	Sequence 4, Appli
752	6	1.4	12	4	US-09-937-837-11	Sequence 11, Appl	825	6	1.4	15	2	US-08-480-774A-5	Sequence 5, Appli
753	6	1.4	12	4	US-09-869-445-1	Sequence 1, Appli	826	6	1.4	15	2	US-08-356-786-14	Sequence 14, Appl
754	6	1.4	12	4	US-09-625-049A-42	Sequence 42, Appl	827	6	1.4	15	2	US-08-621-751A-17	Sequence 17, Appl
755	6	1.4	12	4	US-09-830-748B-12	Sequence 12, Appl	828	6	1.4	15	2	US-08-385-335A-7	Sequence 7, Appli
756	6	1.4	12	5	PCT-US91-09133-13	Sequence 13, Appl	829	6	1.4	15	2	US-08-647-449-21	Sequence 21, Appl
757	6	1.4	12	5	PCT-US93-11138-7	Sequence 7, Appli	830	6	1.4	15	2		



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832	6	1.4	15	2	US-08-752-844-45	Sequence 45, Appl	905	6	1.4	15	4	US-08-840-713-49	Sequence 49, Appl
833	6	1.4	15	2	US-08-465-473B-17	Sequence 17, Appl	906	6	1.4	15	4	US-09-696-322-67	Sequence 67, Appl
834	6	1.4	15	2	US-08-891-848-19	Sequence 19, Appl	907	6	1.4	15	4	US-09-717-391-67	Sequence 67, Appl
835	6	1.4	15	2	US-08-438-190A-1	Sequence 1, Appl	908	6	1.4	15	4	US-09-293-533-45	Sequence 45, Appl
836	6	1.4	15	2	US-08-438-190A-2	Sequence 2, Appl	909	6	1.4	15	4	US-09-315-574-1	Sequence 1, Appl
837	6	1.4	15	2	US-08-438-190A-4	Sequence 4, Appl	910	6	1.4	15	4	US-09-696-313-67	Sequence 67, Appl
838	6	1.4	15	2	US-08-955-848A-45	Sequence 45, Appl	911	6	1.4	15	4	US-09-422-375-2	Sequence 2, Appl
839	6	1.4	15	2	US-08-656-906-27	Sequence 27, Appl	912	6	1.4	15	4	US-09-354-832B-21	Sequence 21, Appl
840	6	1.4	15	2	US-08-484-905-8	Sequence 8, Appl	913	6	1.4	15	4	US-09-491-894A-9	Sequence 9, Appl
841	6	1.4	15	2	US-08-484-905-18	Sequence 18, Appl	914	6	1.4	15	4	US-09-223-040-10	Sequence 10, Appl
842	6	1.4	15	2	US-08-591-196-45	Sequence 45, Appl	915	6	1.4	15	4	US-09-557-274-23	Sequence 23, Appl
843	6	1.4	15	2	US-08-665-202-1	Sequence 1, Appl	916	6	1.4	15	4	US-09-240-307-67	Sequence 67, Appl
844	6	1.4	15	2	US-08-331-397B-32	Sequence 32, Appl	917	6	1.4	15	4	US-09-411-067C-3	Sequence 3, Appl
845	6	1.4	15	2	US-08-759-804A-32	Sequence 32, Appl	918	6	1.4	15	4	US-09-746-359A-72	Sequence 72, Appl
846	6	1.4	15	2	US-08-889-291-31	Sequence 31, Appl	919	6	1.4	15	4	US-09-703-399A-80	Sequence 80, Appl
847	6	1.4	15	2	US-08-350-215-1	Sequence 1, Appl	920	6	1.4	15	4	US-09-700-820C-1	Sequence 1, Appl
848	6	1.4	15	3	US-08-350-215-2	Sequence 2, Appl	921	6	1.4	15	4	US-09-549-067A-34	Sequence 34, Appl
849	6	1.4	15	3	US-08-350-215-4	Sequence 4, Appl	922	6	1.4	15	4	US-09-287-849-46	Sequence 46, Appl
850	6	1.4	15	3	US-08-654-623-13	Sequence 13, Appl	923	6	1.4	15	4	US-09-380-484A-16	Sequence 16, Appl
851	6	1.4	15	3	US-08-654-623-29	Sequence 29, Appl	924	6	1.4	15	4	US-10-108-077-4	Sequence 4, Appl
852	6	1.4	15	3	US-08-481-985B-8	Sequence 8, Appl	925	6	1.4	15	4	US-09-719-243-11	Sequence 11, Appl
853	6	1.4	15	3	US-08-481-985B-18	Sequence 18, Appl	926	6	1.4	15	4	US-09-719-243-12	Sequence 12, Appl
854	6	1.4	15	3	US-08-920-610-9	Sequence 9, Appl	927	6	1.4	15	4	US-09-239-043D-2100	Sequence 2100, App
855	6	1.4	15	3	US-08-483-749A-29	Sequence 29, Appl	928	6	1.4	15	4	US-09-724-108-25	Sequence 25, Appl
856	6	1.4	15	3	US-09-287-145A-1	Sequence 1, Appl	929	6	1.4	15	4	US-09-867-262-4	Sequence 4, Appl
857	6	1.4	15	3	US-09-287-145A-2	Sequence 2, Appl	930	6	1.4	15	4	US-09-009-388C-25	Sequence 25, Appl
858	6	1.4	15	3	US-09-287-145A-4	Sequence 4, Appl	931	6	1.4	15	4	US-10-087-426-4	Sequence 4, Appl
859	6	1.4	15	3	US-08-881-037-111	Sequence 111, App	932	6	1.4	15	4	US-09-498-557-17	Sequence 17, Appl
860	6	1.4	15	3	US-08-949-758-1	Sequence 1, Appl	933	6	1.4	15	4	US-10-099-816B-4	Sequence 4, Appl
861	6	1.4	15	3	US-08-621-859-67	Sequence 67, Appl	934	6	1.4	15	4	US-09-885-551A-4	Sequence 4, Appl
862	6	1.4	15	3	US-09-046-985-13	Sequence 13, Appl	935	6	1.4	15	4	US-10-309-587A-2	Sequence 2, Appl
863	6	1.4	15	3	US-09-296-595-18	Sequence 18, Appl	936	6	1.4	15	4	US-09-554-941-14	Sequence 14, Appl
864	6	1.4	15	3	US-09-070-637-12	Sequence 12, Appl	937	6	1.4	15	4	US-09-726-219A-15	Sequence 15, Appl
865	6	1.4	15	3	US-08-501-253A-9	Sequence 9, Appl	938	6	1.4	15	4	US-09-726-219A-269	Sequence 269, App
866	6	1.4	15	3	US-09-002-753A-23	Sequence 23, Appl	939	6	1.4	15	4	US-09-726-219A-270	Sequence 270, App
867	6	1.4	15	3	US-08-370-476-8	Sequence 8, Appl	940	6	1.4	15	4	US-09-726-219A-272	Sequence 272, App
868	6	1.4	15	3	US-08-370-476-18	Sequence 18, Appl	941	6	1.4	15	4	US-09-581-345-6	Sequence 6, Appl
869	6	1.4	15	3	US-09-075-511-67	Sequence 67, Appl	942	6	1.4	15	4	US-09-798-689-17	Sequence 17, Appl
870	6	1.4	15	3	US-09-098-244-31	Sequence 31, Appl	943	6	1.4	15	4	US-09-936-885A-42	Sequence 42, Appl
871	6	1.4	15	3	US-09-099-015-67	Sequence 67, Appl	944	6	1.4	15	4	US-08-537-871A-59	Sequence 59, Appl
872	6	1.4	15	3	US-08-737-629-13	Sequence 13, Appl	945	6	1.4	15	4	PCT-US95-15696-14	Sequence 14, Appl
873	6	1.4	15	3	US-09-217-847-27	Sequence 27, Appl	946	6	1.4	15	5	PCT-US96-10435-6	Sequence 6, Appl
874	6	1.4	15	3	US-08-646-265A-111	Sequence 111, App	947	6	1.4	15	5	US-08-331-398A-54	Sequence 54, Appl
875	6	1.4	15	3	US-08-487-761-2	Sequence 2, Appl	948	6	1.4	16	1	US-08-442-461D-21	Sequence 21, Appl
876	6	1.4	15	3	US-09-474-743-13	Sequence 13, Appl	949	6	1.4	16	2	US-08-385-335A-6	Sequence 6, Appl
877	6	1.4	15	3	US-08-890-929-9	Sequence 9, Appl	950	6	1.4	16	2	US-08-750-128-9	Sequence 9, Appl
878	6	1.4	15	3	US-09-281-792B-21	Sequence 21, Appl	951	6	1.4	16	2	US-08-331-397B-54	Sequence 54, Appl
879	6	1.4	15	3	US-08-743-168B-6	Sequence 6, Appl	952	6	1.4	16	2	US-09-434-774-13	Sequence 13, Appl
880	6	1.4	15	3	US-09-227-693-32	Sequence 32, Appl	953	6	1.4	16	3	US-09-440-325A-3	Sequence 3, Appl
881	6	1.4	15	3	US-09-367-953B-21	Sequence 21, Appl	954	6	1.4	16	3	US-09-528-760A-4	Sequence 4, Appl
882	6	1.4	15	3	US-09-165-060-67	Sequence 67, Appl	955	6	1.4	16	3	US-08-983-035A-54	Sequence 54, Appl
883	6	1.4	15	3	US-08-635-928-34	Sequence 34, Appl	956	6	1.4	16	3	US-09-397-992A-20	Sequence 20, Appl
884	6	1.4	15	3	US-09-140-084-20	Sequence 20, Appl	957	6	1.4	16	3	US-09-347-504-15	Sequence 15, Appl
885	6	1.4	15	3	US-08-525-539A-67	Sequence 67, Appl	958	6	1.4	16	3	US-09-493-565-8	Sequence 8, Appl
886	6	1.4	15	3	US-08-479-737-45	Sequence 45, Appl	959	6	1.4	16	4	US-09-240-179-56	Sequence 56, Appl
887	6	1.4	15	3	US-09-240-310-67	Sequence 67, Appl	960	6	1.4	16	4	US-09-715-994-4	Sequence 4, Appl
888	6	1.4	15	3	US-09-556-111-1	Sequence 1, Appl	961	6	1.4	16	4	US-09-347-926-23	Sequence 23, Appl
889	6	1.4	15	3	US-09-556-111-2	Sequence 2, Appl	962	6	1.4	16	4	US-09-229-007A-7	Sequence 7, Appl
890	6	1.4	15	3	US-09-556-111-4	Sequence 4, Appl	963	6	1.4	16	4	US-09-796-110-4	Sequence 4, Appl
891	6	1.4	15	3	US-09-375-314-31	Sequence 31, Appl	964	6	1.4	16	4	US-09-712-529-7	Sequence 7, Appl
892	6	1.4	15	3	US-09-590-778-67	Sequence 67, Appl	965	6	1.4	16	4	US-09-731-558-10	Sequence 10, Appl
893	6	1.4	15	3	US-09-192-838B-5	Sequence 5, Appl	966	6	1.4	16	4	US-09-716-793A-4	Sequence 4, Appl
894	6	1.4	15	3	US-09-535-754-4	Sequence 4, Appl	967	6	1.4	16	4	US-09-846-996A-3	Sequence 3, Appl
895	6	1.4	15	3	US-09-590-774-67	Sequence 67, Appl	968	6	1.4	16	4	US-09-229-037-12	Sequence 12, Appl
896	6	1.4	15	3	US-09-619-550-67	Sequence 67, Appl	969	6	1.4	16	4	US-09-971-843-20	Sequence 20, Appl
897	6	1.4	15	4	US-08-475-442A-45	Sequence 45, Appl	970	6	1.4	16	4	US-09-740-510-4	Sequence 4, Appl
898	6	1.4	15	4	US-09-240-734-67	Sequence 67, Appl	971	6	1.4	16	4	US-09-555-352-34	Sequence 34, Appl
899	6	1.4	15	4	US-09-724-297-25	Sequence 25, Appl	972	6	1.4	16	4	US-09-951-843-4	Sequence 4, Appl
900	6	1.4	15	4	US-09-470-191-97	Sequence 97, Appl	973	6	1.4	16	4	US-09-395-448-12	Sequence 12, Appl
901	6	1.4	15	4	US-09-495-052-32	Sequence 32, Appl	974	6	1.4	16	4	US-09-478-681-12	Sequence 12, Appl
902	6	1.4	15	4	US-09-767-395-31	Sequence 31, Appl	975	6	1.4	16	4	US-09-634-368-17	Sequence 17, Appl
903	6	1.4	15	4	US-09-146-979-98	Sequence 98, Appl	976	6	1.4	16	4		

977	6	1.4	16	4	US-10-161-499-15	Sequence 15, Appl	1050	6	1.4	20	3	US-09-025-769B-1	Sequence 1, Appl
978	6	1.4	16	4	US-09-779-233-35	Sequence 35, Appl	1051	6	1.4	20	3	US-09-067-615-81	Sequence 81, Appl
979	6	1.4	16	4	US-09-873-135-4	Sequence 4, Appl	1052	6	1.4	20	3	US-09-067-615-89	Sequence 89, Appl
980	6	1.4	16	4	US-10-212-201A-7	Sequence 7, Appl	1053	6	1.4	20	3	US-09-425-585-12	Sequence 12, Appl
981	6	1.4	16	4	US-09-582-761B-48	Sequence 48, Appl	1054	6	1.4	20	4	US-09-603-663-75	Sequence 75, Appl
982	6	1.4	16	4	US-09-925-796-12	Sequence 12, Appl	1055	6	1.4	20	4	US-09-603-658-75	Sequence 75, Appl
983	6	1.4	16	4	US-09-941-450-12	Sequence 12, Appl	1056	6	1.4	20	4	US-09-602-373A-75	Sequence 75, Appl
984	6	1.4	16	4	US-10-113-424-7	Sequence 7, Appl	1057	6	1.4	20	4	US-08-716-249-9	Sequence 9, Appl
985	6	1.4	16	4	US-09-716-637-10	Sequence 10, Appl	1058	6	1.4	20	4	US-09-422-375-1	Sequence 1, Appl
986	6	1.4	16	4	US-09-968-362A-23	Sequence 23, Appl	1059	6	1.4	20	4	US-09-333-213-3	Sequence 3, Appl
987	6	1.4	16	4	US-09-625-049A-39	Sequence 39, Appl	1060	6	1.4	20	4	US-09-953-321-12	Sequence 12, Appl
988	6	1.4	16	4	US-09-706-243A-12	Sequence 12, Appl	1061	6	1.4	20	4	US-09-490-070A-1	Sequence 1, Appl
989	6	1.4	16	4	US-10-212-355-7	Sequence 7, Appl	1062	6	1.4	20	4	US-09-490-153-1	Sequence 1, Appl
990	6	1.4	17	1	US-08-463-163-5	Sequence 5, Appl	1063	6	1.4	20	4	US-08-302-758B-10	Sequence 10, Appl
991	6	1.4	17	2	US-08-484-905-10	Sequence 10, Appl	1064	6	1.4	20	4	US-10-077-210-3	Sequence 3, Appl
992	6	1.4	17	3	US-08-481-985B-10	Sequence 10, Appl	1065	6	1.4	20	4	US-09-490-324-1	Sequence 1, Appl
993	6	1.4	17	3	US-08-370-476-10	Sequence 10, Appl	1066	6	1.4	20	5	PCT-US95-04468-55	Sequence 55, Appl
994	6	1.4	17	3	US-08-890-929-1	Sequence 1, Appl	1067	6	1.4	20	5	PCT-US95-09816A-81	Sequence 81, Appl
995	6	1.4	17	4	US-09-646-028-57	Sequence 57, Appl	1068	6	1.4	20	5	PCT-US95-09816A-89	Sequence 89, Appl
996	6	1.4	17	4	US-09-634-368-21	Sequence 21, Appl	1069	6	1.4	21	1	US-07-679-052A-9	Sequence 9, Appl
997	6	1.4	17	4	US-09-634-368-32	Sequence 32, Appl	1070	6	1.4	21	2	US-08-484-905-14	Sequence 14, Appl
998	6	1.4	17	4	US-08-346-293-9	Sequence 9, Appl	1071	6	1.4	21	3	US-08-851-749-1	Sequence 1, Appl
999	6	1.4	18	1	US-07-972-032-84	Sequence 84, Appl	1072	6	1.4	21	3	US-08-481-985B-14	Sequence 14, Appl
1000	6	1.4	18	1	US-08-207-169A-7	Sequence 7, Appl	1073	6	1.4	21	3	US-08-370-476-14	Sequence 14, Appl
1001	6	1.4	18	1	US-08-642-255-135	Sequence 135, Appl	1074	6	1.4	21	4	US-09-446-787B-4	Sequence 4, Appl
1002	6	1.4	18	3	US-08-469-318-188	Sequence 188, Appl	1075	6	1.4	21	4	US-08-406-824A-17	Sequence 17, Appl
1003	6	1.4	18	3	US-08-469-318-189	Sequence 189, Appl	1076	6	1.4	21	4	US-09-512-563C-26	Sequence 26, Appl
1004	6	1.4	18	3	US-08-469-318-190	Sequence 190, Appl	1077	6	1.4	21	4	US-09-512-563C-26	Sequence 26, Appl
1005	6	1.4	18	3	US-08-468-609A-188	Sequence 188, Appl	1078	6	1.4	21	4	US-09-625-049A-38	Sequence 38, Appl
1006	6	1.4	18	3	US-08-468-609A-189	Sequence 189, Appl	1079	6	1.4	21	6	5182195-7	Patent No. 5182195
1007	6	1.4	18	3	US-08-468-609A-190	Sequence 190, Appl	1080	6	1.4	21	6	5182195-7	Patent No. 5182195
1008	6	1.4	18	3	US-08-949-758-2	Sequence 2, Appl	1081	6	1.4	22	1	US-08-264-003-14	Sequence 14, Appl
1009	6	1.4	18	3	US-08-446-872A-188	Sequence 188, Appl	1082	6	1.4	22	1	US-08-225-224-56	Sequence 56, Appl
1010	6	1.4	18	3	US-08-446-872A-189	Sequence 189, Appl	1083	6	1.4	22	3	US-08-722-258-56	Sequence 56, Appl
1011	6	1.4	18	3	US-08-446-872A-190	Sequence 190, Appl	1084	6	1.4	22	3	US-08-469-318-196	Sequence 196, Appl
1012	6	1.4	18	3	US-09-215-212-6	Sequence 6, Appl	1085	6	1.4	22	3	US-08-446-872A-196	Sequence 196, Appl
1013	6	1.4	18	4	US-08-762-227A-188	Sequence 188, Appl	1086	6	1.4	22	4	US-08-762-227A-196	Sequence 196, Appl
1014	6	1.4	18	4	US-08-762-227A-189	Sequence 189, Appl	1087	6	1.4	22	4	US-08-406-824A-24	Sequence 24, Appl
1015	6	1.4	18	4	US-08-762-227A-190	Sequence 190, Appl	1088	6	1.4	22	4	US-09-376-463-18	Sequence 18, Appl
1016	6	1.4	18	4	US-09-634-368-19	Sequence 19, Appl	1089	6	1.4	22	5	PCT-US95-01185-196	Sequence 196, Appl
1017	6	1.4	18	5	PCT-US95-01185-188	Sequence 188, Appl	1090	6	1.4	22	5	PCT-US95-04468-56	Sequence 56, Appl
1018	6	1.4	18	5	PCT-US95-01185-189	Sequence 189, Appl	1091	6	1.4	23	3	US-09-215-212-5	Sequence 5, Appl
1019	6	1.4	18	5	PCT-US95-01185-190	Sequence 190, Appl	1092	6	1.4	24	2	US-08-256-156A-2	Sequence 2, Appl
1020	6	1.4	18	6	5182195-2	Patent No. 5182195	1093	6	1.4	24	2	US-08-902-623-16	Sequence 16, Appl
1021	6	1.4	18	6	5182195-2	Patent No. 5182195	1094	6	1.4	24	4	US-09-643-657-35	Sequence 35, Appl
1022	6	1.4	19	1	US-07-679-052A-1	Sequence 1, Appl	1095	6	1.4	24	4	US-09-851-271A-12	Sequence 12, Appl
1023	6	1.4	19	2	US-08-448-418-90	Sequence 90, Appl	1096	6	1.4	25	4	US-09-254-832B-22	Sequence 22, Appl
1024	6	1.4	19	2	US-08-484-905-12	Sequence 12, Appl	1097	6	1.4	25	4	US-09-376-463-4	Sequence 4, Appl
1025	6	1.4	19	2	US-09-018-760-2	Sequence 2, Appl	1098	6	1.4	26	1	US-08-281-702A-6	Sequence 6, Appl
1026	6	1.4	19	3	US-08-481-985B-12	Sequence 12, Appl	1099	6	1.4	26	2	US-08-618-917-6	Sequence 6, Appl
1027	6	1.4	19	3	US-08-993-380-2	Sequence 2, Appl	1100	6	1.4	26	2	US-08-596-387B-97	Sequence 97, Appl
1028	6	1.4	19	3	US-08-370-476-12	Sequence 12, Appl	1101	6	1.4	26	3	US-08-545-196B-58	Sequence 58, Appl
1029	6	1.4	19	4	US-08-716-249-1	Sequence 1, Appl	1102	6	1.4	26	3	US-09-439-897-63	Sequence 63, Appl
1030	6	1.4	19	4	US-09-368-819A-6	Sequence 6, Appl	1103	6	1.4	26	3	US-09-067-615-97	Sequence 97, Appl
1031	6	1.4	19	4	US-09-146-979-90	Sequence 90, Appl	1104	6	1.4	26	5	PCT-US95-09816A-97	Sequence 97, Appl
1032	6	1.4	19	4	US-09-634-368-25	Sequence 25, Appl	1105	6	1.4	27	4	US-09-270-767-59868	Sequence 59868, A
1033	6	1.4	19	4	US-08-302-756B-5	Sequence 5, Appl	1106	6	1.4	28	1	US-08-478-312-16	Sequence 16, Appl
1034	6	1.4	19	4	US-09-376-463-22	Sequence 22, Appl	1107	6	1.4	28	1	US-08-485-302-16	Sequence 16, Appl
1035	6	1.4	20	1	US-07-987-286-18	Sequence 18, Appl	1108	6	1.4	28	1	US-08-476-169-12	Sequence 12, Appl
1036	6	1.4	20	1	US-08-225-224-55	Sequence 55, Appl	1109	6	1.4	28	1	US-08-484-083-12	Sequence 12, Appl
1037	6	1.4	20	2	US-08-596-387B-81	Sequence 81, Appl	1110	6	1.4	28	2	US-08-400-115-21	Sequence 21, Appl
1038	6	1.4	20	2	US-08-596-387B-89	Sequence 89, Appl	1111	6	1.4	28	3	US-08-957-001B-25	Sequence 25, Appl
1039	6	1.4	20	2	US-08-614-626-18	Sequence 18, Appl	1112	6	1.4	28	3	US-09-496-301-25	Sequence 25, Appl
1040	6	1.4	20	2	US-08-934-915-19	Sequence 19, Appl	1113	6	1.4	28	3	US-09-215-212-4	Sequence 4, Appl
1041	6	1.4	20	2	US-08-934-915-95	Sequence 95, Appl	1114	6	1.4	28	4	US-09-235-230-12	Sequence 12, Appl
1042	6	1.4	20	2	US-08-751-767A-14	Sequence 14, Appl	1115	6	1.4	29	1	US-08-478-312-14	Sequence 14, Appl
1043	6	1.4	20	3	US-08-851-749-6	Sequence 6, Appl	1116	6	1.4	29	1	US-08-478-312-17	Sequence 17, Appl
1044	6	1.4	20	3	US-08-654-623-15	Sequence 15, Appl	1117	6	1.4	29	1	US-08-485-302-14	Sequence 14, Appl
1045	6	1.4	20	3	US-08-722-258-55	Sequence 55, Appl	1118	6	1.4	29	1	US-08-485-302-17	Sequence 17, Appl
1046	6	1.4	20	3	US-09-046-985-14	Sequence 14, Appl	1119	6	1.4	29	1	US-08-476-169-10	Sequence 10, Appl
1047	6	1.4	20	3	US-09-474-743-14	Sequence 14, Appl	1120	6	1.4	29	1	US-08-476-169-13	Sequence 13, Appl
1048	6	1.4	20	3	US-09-178-115-116	Sequence 116, Appl	1121	6	1.4	29	1	US-08-484-083-10	Sequence 10, Appl
1049	6	1.4	20	3	US-09-177-776-116	Sequence 116, Appl	1122	6	1.4	29	1	US-08-484-083-13	Sequence 13, Appl

1123	6	1.4	29	4	US-09-270-767-35666	Sequence 35666, A	1196	6	1.4	36	4	US-08-762-227A-50	Sequence 50, Appl
1124	6	1.4	29	4	US-09-270-767-50883	Sequence 50883, A	1197	6	1.4	36	4	US-09-140-749-12	Sequence 12, Appl
1125	6	1.4	29	4	US-09-419-381-48	Sequence 48, Appl	1198	6	1.4	36	4	US-09-510-238A-9	Sequence 9, Appl
1126	6	1.4	30	1	US-08-478-312-18	Sequence 18, Appl	1199	6	1.4	36	4	US-09-936-885A-5	Sequence 5, Appl
1127	6	1.4	30	1	US-08-485-302-18	Sequence 18, Appl	1200	6	1.4	36	5	PCT-US95-01185-50	Sequence 50, Appl
1128	6	1.4	30	1	US-08-476-169-14	Sequence 14, Appl	1201	6	1.4	37	1	US-08-346-293-26	Sequence 26, Appl
1129	6	1.4	30	1	US-08-484-083-14	Sequence 14, Appl	1202	6	1.4	37	4	US-09-975-413A-14	Sequence 14, Appl
1130	6	1.4	31	1	US-08-478-312-15	Sequence 15, Appl	1203	6	1.4	37	4	US-09-975-413A-17	Sequence 17, Appl
1131	6	1.4	31	1	US-08-478-312-19	Sequence 19, Appl	1204	6	1.4	37	4	US-09-975-413A-23	Sequence 23, Appl
1132	6	1.4	31	1	US-08-485-302-15	Sequence 15, Appl	1205	6	1.4	38	4	US-09-446-787B-1	Sequence 1, Appl
1133	6	1.4	31	1	US-08-485-302-19	Sequence 19, Appl	1206	6	1.4	39	3	US-08-941-445A-37	Sequence 37, Appl
1134	6	1.4	31	1	US-08-476-169-11	Sequence 11, Appl	1207	6	1.4	39	3	US-09-314-268-98	Sequence 98, Appl
1135	6	1.4	31	1	US-08-476-169-15	Sequence 15, Appl	1208	6	1.4	39	4	US-09-857-401B-4	Sequence 4, Appl
1136	6	1.4	31	1	US-08-484-083-11	Sequence 11, Appl	1209	6	1.4	40	3	US-08-815-190A-17	Sequence 17, Appl
1137	6	1.4	31	1	US-08-484-083-15	Sequence 15, Appl	1210	6	1.4	40	4	US-09-333-213-1	Sequence 1, Appl
1138	6	1.4	31	3	US-08-789-333B-12	Sequence 12, Appl	1211	6	1.4	42	1	US-08-078-683A-12	Sequence 12, Appl
1139	6	1.4	31	3	US-09-169-015-22	Sequence 22, Appl	1212	6	1.4	42	1	US-08-377-687-39	Sequence 39, Appl
1140	6	1.4	31	3	US-08-743-168B-5	Sequence 5, Appl	1213	6	1.4	42	2	US-08-777-192-39	Sequence 39, Appl
1141	6	1.4	31	3	US-09-133-944-12	Sequence 12, Appl	1214	6	1.4	42	2	US-08-143-311B-4	Sequence 4, Appl
1142	6	1.4	31	3	US-09-507-819-64	Sequence 64, Appl	1215	6	1.4	42	3	US-08-971-982-39	Sequence 39, Appl
1143	6	1.4	31	4	US-09-208-827-13	Sequence 13, Appl	1216	6	1.4	42	4	US-08-753-851-4	Sequence 4, Appl
1144	6	1.4	31	4	US-08-787-738B-12	Sequence 12, Appl	1217	6	1.4	42	4	US-08-471-970A-12	Sequence 12, Appl
1145	6	1.4	31	4	US-09-157-748-15	Sequence 15, Appl	1218	6	1.4	42	4	US-09-723-677B-12	Sequence 12, Appl
1146	6	1.4	31	4	US-09-800-170-65	Sequence 65, Appl	1219	6	1.4	43	4	US-09-376-463-26	Sequence 26, Appl
1147	6	1.4	31	4	US-09-641-576-64	Sequence 64, Appl	1220	6	1.4	44	1	US-08-361-920-15	Sequence 15, Appl
1148	6	1.4	31	4	US-09-626-581B-25	Sequence 25, Appl	1221	6	1.4	44	1	US-08-479-939-15	Sequence 15, Appl
1149	6	1.4	31	4	US-09-415-765B-25	Sequence 25, Appl	1222	6	1.4	44	1	US-08-483-432-15	Sequence 15, Appl
1150	6	1.4	31	4	US-09-486-814A-10	Sequence 10, Appl	1223	6	1.4	45	1	US-08-451-947-97	Sequence 97, Appl
1151	6	1.4	31	4	US-09-626-580C-25	Sequence 25, Appl	1224	6	1.4	45	2	US-08-424-826A-97	Sequence 97, Appl
1152	6	1.4	31	4	US-09-749-959-21	Sequence 21, Appl	1225	6	1.4	45	2	US-08-935-450-11	Sequence 11, Appl
1153	6	1.4	31	4	US-10-043-074-13	Sequence 13, Appl	1226	6	1.4	45	3	US-08-928-694-97	Sequence 97, Appl
1154	6	1.4	31	4	US-08-437-943B-60	Sequence 60, Appl	1227	6	1.4	45	3	US-08-900-230-7	Sequence 7, Appl
1155	6	1.4	31	4	US-09-270-767-37318	Sequence 37318, A	1228	6	1.4	45	4	US-08-450-842-97	Sequence 97, Appl
1156	6	1.4	31	4	US-09-270-767-52535	Sequence 52535, A	1229	6	1.4	45	4	US-08-451-390-97	Sequence 97, Appl
1157	6	1.4	31	4	US-09-285-912A-75	Sequence 75, Appl	1230	6	1.4	45	4	US-09-338-123-11	Sequence 11, Appl
1158	6	1.4	31	4	US-09-578-030-16	Sequence 16, Appl	1231	6	1.4	45	5	PCT-US91-06950-97	Sequence 97, Appl
1159	6	1.4	31	4	US-09-916-940-12	Sequence 12, Appl	1232	6	1.4	46	4	US-08-257-029-5	Sequence 5, Appl
1160	6	1.4	31	4	US-09-419-381-59	Sequence 59, Appl	1233	6	1.4	46	4	US-08-896-063-5	Sequence 5, Appl
1161	6	1.4	31	4	US-10-142-662-26	Sequence 26, Appl	1234	6	1.4	47	3	US-09-314-268-97	Sequence 97, Appl
1162	6	1.4	31	4	US-10-096-550-12	Sequence 12, Appl	1235	6	1.4	47	4	US-09-376-463-32	Sequence 32, Appl
1163	6	1.4	31	5	PCT-US96-10435-12	Sequence 12, Appl	1236	6	1.4	48	1	US-07-796-361A-15	Sequence 15, Appl
1164	6	1.4	31	5	PCT-US96-10435-5	Sequence 5, Appl	1237	6	1.4	48	4	US-09-270-767-59367	Sequence 59367, A
1165	6	1.4	32	1	US-08-478-312-20	Sequence 20, Appl	1238	6	1.4	48	4	US-09-376-463-29	Sequence 29, Appl
1166	6	1.4	32	1	US-08-485-302-20	Sequence 20, Appl	1239	6	1.4	49	3	US-08-963-851-3	Sequence 3, Appl
1167	6	1.4	32	1	US-08-476-169-16	Sequence 16, Appl	1240	6	1.4	51	3	US-08-941-445A-19	Sequence 19, Appl
1168	6	1.4	32	1	US-08-484-083-16	Sequence 16, Appl	1241	6	1.4	51	4	US-09-336-536-71	Sequence 71, Appl
1169	6	1.4	32	1	US-08-464-531-34	Sequence 34, Appl	1242	6	1.4	54	1	US-07-972-032-59	Sequence 59, Appl
1170	6	1.4	32	2	US-08-461-598-34	Sequence 34, Appl	1243	6	1.4	54	1	US-08-497-134A-16	Sequence 16, Appl
1171	6	1.4	32	3	US-08-322-137-34	Sequence 34, Appl	1244	6	1.4	54	1	US-08-209-747-29	Sequence 29, Appl
1172	6	1.4	32	3	US-08-743-168B-47	Sequence 47, Appl	1245	6	1.4	54	1	US-08-458-298-29	Sequence 29, Appl
1173	6	1.4	32	3	US-08-743-168B-48	Sequence 48, Appl	1246	6	1.4	54	1	US-08-642-255-71	Sequence 71, Appl
1174	6	1.4	32	3	US-08-743-168B-49	Sequence 49, Appl	1247	6	1.4	54	4	US-09-513-999C-6289	Sequence 6289, Ap
1175	6	1.4	32	3	US-08-743-168B-50	Sequence 50, Appl	1248	6	1.4	55	3	US-09-029-424-17	Sequence 17, Appl
1176	6	1.4	32	3	US-08-743-168B-51	Sequence 51, Appl	1249	6	1.4	55	3	US-09-361-707-76	Sequence 76, Appl
1177	6	1.4	32	3	US-08-743-168B-52	Sequence 52, Appl	1250	6	1.4	55	3	US-09-361-707-77	Sequence 77, Appl
1178	6	1.4	32	3	US-08-743-168B-53	Sequence 53, Appl	1251	6	1.4	55	3	US-09-361-707-78	Sequence 78, Appl
1179	6	1.4	32	4	US-09-563-222C-100	Sequence 100, App	1252	6	1.4	55	3	US-09-361-707-79	Sequence 79, Appl
1180	6	1.4	32	4	US-09-377-502-48	Sequence 48, Appl	1253	6	1.4	55	3	US-09-361-707-80	Sequence 80, Appl
1181	6	1.4	33	1	US-08-478-312-21	Sequence 21, Appl	1254	6	1.4	55	3	US-09-361-707-81	Sequence 81, Appl
1182	6	1.4	33	1	US-08-485-302-21	Sequence 21, Appl	1255	6	1.4	55	3	US-09-361-707-82	Sequence 82, Appl
1183	6	1.4	33	1	US-08-476-169-17	Sequence 17, Appl	1256	6	1.4	55	3	US-09-361-707-83	Sequence 83, Appl
1184	6	1.4	33	1	US-08-484-083-17	Sequence 17, Appl	1257	6	1.4	55	3	US-09-361-707-84	Sequence 84, Appl
1185	6	1.4	33	1	US-09-215-212-3	Sequence 3, Appl	1258	6	1.4	55	3	US-09-361-707-85	Sequence 85, Appl
1186	6	1.4	34	4	US-09-270-767-57471	Sequence 57471, A	1259	6	1.4	55	3	US-09-361-707-86	Sequence 86, Appl
1187	6	1.4	35	4	US-09-975-413A-13	Sequence 13, Appl	1260	6	1.4	55	3	US-09-361-707-87	Sequence 87, Appl
1188	6	1.4	35	4	US-09-975-413A-16	Sequence 16, Appl	1261	6	1.4	55	3	US-09-361-707-88	Sequence 88, Appl
1189	6	1.4	36	2	US-08-470-775-11	Sequence 11, Appl	1262	6	1.4	55	3	US-09-361-707-89	Sequence 89, Appl
1190	6	1.4	36	3	US-08-469-318-50	Sequence 50, Appl	1263	6	1.4	55	3	US-09-361-707-90	Sequence 90, Appl
1191	6	1.4	36	3	US-08-468-609A-50	Sequence 50, Appl	1264	6	1.4	55	3	US-09-361-707-91	Sequence 91, Appl
1192	6	1.4	36	3	US-08-192-325B-50	Sequence 50, Appl	1265	6	1.4	55	3	US-09-361-707-92	Sequence 92, Appl
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## ALIGNMENTS

## RESULT 1

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; Sequence 256, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
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; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
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; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
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; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725

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; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22487
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22487

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Query Match          3.2%; Score 14; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 270 GSSSGSSSGSSSG 283
DB 68 GSSSGSSSGSSSG 81

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RESULT 5
US-09-248-796A-23892
; Sequence 23892, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23892
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23892

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Query Match          2.7%; Score 12; DB 4; Length 80;
Best Local Similarity 100.0%; Pred. No. 0.01;
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QY 279 GSSSGSSSGSS 290
DB 49 GSSSGSSSGSS 60

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RESULT 6
US-09-949-016-7198
; Sequence 7198, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7198
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Human

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US-09-949-016-7198

Query Match 2.5%; Score 11; DB 4; Length 663;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 GSSGSSGSSG 285

Db 578 GSSGSSGSSG 588

RESULT 7

US-09-248-796A-22352  
; Sequence 22352, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 22352  
; LENGTH: 180  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-22352

Query Match 2.3%; Score 10; DB 4; Length 180;

Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 270 GSSGSSGSSG 279

Db 68 GSSGSSGSSG 77

RESULT 8

US-09-949-016-9109  
; Sequence 9109, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9109  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9109

Query Match 2.3%; Score 10; DB 4; Length 214;

Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 SSSGSSGSSG 281

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Db 118 SSSGSSGSSG 127

RESULT 9

US-09-949-016-6315  
; Sequence 6315, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6315  
; LENGTH: 441  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6315

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Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 SSSGSSGSSG 281

Db 345 SSSGSSGSSG 354

RESULT 10

US-09-248-796A-26119  
; Sequence 26119, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 26119  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-26119

Query Match 2.3%; Score 10; DB 4; Length 541;

Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 SGSSGSSGSSG 283

Db 407 SGSSGSSGSSG 416

RESULT 11

US-09-134-000C-6510  
; Sequence 6510, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:

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; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6510
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-6510

Query Match      2.0%; Score 9; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 ACLLALCL 16
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Db      32 ACLLALCL 40

RESULT 12
US-09-107-532A-5997
; Sequence 5997, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5997:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...184
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; SEQUENCE DESCRIPTION: SEQ ID NO: 5997:
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Db      32 ACLLALCL 40

RESULT 13
US-09-248-796A-14345
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; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14345
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-14345

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Best Local Similarity 100.0%; Pred. No. 15;
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QY      274 SGSSSGSS 282
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Db      345 SGSSSGSS 353

RESULT 14
US-09-270-767-43154
; Sequence 43154, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43154
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-43154

Query Match      2.0%; Score 9; DB 4; Length 512;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      269 SGSSSGSS 277
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Db      308 SGSSSGSS 316

RESULT 15
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US-09-381-656-1
; Sequence 1, Application US/09381656
; Patent No. 6645509
; GENERAL INFORMATION:
; APPLICANT: SERRE, Guy Bruno Rene
; APPLICANT: SIMON, Michel
; APPLICANT: WEBER-VIVAT, Marina
; TITLE OF INVENTION: POLYPEPTIDE EXPRESSED IN THE HORNY LAYER OF EPIDERMIS
; TITLE OF INVENTION: AND USE THEREOF
; FILE REFERENCE: 016800-336
; CURRENT APPLICATION NUMBER: US/09/381,656
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: FR 97/03899
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: FR 97/11317
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Human
US-09-381-656-1

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Db      88 SSGSSSGSS 96

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#### SUMMARIES

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516	440	100.0	440	14	US-10-223-085-150
522	440	100.0	440	14	US-10-219-065-156
565	440	100.0	440	14	US-10-223-084-150
566	440	100.0	440	14	US-10-223-088-150
567	440	100.0	440	14	US-10-223-090-150
573	440	100.0	440	14	US-10-223-087-150
586	440	100.0	440	14	US-10-223-083-150
592	440	100.0	440	14	US-10-223-089-150
618	440	100.0	440	14	US-10-174-587-202
688	440	100.0	440	14	US-10-063-742-52
764	440	100.0	440	14	US-10-013-909A-52
769	440	100.0	440	14	US-10-223-081-150
807	440	100.0	440	14	US-10-223-082-150

839	440	100.0	440	15	US-10-305-654-150	Sequence 150, App
848	440	100.0	440	15	US-10-081-056-150	Sequence 150, App
859	440	100.0	440	17	US-10-972-317-52	Sequence 52, Appl
860	178	40.5	386	14	US-10-050-704-100	Sequence 100, App
861	178	40.5	386	16	US-10-798-512-100	Sequence 100, App
862	55	12.5	116	10	US-09-764-891-2877	Sequence 2877, Ap
863	15	3.4	1751	15	US-10-282-122A-53633	Sequence 53633, A
864	11	2.5	1779	16	US-10-437-963-199226	Sequence 199226,
865	11	2.5	202	14	US-10-156-761-11822	Sequence 11822, A
866	11	2.5	270	16	US-10-755-889-660	Sequence 660, App
867	11	2.5	270	17	US-10-959-539-9	Sequence 9, Appli
868	11	2.5	415	15	US-10-268-913-4	Sequence 4, Appli
869	11	2.5	452	14	US-10-004-2198-9	Sequence 9, Appli
870	11	2.5	473	14	US-10-004-2198-4	Sequence 3, Appli
871	11	2.5	520	15	US-10-268-919-3	Sequence 56, Appl
872	11	2.5	953	15	US-10-369-022-56	Sequence 98, Appl
873	11	2.5	953	15	US-10-042-865-98	Sequence 97, Appl
874	11	2.5	954	15	US-10-042-865-97	Sequence 187, App
875	11	2.5	954	15	US-10-263-929-187	Sequence 326, App
876	10	2.3	10	10	US-09-572-404B-326	Sequence 5, Appli
877	10	2.3	15	16	US-10-682-675-5	Sequence 59331, A
878	10	2.3	102	16	US-10-767-701-59331	Sequence 23, Appl
879	10	2.3	119	14	US-10-072-977-23	Sequence 14299, A
880	10	2.3	165	14	US-10-156-761-14299	Sequence 7, Appli
881	10	2.3	368	15	US-10-268-919-7	Sequence 110978,
882	10	2.3	441	15	US-10-295-027-512	Sequence 14, Appl
883	10	2.3	454	16	US-10-437-963-110978	Sequence 5, Appli
884	10	2.3	455	14	US-10-004-2198-14	Sequence 204, App
885	10	2.3	476	14	US-10-004-2198-1	Sequence 324, App
886	10	2.3	476	15	US-10-268-919-5	Sequence 255309,
887	10	2.3	628	15	US-10-282-122A-53269	Sequence 276650,
888	10	2.3	866	14	US-10-081-872-204	Sequence 71, App
889	10	2.3	866	15	US-10-385-305-204	Sequence 71, App
890	9	2.0	10	10	US-09-572-404B-324	Sequence 146838,
891	9	2.0	71	15	US-10-424-599-255309	Sequence 263513,
892	9	2.0	84	15	US-10-424-599-276650	Sequence 731, App
893	9	2.0	111	15	US-10-316-175-72	Sequence 281257,
894	9	2.0	146	15	US-10-316-175-71	Sequence 1291, Ap
895	9	2.0	146	15	US-10-425-114-55131	Sequence 836, App
896	9	2.0	162	15	US-10-424-599-146838	Sequence 34046, A
897	9	2.0	164	15	US-10-424-599-263513	Sequence 201367,
898	9	2.0	175	9	US-09-925-297-731	Sequence 195851,
899	9	2.0	176	15	US-10-424-599-281257	Sequence 150318,
900	9	2.0	199	9	US-09-764-864-1291	Sequence 168724,
901	9	2.0	201	9	US-09-764-864-836	Sequence 10974, A
902	9	2.0	219	14	US-10-029-386-34046	Sequence 201378,
903	9	2.0	244	16	US-10-437-963-201367	Sequence 124370,
904	9	2.0	269	16	US-10-437-963-195851	Sequence 1582, Ap
905	9	2.0	337	15	US-10-424-599-150318	Sequence 12, Appl
906	9	2.0	365	15	US-10-424-599-168724	Sequence 16, Appl
907	9	2.0	420	14	US-10-156-761-10974	Sequence 61, Appl
908	9	2.0	420	16	US-10-437-963-201378	Sequence 3, Appli
909	9	2.0	441	16	US-10-437-963-124370	Sequence 15, Appl
910	9	2.0	476	9	US-09-925-300-1582	Sequence 6, Appli
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912	9	2.0	486	17	US-10-883-805-16	Sequence 4977, Ap
913	9	2.0	529	14	US-10-164-230-61	Sequence 1666, Ap
914	9	2.0	529	14	US-10-204-884-3	Sequence 4978, Ap
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916	9	2.0	529	17	US-10-883-805-6	Sequence 17, Appl
917	9	2.0	634	15	US-10-108-260A-3174	Sequence 16, Appl
918	9	2.0	668	15	US-10-335-977-4977	Sequence 152, App
919	9	2.0	675	15	US-10-389-566-1666	Sequence 316, App
920	9	2.0	677	15	US-10-335-977-4978	Sequence 3316, Ap
921	9	2.0	720	16	US-10-437-963-124368	Sequence 3328, Ap
922	9	2.0	1795	8	US-08-973-363-17	Sequence 33, Appl
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927	8	1.8	10	10	US-09-572-404B-3328	
928	8	1.8	10	10	US-10-365-095-33	
929	8	1.8	16	15	US-10-365-095-10	

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933	8	1.8	54	15	US-10-421-599-217531	Sequence 301, App	1006	8	1.8	381	15	US-10-295-027-560	Sequence 660, App
934	8	1.8	62	10	US-09-903-190-137	Sequence 127, App	1007	8	1.8	388	15	US-10-425-114-72685	Sequence 72685, A
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984	8	1.8	311	14	US-10-025-806-74	Sequence 74, Appl	1057	8	1.8	646	17	US-10-893-588-27	Sequence 27, Appl
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997	8	1.8	334	14	US-10-335-394-53	Sequence 53, Appl	1070	8	1.8	724	15	US-10-108-260A-3263	Sequence 3263, Ap
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1083	8	1.8	766	15	US-10-288-798-14	Sequence 14, Appli	1156	1.6	10	10	US-09-572-404B-44	Sequence 44, Appl
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1125	8	1.8	1199	14	US-10-024-197-2	Sequence 2, Appli	1198	1.6	26	15	US-10-253-493-424	Sequence 424, App
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1136	8	1.8	1394	16	US-10-618-941-132	Sequence 132, App	1209	1.6	38	14	US-10-148-306-2	Sequence 2, Appli
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1414	7	1.6	199	14	US-10-156-761-11345	Sequence 11345, A	1487	7	1.6	238	15	US-10-425-114-54825	Sequence 54825, A
1415	7	1.6	199	14	US-10-021-660-82	Sequence 82, Appli	1488	7	1.6	238	15	US-10-634-862-42	Sequence 42, Appli
1416	7	1.6	201	16	US-10-767-701-38455	Sequence 38455, A	1489	7	1.6	238	15	US-10-437-963-145158	Sequence 145158,
1417	7	1.6	203	15	US-10-424-599-239741	Sequence 239741,	1490	7	1.6	241	15	US-10-424-599-225595	Sequence 225595,
1418	7	1.6	204	15	US-10-424-599-256803	Sequence 256803,	1491	7	1.6	242	9	US-09-887-853-6	Sequence 6, Appli
1419	7	1.6	204	16	US-10-437-963-175115	Sequence 175115,	1492	7	1.6	243	17	US-10-683-547-6	Sequence 6, Appli
1420	7	1.6	205	13	US-09-919-038-258	Sequence 258, App	1493	7	1.6	244	15	US-10-424-599-146309	Sequence 146309,
1421	7	1.6	205	13	US-10-081-218-1	Sequence 1, Appli	1494	7	1.6	246	15	US-10-424-599-146308	Sequence 146308,
1422	7	1.6	205	14	US-10-050-704-98	Sequence 98, Appli	1495	7	1.6	246	15	US-10-424-599-146308	Sequence 8493, Ap
1423	7	1.6	205	15	US-10-424-599-176535	Sequence 176535,	1496	7	1.6	247	16	US-10-335-977-8493	Sequence 8493, Ap
1424	7	1.6	205	16	US-10-424-986-10	Sequence 10, Appli	1497	7	1.6	247	16	US-10-437-963-164964	Sequence 164964,
1425	7	1.6	205	16	US-10-798-512-98	Sequence 98, Appli	1498	7	1.6	248	15	US-09-934-455-214	Sequence 214, App
1426	7	1.6	209	15	US-10-424-599-258441	Sequence 258441,	1499	7	1.6	248	15	US-10-225-066A-4	Sequence 4, Appli
1427	7	1.6	209	16	US-10-437-963-127261	Sequence 127261,	1500	7	1.6	248	15	US-10-374-780A-270	Sequence 270, App
1428	7	1.6	211	14	US-10-016-986-34	Sequence 34, Appli				249	10	US-09-880-748-689	Sequence 689, App
1429	7	1.6	211	15	US-10-225-066A-514	Sequence 514, App							
1430	7	1.6	211	15	US-10-273-973-16	Sequence 16, Appli							
1431	7	1.6	211	15	US-10-225-067-62	Sequence 62, Appli							
1432	7	1.6	211	15	US-10-374-780A-66	Sequence 66, Appli							
1433	7	1.6	211	15	US-10-412-699B-1766	Sequence 1766, Ap							
1434	7	1.6	211	16	US-10-437-963-114922	Sequence 114922,							
1435	7	1.6	214	16	US-10-437-963-119143	Sequence 119143,							
1436	7	1.6	215	16	US-10-437-963-115946	Sequence 115946,							
1437	7	1.6	216	10	US-09-795-872-5	Sequence 5, Appli							
1438	7	1.6	216	16	US-10-437-963-161235	Sequence 161235,							
1439	7	1.6	216	16	US-10-662-824-5	Sequence 5, Appli							
1440	7	1.6	216	16	US-10-767-701-32345	Sequence 32345, A							

Search completed: April 7, 2005, 00:36:25  
Job time : 152 secs

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OM protein - protein search, using sw model

Run on: April 7, 2005, 00:25:58 ; Search time 46 Seconds  
(without alignments)  
920.334 Million cell updates/sec

Title: US-10-063-561-52

Perfect score: 440

Sequence: 1 MKFGQPLACLLALCLGSGE.....KLGFINWDINKDQRSSRIP 440

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

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Post-processing: Listing first 1500 summaries

Database :

PIR\_79:\*

1: pir1:\*

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4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	3.0	1428	2 T08852	lustrin A - Califo
2	12	2.7	683	2 A82704	1,4-beta-cellobios
3	11	2.5	644	2 S39356	transcription fact
4	11	2.5	954	1 S68178	mixed-lineage prot
5	11	2.5	1570	2 T18272	1-phosphatidylinos
6	10	2.3	441	2 G01758	transcription fact
7	10	2.3	510	2 T37541	probable glycolipi
8	10	2.3	542	2 T06728	pectate lyase (EC
9	10	2.3	643	1 KRH02	keratin 1, type II
10	10	2.3	710	2 S28014	outD protein - Erw
11	10	2.3	1469	2 T09219	basal transcriptio
12	10	2.3	1891	2 T13594	hypothetical prote
13	10	2.3	1920	2 T13893	gene binding respon
14	9	2.0	235	2 D87278	DNA-binding respon
15	9	2.0	275	2 F84088	N-acetylmuramoyl-L
16	9	2.0	326	2 C96735	unknown protein F2
17	9	2.0	502	2 A48679	differentiated ker
18	9	2.0	535	2 S66148	gene pipsqueak pro
19	9	2.0	549	2 T20720	hypothetical prote
20	9	2.0	668	1 S54304	taxis sensor histi
21	9	2.0	668	2 E84253	chemotaxis protein
22	9	2.0	668	2 C71868	hypothetical prote
23	9	2.0	675	2 S25005	dnak-type molecula
24	9	2.0	712	2 B47021	pectic enzyme secr
25	9	2.0	1085	2 S66149	gene pipsqueak pro
26	9	2.0	1097	2 T13033	cyclin F - fruit f
27	9	2.0	1130	2 T19148	hypothetical prote
28	9	2.0	1306	2 S25370	MSB2 protein - yea
29	9	2.0	1711	1 A47392	chromodomain-helic

hypothetical prote  
hypothetical prote  
hypothetical prote  
sericin MG-1 - gre  
hypothetical prote  
hypothetical prote  
keratin-like prote  
hypothetical prote  
hypothetical expor  
probable membrane  
nucleic acid-bindin  
SOL2 protein - yea  
loricrin - human  
protein kinase ADK  
hypothetical prote  
homeotic protein e  
hypothetical prote  
glycine-rich prote  
hypothetical prote  
transcription fact  
hypothetical prote  
3-phosphoshikimate  
T-cell surface gly  
hypothetical prote  
unusual floral org  
probable disease r  
ADK1 [imported] -  
probable regulator  
transcription fact  
glutamy1-trNA amid  
loricrin - mouse  
hypothetical glyci  
amidase (EC 3.5.1.  
probable glu-trNA  
hypothetical prote  
hypothetical prote  
ETS2 repressor fac  
amidase (EC 3.5.1.  
cellulase (EC 3.2.  
probable matrix me  
protein kinase Dyr  
amidase family pro  
hypothetical prote  
hypothetical prote  
protein kinase Dyr  
probable protein k  
heat shock protein  
UL25 protein - hum  
BRcore-Q1-21 prote  
wingless receptor  
probable hydroxama  
hydroxamate-type f  
major ampullate fi  
BRcore-TNT1-Q1-21  
ZC21.4 protein - C  
Down-syndrome-crit  
kinesin-like prote  
kinesin-like prote  
hypothetical glyci  
transcription fact  
myosin Myok - Dict  
hypothetical prote  
bacteriocin BCNS -  
hypally regulated  
segment protein 6  
macrophage colony-  
macrophage colony-  
hypothetical prote  
sterol regulatory  
probable serine/th  
serine/threonine p

103	8	1.8	1233	2	T30989	serine/threonine p	176	7	1.6	272	2	E96946	periplasmic amino
104	8	1.8	1585	2	T31611	hypothetical prote	177	7	1.6	272	2	S73796	hypothetical prote
105	8	1.8	1723	2	H86357	polymorphic membra	178	7	1.6	273	2	F83221	plant-metabolite d
106	8	1.8	1723	2	E72067	polymorphic membra	179	7	1.6	276	2	F83919	hypothetical prote
107	8	1.8	1732	2	C81601	MHC class III hist	180	7	1.6	277	2	T32460	ribose-phosphate p
108	8	1.8	1870	2	S37671	MHC class III hist	181	7	1.6	282	2	F75020	neutrophil protein
109	8	1.8	1872	2	S36152	MHC class III hist	182	7	1.6	284	2	A35419	CAMP-binding protei
110	8	1.8	2142	2	B35098	MHC class III hist	183	7	1.6	287	2	A49752	hypothetical prote
111	8	1.8	2761	2	T29285	hypothetical prote	184	7	1.6	292	2	C71448	hypothetical prote
112	8	1.8	3759	2	A35085	trithorax protein	185	7	1.6	293	1	DDBP32	helix-destabilizin
113	7	1.6	91	2	H91035	hypothetical prote	186	7	1.6	293	1	DDBP36	helix-destabilizin
114	7	1.6	91	2	B85880	hypothetical prote	187	7	1.6	294	2	AC3642	2,5-diketo-D-gluc
115	7	1.6	91	2	H97856	hypothetical prote	188	7	1.6	296	2	A47318	RNA-binding protei
116	7	1.6	102	2	JC1150	hypothetical prote	189	7	1.6	296	2	I53142	gene Merc protein
117	7	1.6	118	2	C84806	probable nonspecif	190	7	1.6	297	2	E83194	Polyamine transpor
118	7	1.6	133	2	B49530	vascular endotheli	191	7	1.6	297	2	B86161	Fi003.14 protein -
119	7	1.6	139	2	B96500	hypothetical prote	192	7	1.6	298	2	T12483	hypothetical prote
120	7	1.6	144	2	JC2102	lectin-related pro	193	7	1.6	299	2	T12483	hypothetical prote
121	7	1.6	145	2	F25929	hemoglobin beta-II	194	7	1.6	301	1	DDBP34	helix-destabilizin
122	7	1.6	150	2	C86224	hypothetical prote	195	7	1.6	304	2	T16535	hypothetical prote
123	7	1.6	154	2	A70508	hypothetical prote	196	7	1.6	312	2	G75514	hypothetical prote
124	7	1.6	155	2	S62558	hypothetical prote	197	7	1.6	313	2	A34677	secretory pathway
125	7	1.6	161	2	S71453	glycine-rich RNA-b	198	7	1.6	316	2	S08169	collagen col-12 pr
126	7	1.6	161	2	AE0357	conserved hypotet	199	7	1.6	316	2	S08170	collagen col-13 pr
127	7	1.6	163	2	T28012	hypothetical prote	200	7	1.6	317	2	S01412	hypothetical prote
128	7	1.6	167	2	S21359	keratin, type I, c	201	7	1.6	317	2	T27485	hypothetical prote
129	7	1.6	167	2	D81031	conserved hypotet	202	7	1.6	321	2	D83813	hypothetical prote
130	7	1.6	170	2	JC2213	hypothetical 14.7K	203	7	1.6	324	2	D48423	homotetic protein e
131	7	1.6	175	2	H81975	hypothetical prote	204	7	1.6	329	2	A48805	insulin-like growt
132	7	1.6	175	2	C70326	hypothetical prote	205	7	1.6	329	2	T45972	hypothetical prote
133	7	1.6	175	2	T47463	serine/proline-ric	206	7	1.6	332	2	S15347	transcription fact
134	7	1.6	177	2	AG1467	transcription anti	207	7	1.6	342	2	S51839	D13F(MVASTI) prote
135	7	1.6	177	2	F96739	hypothetical prote	208	7	1.6	343	2	T05221	hypothetical prote
136	7	1.6	178	2	G96667	unknown protein, 5	209	7	1.6	345	2	G83148	DNA polymerase III
137	7	1.6	182	2	A02947	keratin, 60K type	210	7	1.6	351	2	T03946	Xnl like-homeo box
138	7	1.6	182	2	A02946	keratin, 59K type	211	7	1.6	357	2	T02785	probable homeotic
139	7	1.6	190	2	A24713	sericin - silkworm	212	7	1.6	359	2	H90301	hypothetical prote
140	7	1.6	193	2	JC6114	melanocyte-specifi	213	7	1.6	361	2	T48029	hypothetical prote
141	7	1.6	196	2	G87484	acylttransferase fa	214	7	1.6	362	2	T52266	nitilase-like pro
142	7	1.6	200	2	I46051	secreted phosphor	215	7	1.6	363	2	TS1341	RNA helicase RH9 l
143	7	1.6	202	2	B87521	Deda family protei	216	7	1.6	366	2	JC7690	Gfi-1-like protein
144	7	1.6	204	2	D84809	hypothetical prote	217	7	1.6	369	2	H72018	chlp3 43 kda prote
145	7	1.6	204	2	B86308	F20D23.10 protein	218	7	1.6	369	2	G86606	CHLPS 43 kda prote
146	7	1.6	211	2	S55885	CCHH finger protei	219	7	1.6	369	2	C81521	conserved hypotet
147	7	1.6	216	2	G70447	flagellar U-ring p	220	7	1.6	371	2	T13021	hypothetical prote
148	7	1.6	221	2	AG1961	hypothetical prote	221	7	1.6	372	2	AG2827	HFLK protein (impo
149	7	1.6	223	1	VCBVCA	coat protein - tob	222	7	1.6	373	2	E97605	protease chain h
150	7	1.6	224	2	T19959	hypothetical prote	223	7	1.6	374	2	A45074	Gal beta 1,3(4)Glc
151	7	1.6	231	2	S62530	hypothetical prote	224	7	1.6	375	2	JN0618	Gal beta 1,3(4)Glc
152	7	1.6	233	2	T24714	hypothetical prote	225	7	1.6	379	2	S42543	hypothetical prote
153	7	1.6	234	2	F46449	hypothetical prote	226	7	1.6	382	1	B42333	transcription fact
154	7	1.6	246	2	AB0589	hypothetical prote	227	7	1.6	384	2	E75295	conserved hypotet
155	7	1.6	247	2	T10524	tonoplast intrinsi	228	7	1.6	385	2	S53087	ubiquinol-cytochro
156	7	1.6	248	2	S26198	H+-transporting tw	229	7	1.6	385	2	S40778	ubiquinol-cytochro
157	7	1.6	248	2	T40415	hypothetical prote	230	7	1.6	386	2	T14243	ubiquinol-cytochro
158	7	1.6	248	2	T33230	hypothetical prote	231	7	1.6	387	1	CBASN	ubiquinol-cytochro
159	7	1.6	253	2	T04842	hypothetical prote	232	7	1.6	387	2	T25452	hypothetical prote
160	7	1.6	253	2	B49752	cAMP-binding prote	233	7	1.6	391	2	C86347	F24U8.6 protein -
161	7	1.6	254	2	S48547	probable membrane	234	7	1.6	399	2	I38901	JNK-activating pro
162	7	1.6	256	2	T44452	amidase yedB (impo	235	7	1.6	401	2	AE3651	amidase (EC 3.5.1.
163	7	1.6	256	2	T03371	glycine-rich prote	236	7	1.6	401	2	T48495	hypothetical prote
164	7	1.6	256	2	T24713	hypothetical prote	237	7	1.6	402	2	JC5270	neuron-specific si
165	7	1.6	257	2	C84533	hypothetical prote	238	7	1.6	405	2	S19355	hypothetical prote
166	7	1.6	258	2	G96798	hypothetical prote	239	7	1.6	406	2	S38170	SRP40 protein - ye
167	7	1.6	258	2	T09031	hypothetical prote	240	7	1.6	417	2	JC7092	Pauli protein - fis
168	7	1.6	259	2	F86475	hypothetical prote	241	7	1.6	419	2	AC1049	HfLK protein (impo
169	7	1.6	262	2	T47659	hypothetical prote	242	7	1.6	419	2	F86113	probable integral
170	7	1.6	263	2	T49870	probable transcrip	243	7	1.6	419	2	F91272	probable integral
171	7	1.6	264	2	JC7772	aquaporin 10 - hum	244	7	1.6	419	2	B43653	probable integral
172	7	1.6	265	2	B96993	probable membrane	245	7	1.6	423	2	G84243	Glu-tRNA amidotran
173	7	1.6	267	1	CTPGP	corticotropin / li	246	7	1.6	424	1	Z3BPF1	coat protein A pre
174	7	1.6	270	2	A60830	keratin, 70K type	247	7	1.6	424	1	Z3BPF2	coat protein A pre
175	7	1.6	271	2	T04666	hypothetical prote	248	7	1.6	424	1	Z3BPM3	coat protein A pre

249	7	1.6	424	2	T43498	hypotheical prote	322	7	1.6	485	2	T44294	glutamyl-tRNA (Gln
250	7	1.6	426	2	A11309	formyl-tetrahydrof	323	7	1.6	486	1	A57601	transcription fact
251	7	1.6	430	2	T21060	hypotheical prote	324	7	1.6	486	2	C86645	Glu-tRNA amidotran
252	7	1.6	433	2	S76485	hypotheical prote	325	7	1.6	486	2	T51582	glutamyl-tRNA (Gln
253	7	1.6	434	1	Z3B9TK	coat protein A - p	326	7	1.6	487	1	AB1938	glutamyl-tRNA (Gln
254	7	1.6	434	2	G64444	amidase - Methanoc	327	7	1.6	487	1	BWSOGM	glcfa protein - Str
255	7	1.6	434	2	H71310	hypotheical prote	328	7	1.6	488	1	QXASBI	mRNA maturase bll
256	7	1.6	434	2	S73331	hypotheical prote	329	7	1.6	488	2	A72554	probable Glu-tRNA
257	7	1.6	436	2	A11316	hypotheical prote	330	7	1.6	488	2	F95050	glutamyl-tRNA (Gln)
258	7	1.6	436	2	A11688	hypotheical prote	331	7	1.6	488	2	B79921	glu-tRNAglu amidot
259	7	1.6	436	2	T15331	hypotheical prote	332	7	1.6	488	2	A55180	homeotic protein H
260	7	1.6	438	2	I50517	retinoid X recepto	333	7	1.6	489	2	D87551	glutamyl-tRNA (Gln)
261	7	1.6	439	2	I57561	transcription fact	334	7	1.6	490	2	B81239	pyruvate kinase II
262	7	1.6	439	2	H86558	N-acetylmutamoyl-L	335	7	1.6	490	2	G82011	pyruvate kinase (E
263	7	1.6	440	2	S37303	sox-4 protein - mo	336	7	1.6	491	2	A81722	glutamyl-tRNA (Gln)
264	7	1.6	442	2	T47788	hypotheical prote	337	7	1.6	491	2	F71568	probable glu-tRNA
265	7	1.6	444	2	T47114	probable 3-carboxy	338	7	1.6	492	2	H72130	glutamyl-tRNA (Gln)
266	7	1.6	445	1	A49447	transcription fact	339	7	1.6	492	2	C86491	Glu tRNA Gln amid
267	7	1.6	446	2	B53376	indoleacetamide hy	340	7	1.6	492	2	AB1030	probable exported
268	7	1.6	447	2	B83465	conserved hypothe	341	7	1.6	493	2	B44761	6-aminohexanoate-c
269	7	1.6	448	2	H90536	hypotheical prote	342	7	1.6	493	2	A44761	6-aminohexanoate-c
270	7	1.6	452	2	T25076	hypotheical prote	343	7	1.6	493	2	B97724	glutamyl-tRNA amid
271	7	1.6	453	1	F64623	amidase - Helicoba	344	7	1.6	493	2	E71725	glutamyl-tRNA amid
272	7	1.6	453	2	A69494	Glu-tRNA amidotran	345	7	1.6	493	2	AG2738	glutamyl-tRNA amid
273	7	1.6	453	2	H81308	Glu-tRNAglu amidot	346	7	1.6	495	1	S52641	heat shock transcr
274	7	1.6	453	2	A71891	glu-tRNA amidotran	347	7	1.6	495	2	AB3594	glutamyl-tRNA (Gln)
275	7	1.6	454	2	D69066	amidase - Methanob	348	7	1.6	496	2	E70142	glu-tRNA amidotran
276	7	1.6	455	1	B25493	indoleacetamide hy	349	7	1.6	496	2	E97519	glutamyl-tRNA (Gln)
277	7	1.6	455	2	A86306	F20D23.27 protein	350	7	1.6	497	2	T35815	probable Glu-tRNA (
278	7	1.6	457	2	A69541	Glu-tRNA amidotran	351	7	1.6	499	2	F86645	amidase [imported]
279	7	1.6	457	2	E96772	hypotheical prote	352	7	1.6	499	2	T36462	hypotheical prote
280	7	1.6	459	2	S13064	1D-myo-inositol-tr	353	7	1.6	502	2	I52637	Ca2+/calmodulin-de
281	7	1.6	461	2	F70571	hypotheical glyci	354	7	1.6	504	2	S74034	amidase (EC 3.5.1.
282	7	1.6	461	2	JN0129	1D-myo-inositol-tr	355	7	1.6	506	2	S75789	6-aminohexanoate-c
283	7	1.6	461	2	C86679	transcription regu	356	7	1.6	507	2	AB2530	amidase [imported]
284	7	1.6	461	2	H84099	cell wall-binding	357	7	1.6	507	2	S05542	hypotheical prote
285	7	1.6	462	1	S30104	indoleacetamide hy	358	7	1.6	510	2	A45338	connexin-56 - Chic
286	7	1.6	462	2	G70753	probable amidase -	359	7	1.6	515	2	S38270	amidase (EC 3.5.1.
287	7	1.6	464	2	AG1933	Glu-tRNA (Gln) amid	360	7	1.6	516	2	AC1540	ATP-dependent RNA
288	7	1.6	464	2	B87573	pyrazinamide/nic	361	7	1.6	520	2	AB1183	ATP-dependent RNA
289	7	1.6	464	2	E82865	conjugal transfer	362	7	1.6	521	2	A37806	amidase (EC 3.5.1.
290	7	1.6	465	2	AC0396	probable amidase [	363	7	1.6	521	2	S15070	amidase (EC 3.5.1.
291	7	1.6	465	2	F75524	hypotheical prote	364	7	1.6	523	2	T23003	hypotheical prote
292	7	1.6	471	2	D95356	probable amidase [	365	7	1.6	524	2	S55097	probable membrane
293	7	1.6	474	2	B85500	proteinase DO (EC	366	7	1.6	525	2	D70878	hypotheical glyci
294	7	1.6	474	2	S45229	proteinase DO (EC	367	7	1.6	526	1	KRBOVI	keratin, 54K type
295	7	1.6	474	2	E90849	proteinase DO (EC	368	7	1.6	530	2	T32812	hypotheical prote
296	7	1.6	474	2	I38240	transcription fact	369	7	1.6	534	2	H71445	probable glycerol-
297	7	1.6	475	2	G72274	glutamyl tRNA-Gln	370	7	1.6	536	2	H71563	hypotheical prote
298	7	1.6	475	2	C86863	N-acetylmutamoyl-L	371	7	1.6	537	2	S50344	asparagilopepsin h
299	7	1.6	476	2	C84643	hypotheical prote	372	7	1.6	543	2	F70726	hypotheical glyci
300	7	1.6	477	2	I64210	hydrolase (aux2) h	373	7	1.6	543	2	B39369	homeotic protein B
301	7	1.6	477	2	T18801	hypotheical prote	374	7	1.6	546	2	B75375	probable amidase -
302	7	1.6	478	1	S73920	amidase homolog G0	375	7	1.6	547	2	C86264	protein F3F19.5 [1
303	7	1.6	478	2	F70322	glutamyl-tRNA (Gln	376	7	1.6	550	1	FGRTA	collagen alpha c
304	7	1.6	478	2	H90246	hypotheical prote	377	7	1.6	551	1	NRECE3	collagen E3 (EC 3.1
305	7	1.6	478	2	D97266	glutamyl-tRNAglu a	378	7	1.6	552	2	S17551	gamma-aminobutyric
306	7	1.6	480	2	A40815	transcription fact	379	7	1.6	554	2	G01928	gamma-aminobutyric
307	7	1.6	480	2	A86427	probable serine/th	380	7	1.6	555	2	D95139	DNA repair protein
308	7	1.6	481	2	E81091	Glu-tRNA (Gln) amid	381	7	1.6	555	2	C98007	DNA repair and gen
309	7	1.6	481	2	C81849	Glu-tRNA (Gln) amid	382	7	1.6	555	2	F86487	unknown protein [1
310	7	1.6	481	2	A27626	sucrose phosphoryl	383	7	1.6	556	2	S06838	gamma-aminobutyric
311	7	1.6	482	2	D75346	glutamyl-tRNA (Gln)	384	7	1.6	556	2	D70940	probable PPG prote
312	7	1.6	483	1	TVRTKA	protein kinase (EC	385	7	1.6	558	2	T23991	hypotheical prote
313	7	1.6	483	1	S77264	amidase slr0877 -	386	7	1.6	560	2	AD1681	formyl-tetrahydrof
314	7	1.6	483	2	AC1294	glutamyl-tRNA (Gln)	387	7	1.6	561	2	C75543	6-aminohexanoate-c
315	7	1.6	483	2	A11665	glutamyl-tRNA (Gln)	388	7	1.6	568	2	S15008	gene disco protein
316	7	1.6	483	2	S27880	Nasopressin recept	389	7	1.6	571	2	T29751	hypotheical prote
317	7	1.6	484	2	H83084	Glu-tRNA (Gln) amid	390	7	1.6	572	2	T08509	trbL protein - Ent
318	7	1.6	484	2	B70586	probable amiA2 pro	391	7	1.6	575	2	T48224	probable homeodoma
319	7	1.6	485	2	C89598	glutamyl-tRNAglu a	392	7	1.6	575	2	S35327	protein kinase 99g
320	7	1.6	485	2	B69795	glutamyl-tRNA (Gln)	393	7	1.6	576	1	S22453	colicin E7 (EC 3.1
321	7	1.6	485	2	F97228	glu-tRNAglu amidot	394	7	1.6	576	2	A26628	homeotic protein I

395	7	1.6	577	2	Tl6333	hypothetical prote	468	7	1.6	816	2	T00919	hypothetical prote
396	7	1.6	577	2	T01945	hypothetical prote	469	7	1.6	821	2	E95245	penicillin-binding
397	7	1.6	581	1	NDECE2	colicin E2 (EC 3.1	470	7	1.6	821	2	B95110	peptidoglycan gly
398	7	1.6	581	1	KRMS2	keratin, type II c	471	7	1.6	822	2	AB0238	neamin storage sys
399	7	1.6	581	2	H69452	hypothetical prote	472	7	1.6	822	2	T47007	hypothetical prote
400	7	1.6	583	2	T39112	probable amidase -	473	7	1.6	835	2	JP0076	hel protein - chic
401	7	1.6	586	2	T51211	hypothetical prote	474	7	1.6	844	2	AD0047	ribonuclease R (EC
402	7	1.6	586	2	T04716	hypothetical prote	475	7	1.6	846	2	A30889	integrin beta chai
403	7	1.6	586	2	JC6500	hypothetical prote	476	7	1.6	850	2	JC5700	Erbb kinase activa
404	7	1.6	587	2	T00316	hnf-3/forkhead tra	477	7	1.6	853	2	S74279	hypothetical prote
405	7	1.6	590	2	A29904	toxr-regulated lip	478	7	1.6	858	2	T18946	probable phospholi
406	7	1.6	592	2	B82759	keratin 5, type II	479	7	1.6	873	2	B53225	ecdysone-induced p
407	7	1.6	594	2	B86456	endo-1,4-beta-gluc	480	7	1.6	898	2	T42131	probable toxR-regu
408	7	1.6	604	2	A39369	protein trihelix D	481	7	1.6	899	2	SL7546	furin (EC 3.4.21-7
409	7	1.6	606	2	H70816	homeotic protein B	482	7	1.6	900	2	C96842	hypothetical prote
410	7	1.6	606	2	SI3367	hypothetical glyci	483	7	1.6	927	2	A48085	transcription fact
411	7	1.6	609	2	B84783	Om(1D) protein - f	484	7	1.6	932	1	A31898	probable phospholi
412	7	1.6	609	2	A49839	probable poly(A) b	485	7	1.6	947	2	T00340	hydroxymethylgluta
413	7	1.6	612	2	S53714	odd-paired - fruit	486	7	1.6	952	2	T52456	hypothetical prote
414	7	1.6	615	2	T20839	probable dinitrifi	487	7	1.6	952	2	T49283	endopeptidase Clp
415	7	1.6	615	2	T34392	hypothetical prote	488	7	1.6	962	2	S60225	AtClpC - Arabidops
416	7	1.6	616	2	A11180	hypothetical prote	489	7	1.6	968	2	T00353	ionotropic glutama
417	7	1.6	618	2	A70989	amidas homolog 1	490	7	1.6	972	2	T49773	hypothetical prote
418	7	1.6	621	2	S75115	hypothetical glyci	491	7	1.6	980	1	TVCTMD	related to actin-1
419	7	1.6	621	2	JC7278	acetohydroxy acid	492	7	1.6	980	1	T49570	macrophage colony-
420	7	1.6	622	2	I37984	adaptor protein co	493	7	1.6	983	2	B88533	hypothetical prote
421	7	1.6	623	1	S33167	keratin 9, type I,	494	7	1.6	998	2	A96827	glutamate receptor
422	7	1.6	631	2	B83404	gene pointed prote	495	7	1.6	1000	2	C82630	hypothetical prote
423	7	1.6	632	2	T32454	hypothetical prote	496	7	1.6	1002	2	T09438	serine proteinase
424	7	1.6	632	2	T27215	hypothetical prote	497	7	1.6	1008	2	F71727	tox-activated lip
425	7	1.6	638	2	S46499	hypothetical prote	498	7	1.6	1011	2	F70620	acriflavin resista
426	7	1.6	640	1	ZYBPT5	NADP-dependent mal	499	7	1.6	1013	2	B82276	hypothetical glyci
427	7	1.6	641	2	T03095	tail protein pb5 -	500	7	1.6	1018	2	T30986	Tox-activated gen
428	7	1.6	647	2	S06450	homeoprotein Sail	501	7	1.6	1029	2	T28956	period protein - C
429	7	1.6	650	2	F72540	steroid hormone re	502	7	1.6	1036	1	GNLJG2	hypothetical prote
430	7	1.6	655	2	T00768	hypothetical prote	503	7	1.6	1043	2	T13733	HIV-1 retropepsin
431	7	1.6	660	2	S50383	polyadenylate-bind	504	7	1.6	1044	2	G98332	RT2-F1 protein - f
432	7	1.6	663	2	T40493	gamma-glutamyltran	505	7	1.6	1044	2	AD2950	rnd multidrug effl
433	7	1.6	666	2	A42296	hnf-3/forkhead tra	506	7	1.6	1047	2	T34946	RND multidrug effl
434	7	1.6	671	2	A35912	lysozyme 2 (EC 3.2	507	7	1.6	1047	2	A59246	probable isoleucyl
435	7	1.6	673	2	T06294	homeotic protein o	508	7	1.6	1063	2	A40253	acidic nuclear pro
436	7	1.6	673	2	T00328	hypothetical prote	509	7	1.6	1070	2	S19686	alpha-glucosidase
437	7	1.6	675	2	S19140	hypothetical prote	510	7	1.6	1076	2	JC2217	major surface glyci
438	7	1.6	678	2	T49984	dnak-type molecula	511	7	1.6	1077	2	A44067	serine-rich protei
439	7	1.6	685	2	T24950	bromodomain protei	512	7	1.6	1079	2	B70807	hypothetical glyci
440	7	1.6	703	2	T05632	hypothetical prote	513	7	1.6	1079	2	C96772	hypothetical glyci
441	7	1.6	709	2	T28712	hypothetical prote	514	7	1.6	1096	2	T08619	probable metallopr
442	7	1.6	710	2	T31502	hypothetical prote	515	7	1.6	1110	2	IS1116	hypothetical prote
443	7	1.6	713	2	T48634	DRH1 DEAD box prot	516	7	1.6	1119	2	AB2239	hypothetical prote
444	7	1.6	714	2	AF2479	ABC transporter AT	517	7	1.6	1121	2	JQ1631	HCRR2 protein - hu
445	7	1.6	716	2	AC2449	ABC transporter AT	518	7	1.6	1133	2	A54164	sterol regulatory
446	7	1.6	720	1	A55160	Trg protein - frul	519	7	1.6	1133	2	T01757	hypothetical prote
447	7	1.6	722	2	AF1956	ABC transporter AT	520	7	1.6	1143	2	T10636	hypothetical prote
448	7	1.6	722	2	S57246	ventral nervous sy	521	7	1.6	1146	2	A55532	myosin-heavy-chain
449	7	1.6	726	2	T34638	hypothetical prote	522	7	1.6	1150	2	T13824	LK6 protein kinase
450	7	1.6	733	2	T28145	RING3 kinase - chi	523	7	1.6	1160	2	T13713	beta3 protein - fr
451	7	1.6	742	2	T00371	hypothetical prote	524	7	1.6	1175	2	S39951	chitin synthase (E
452	7	1.6	749	2	A70812	hypothetical glyci	525	7	1.6	1187	2	C84568	hypothetical prote
453	7	1.6	754	2	T18238	lysophospholipase	526	7	1.6	1189	2	T17088	homodomain-intera
454	7	1.6	754	2	F87185	phosphoribosylform	527	7	1.6	1200	2	C96025	hypothetical expor
455	7	1.6	754	2	A56619	female sterile hom	528	7	1.6	1205	2	AH2486	hypothetical prote
456	7	1.6	759	2	B83474	probable type II s	529	7	1.6	1208	2	T23467	hypothetical prote
457	7	1.6	760	1	S07896	transcription fact	530	7	1.6	1212	2	T44236	hypothetical prote
458	7	1.6	781	1	TVFFDF	protein kinase Dra	531	7	1.6	1215	2	IS2882	hypothetical prote
459	7	1.6	781	2	H87531	methy-accepting c	532	7	1.6	1217	2	S52714	sericinB - silkw
460	7	1.6	781	2	S37032	gene IL5 protein -	533	7	1.6	1217	2	JS0069	hypothetical p1 op
461	7	1.6	786	2	G85073	probable myosin-li	534	7	1.6	1218	2	A34598	ecdysone-induced p
462	7	1.6	788	2	C84616	similar to mammali	535	7	1.6	1237	2	SL4201	probable adenylate
463	7	1.6	788	2	JS0747	regulatory protein	536	7	1.6	1242	2	S14201	hypothetical prote
464	7	1.6	795	2	T25116	hypothetical prote	537	7	1.6	1249	2	T26294	hypothetical prote
465	7	1.6	798	2	T21369	hypothetical prote	538	7	1.6	1268	2	G85154	hypothetical prote
466	7	1.6	799	2	T02456	protein kinase hom	539	7	1.6	1269	2	S35366	furin (EC 3.4.21.7
467	7	1.6	806	2	F69899	phage-related pre-	540	7	1.6	1325	1	S73723	probable lipoprote

541	7	1.6	1335	2	A82494	TagA-related prote	614	6	1.4	71	2	T32501	hypothetical prote
542	7	1.6	1361	2	C71403	hypothetical 15.1K	615	6	1.4	71	2	T29977	hypothetical prote
543	7	1.6	1367	1	IGHUR1	insulin-like growt	616	6	1.4	72	2	B90762	hypothetical prote
544	7	1.6	1371	2	A33837	insulin-like growt	617	6	1.4	73	2	T34599	hypothetical prote
545	7	1.6	1394	2	B34598	ecdysone-induced p	618	6	1.4	75	2	D95085	hypothetical prote
546	7	1.6	1403	2	S64142	hypothetical prote	619	6	1.4	75	2	E86841	hypothetical prote
547	7	1.6	1411	2	T48529	hypothetical prote	620	6	1.4	76	2	H30517	ig heavy chain V-A
548	7	1.6	1433	2	S54587	Cat8 protein - yea	621	6	1.4	76	2	D82844	carbon storage reg
549	7	1.6	1436	2	S05920	probable PPE prote	622	6	1.4	77	2	AE2966	hypothetical prote
550	7	1.6	1443	2	S05979	steroid hormone re	623	6	1.4	80	2	T10550	hypothetical prote
551	7	1.6	1464	2	T13716	bazooka gene prote	624	6	1.4	81	2	A49736	collagen alpha 3(I
552	7	1.6	1487	2	T02850	hypothetical prote	625	6	1.4	81	2	A95319	SyrA protein invol
553	7	1.6	1489	2	D70807	hypothetical glyci	626	6	1.4	82	2	T52378	probable transport
554	7	1.6	1538	2	H70846	hypothetical glyci	627	6	1.4	82	2	T33088	hypothetical prote
555	7	1.6	1584	2	T18276	hypothetical glyci	628	6	1.4	82	2	AF3259	hypothetical prote
556	7	1.6	1612	2	JC5210	protein-tyrosine k	629	6	1.4	82	2	AH2065	hypothetical prote
557	7	1.6	1616	2	T17884	DNA (cytosine-5-) -	630	6	1.4	83	2	G82744	hypothetical prote
558	7	1.6	1677	2	T43021	S-layer protein -	631	6	1.4	85	2	T07090	metallothionein-II
559	7	1.6	1718	2	T14603	vitellogenin precu	632	6	1.4	85	2	T16739	hypothetical prote
560	7	1.6	1726	2	T30810	hypothetical prote	633	6	1.4	86	2	AI2732	conserved hypothet
561	7	1.6	1741	2	T13610	chromatin structur	634	6	1.4	86	2	C97514	hypothetical prote
562	7	1.6	1768	2	T13349	parallel sister ch	635	6	1.4	88	1	WMAD9	hypothetical prote
563	7	1.6	1777	2	T34369	hypothetical prote	636	6	1.4	89	2	E87288	early E1B 9K prote
564	7	1.6	1782	2	S45289	hypothetical prote	637	6	1.4	90	2	C69480	ribosomal protein
565	7	1.6	1791	2	T02345	vitellogenin precu	638	6	1.4	90	2	S00060	phospholipid trans
566	7	1.6	1839	1	OYBYK	hypothetical prote	639	6	1.4	91	2	T31244	hypothetical prote
567	7	1.6	1842	2	T43409	adenylate cyclase	640	6	1.4	92	2	S52277	hypothetical prote
568	7	1.6	1842	2	T38781	probable fatty-aci	641	6	1.4	94	2	C32529	ig lambda chain V
569	7	1.6	1912	2	T29088	fatty acid synthas	642	6	1.4	95	2	PH0864	ig kappa chain V r
570	7	1.6	1969	2	T08875	vitellogenin I pre	643	6	1.4	95	2	E83065	hypothetical prote
571	7	1.6	1970	2	T03284	histidine kinase h	644	6	1.4	96	2	S36060	hypothetical prote
572	7	1.6	2023	2	T13154	myoblast city prot	645	6	1.4	96	2	AG2795	conserved hypothet
573	7	1.6	2038	2	A43742	polycarb protein e	646	6	1.4	96	2	G97574	hypothetical 11.0K
574	7	1.6	2061	2	T13751	female sterile hom	647	6	1.4	98	2	S26933	ig heavy chain V r
575	7	1.6	2064	2	G82562	transcription fact	648	6	1.4	99	2	S14881	hypothetical prote
576	7	1.6	2174	2	E95365	bacteriocin XP2407	649	6	1.4	100	2	T04807	hypothetical prote
577	7	1.6	2182	2	T28634	hypothetical glyci	650	6	1.4	100	2	A72572	SM73 protein homol
578	7	1.6	2406	2	A54148	variant-specific s	651	6	1.4	101	2	I57492	hypothetical prote
579	7	1.6	2515	2	S47008	odx protein - fru	652	6	1.4	101	2	C90564	lipoprotein C-I
580	7	1.6	2528	2	T20719	tenascin-like prot	653	6	1.4	101	2	G72698	lipoprotein (impor
581	7	1.6	2528	2	T20719	hypothetical prote	654	6	1.4	101	2	G75188	hypothetical prote
582	7	1.6	2738	2	E88320	hypothetical prote	655	6	1.4	102	2	C81002	hypothetical prote
583	7	1.6	2946	2	T15840	protein F07A11.6 l	656	6	1.4	102	2	E72482	probable periplasm
584	7	1.6	3016	2	S77300	hypothetical prote	657	6	1.4	102	2	S08462	hypothetical prote
585	7	1.6	3078	2	T28432	hypothetical prote	658	6	1.4	103	2	S08462	ig heavy chain V r
586	7	1.6	3190	2	T13828	variant-specific s	659	6	1.4	104	1	KVRBXP	ig kappa chain V r
587	7	1.6	3386	2	T22813	CREB-binding prote	660	6	1.4	104	2	JC4190	holotricin 3 precu
588	7	1.6	13288	2	T03099	hypothetical prote-	661	6	1.4	105	1	A46264	thioredoxin 1 - sl
589	7	1.4	15	2	E56978	mucin, submaxillar	662	6	1.4	105	2	S49533	anti-Sm antibody V
590	6	1.4	28	2	PQ0263	collagen alpha 2(X	663	6	1.4	105	2	S44838	K02D10.3 protein -
591	6	1.4	29	2	A41683	dnaK-type molecula	664	6	1.4	105	2	A42694	homeodomain protei
592	6	1.4	42	2	A35494	hyaluronate recept	665	6	1.4	106	1	L4HUKN	ig lambda chain V-
593	6	1.4	47	2	B35249	scatter protein 90	666	6	1.4	106	2	S40091	ig light chain - m
594	6	1.4	47	2	H90945	ig lambda chain V	667	6	1.4	107	1	ERADT1	early E3A 12.5K pr
595	6	1.4	47	2	C85794	hypothetical prote	668	6	1.4	107	2	C72766	hypothetical prote
596	6	1.4	47	2	B64944	hypothetical prote	669	6	1.4	107	2	G83348	hypothetical prote
597	6	1.4	48	2	T14521	H+-transporting tw	670	6	1.4	107	2	B85356	glycine-rich prote
598	6	1.4	52	2	S69113	collagen alpha 3(I	671	6	1.4	108	1	K1HUAU	ig kappa chain V-I
599	6	1.4	53	2	S12520	core protein A1 -	672	6	1.4	108	1	L3HUSH	ig lambda chain V-
600	6	1.4	53	2	H84193	hypothetical prote	673	6	1.4	108	2	S38498	ig lambda chain -
601	6	1.4	56	2	T02946	hypothetical prote	674	6	1.4	108	2	S47184	ig kappa chain V r
602	6	1.4	59	2	F69040	hypothetical prote	675	6	1.4	108	2	PS0073	ig kappa chain V r
603	6	1.4	60	1	WZV2A7	5K HindIII-C prote	676	6	1.4	108	2	C72777	hypothetical prote
604	6	1.4	63	2	C26796	ig heavy chain V r	677	6	1.4	109	2	B72586	hypothetical prote
605	6	1.4	63	2	C83524	probable cold-shoc	678	6	1.4	109	2	S19663	ig lambda chain V
606	6	1.4	63	2	H70930	probable lppr prot	679	6	1.4	109	2	G74151	ig kappa chain V r
607	6	1.4	64	2	FC1237	peptidylprolyl iso	680	6	1.4	109	2	G27473	hypothetical prote
608	6	1.4	64	2	A86333	hypothetical prote	681	6	1.4	110	1	R6BY24	60s acidic ribosom
609	6	1.4	66	2	S22529	cold-regulated pro	682	6	1.4	110	1	S40402	protein-export pro
610	6	1.4	67	2	T17658	hypothetical prote	683	6	1.4	110	2	S36272	ig lambda chain V
611	6	1.4	70	2	T23415	hypothetical prote	684	6	1.4	110	2	A85981	ig lambda chain V
612	6	1.4	70	2	T26824	hypothetical prote	685	6	1.4	110	2	AD0902	protein export mem
613	6	1.4	70	2	T32870	hypothetical prote	686	6	1.4	110	2	F91135	protein-export pro

687	6	1.4	110	2	S16496	hypothetical prote	760	6	1.4	133	2	A28565	Ig lambda chain pr
688	6	1.4	110	2	B70601	hypothetical prote	761	6	1.4	133	2	B85754	prophage p12 prote
689	6	1.4	111	2	S69911	Ig V-D-J region (R	762	6	1.4	133	2	D86175	hypothetical prote
690	6	1.4	111	2	F82962	hypothetical prote	763	6	1.4	133	2	C86473	arabinogalactan-pr
691	6	1.4	113	2	S43583	F26F3.3 protein -	764	6	1.4	135	2	AB3626	nr1 protein (limpo
692	6	1.4	113	2	H84725	hypothetical prote	765	6	1.4	135	2	S48141	hypoglycemic hormo
693	6	1.4	113	2	S33779	hypothetical prote	766	6	1.4	135	2	S48142	hypoglycemic hormo
694	6	1.4	113	2	G88947	protein C39F7.3 fi	767	6	1.4	135	2	F83611	hypothetical prote
695	6	1.4	113	2	G95390	protein [imported	768	6	1.4	136	2	T02870	globulin 2 precurs
696	6	1.4	114	2	B45036	Pur beta - human (	769	6	1.4	136	2	S37924	hypothetical prote
697	6	1.4	115	2	S44112	Ig heavy chain V r	770	6	1.4	136	2	T31126	hypothetical prote
698	6	1.4	115	2	S13726	Ig lambda chain V	771	6	1.4	136	2	C95291	hypothetical prote
699	6	1.4	116	1	HVRK	Ig heavy chain pre	772	6	1.4	137	2	T04930	glycine-rich cell
700	6	1.4	116	1	Z6BPIK	coat protein D - p	773	6	1.4	137	2	G72666	hypothetical prote
701	6	1.4	116	2	S45909	probable membrane	774	6	1.4	137	2	B82998	hypothetical prote
702	6	1.4	116	2	T48427	hypothetical prote	775	6	1.4	138	2	S24106	envelope protein -
703	6	1.4	117	2	S24658	Ig heavy chain V r	776	6	1.4	138	2	S24082	hypothetical 15K p
704	6	1.4	117	2	S24656	Ig heavy chain V r	777	6	1.4	138	2	JT0593	hypothetical prote
705	6	1.4	117	2	S24661	Ig heavy chain V r	778	6	1.4	138	2	C87389	hypothetical prote
706	6	1.4	117	2	F70881	Ig heavy chain V r	779	6	1.4	139	2	B33910	sal homeotic prote
707	6	1.4	117	2	S69301	hypothetical prote	780	6	1.4	139	2	H83287	protein par-1 (imp
708	6	1.4	117	2	T45695	hypothetical prote	781	6	1.4	139	2	F84701	hypothetical prote
709	6	1.4	117	2	S69471	hypothetical prote	782	6	1.4	139	2	T03372	high mobility grou
710	6	1.4	118	2	A32529	Ig lambda chain pr	783	6	1.4	140	2	JC4607	hydrophobin 1 prec
711	6	1.4	118	2	A72654	hypothetical prote	784	6	1.4	140	2	A64886	ydar protein - Esc
712	6	1.4	118	2	F87447	hypothetical prote	785	6	1.4	141	2	C32536	T-cell receptor al
713	6	1.4	119	2	S24655	Ig heavy chain V r	786	6	1.4	141	2	H85609	kinase [imported]
714	6	1.4	119	2	S24657	Ig heavy chain V r	787	6	1.4	141	2	T17493	citrate utilizatio
715	6	1.4	119	2	S24659	Ig heavy chain V r	788	6	1.4	141	2	A27249	vitelline membrane
716	6	1.4	119	2	PH1533	Ig H chain V regio	789	6	1.4	141	2	T46427	hypothetical prote
717	6	1.4	119	2	S30526	Ig lambda chain V	790	6	1.4	142	1	HARB	hemoglobin alpha c
718	6	1.4	119	2	A97825	50S ribosomal prot	791	6	1.4	142	2	S00262	sal homeotic prote
719	6	1.4	119	2	D71671	ribosomal protein	792	6	1.4	142	2	C33910	sal homeotic prote
720	6	1.4	120	2	S11090	FK506-binding prot	793	6	1.4	142	2	F70517	hypothetical prote
721	6	1.4	120	2	S24654	Ig heavy chain V r	794	6	1.4	143	2	T12144	hypothetical prote
722	6	1.4	120	2	PS0055	Ig lambda chain pr	795	6	1.4	143	2	G72492	hypothetical prote
723	6	1.4	120	2	PS0056	Ig lambda chain pr	796	6	1.4	144	2	T15047	RNA binding protei
724	6	1.4	120	2	A54256	Ig heavy chain V r	797	6	1.4	144	2	T18867	hypothetical prote
725	6	1.4	120	2	A34871	Ig kappa chain V r	798	6	1.4	144	2	F72556	hypothetical prote
726	6	1.4	120	2	T51754	endo-xyloglucan tr	799	6	1.4	144	2	T25028	hypothetical prote
727	6	1.4	120	2	A13137	hypothetical prote	800	6	1.4	144	2	S68454	SKB7 protein homol
728	6	1.4	121	2	S24660	Ig heavy chain V r	801	6	1.4	145	2	C83639	hypothetical prote
729	6	1.4	122	1	R5HG12	ribosomal protein	802	6	1.4	146	2	S02083	Ig lambda chain V-
730	6	1.4	122	2	T48951	hypothetical prote	803	6	1.4	146	2	S71256	ribosomal protein
731	6	1.4	122	2	AD2072	hypothetical prote	804	6	1.4	146	2	C82254	conserved hypotet
732	6	1.4	123	2	S40378	Ig kappa chain - h	805	6	1.4	146	2	AP2642	conserved hypotet
733	6	1.4	124	1	NRGPA	pancreatic ribonuc	806	6	1.4	147	1	VBHU	transthyretin prec
734	6	1.4	124	1	NROZ	pancreatic ribonuc	807	6	1.4	147	1	VBRT	transthyretin prec
735	6	1.4	124	1	TVVPBJ	small T antigen -	808	6	1.4	147	1	VBRT	transthyretin prec
736	6	1.4	124	2	S24653	Ig heavy chain V r	809	6	1.4	147	2	S05320	transthyretin prec
737	6	1.4	124	2	JS0515	hypothetical 12.4K	810	6	1.4	147	2	C84049	hypothetical prote
738	6	1.4	124	2	T19000	hypothetical prote	811	6	1.4	147	2	B63040	hypothetical prote
739	6	1.4	124	2	AE2521	transposase alr734	812	6	1.4	148	2	S07196	meiosis and sporul
740	6	1.4	125	2	S72665	Ig V-D-J region (R	813	6	1.4	148	2	E87609	hypothetical prote
741	6	1.4	125	2	H90062	conserved hypotet	814	6	1.4	148	2	S10238	leghemoglobin glb3
742	6	1.4	125	2	T49356	hypothetical prote	815	6	1.4	148	2	E95384	protein [imported
743	6	1.4	127	1	VERB	transthyretin - ra	816	6	1.4	149	2	A83696	nitrogen fixation
744	6	1.4	127	2	S40380	Ig kappa chain V-J	817	6	1.4	149	2	S67473	transthyretin prec
745	6	1.4	127	2	PH1420	Ig heavy chain V r	818	6	1.4	149	2	T23179	hypothetical prote
746	6	1.4	127	2	PH1421	Ig heavy chain V r	819	6	1.4	149	2	F75509	hypothetical prote
747	6	1.4	127	2	S70444	Ig lambda chain pr	820	6	1.4	150	2	S17827	transthyretin prec
748	6	1.4	127	2	AB1063	phage immunity rep	821	6	1.4	150	2	S65955	transthyretin prec
749	6	1.4	127	2	F69377	molybdenum-pterin-	822	6	1.4	150	2	F83061	peptide n-acetyltr
750	6	1.4	127	2	G98316	hypothetical prote	823	6	1.4	150	2	C95233	conserved hypotet
751	6	1.4	127	2	JC1273	ribosomal protein	824	6	1.4	150	2	T21489	hypothetical prote
752	6	1.4	128	2	D71328	probable flagellar	825	6	1.4	150	2	F86299	hypothetical prote
753	6	1.4	129	2	T36916	hypothetical prote	826	6	1.4	150	2	AG3397	hypothetical membr
754	6	1.4	129	2	H72806	probable DNA prima	827	6	1.4	151	2	H69991	hypothetical prote
755	6	1.4	130	2	B32456	Ig kappa chain pre	828	6	1.4	151	2	A69823	hypothetical prote
756	6	1.4	130	2	T22004	hypothetical prote	829	6	1.4	152	2	JC1521	synaptobrevin isof
757	6	1.4	132	2	PL0114	Ig lambda chain pr	830	6	1.4	152	2	A97003	probable beta-D-ga
758	6	1.4	132	2	A55410	Ig light chain V r	831	6	1.4	152	2	G96010	hypothetical expor
759	6	1.4	132	2	S04937	Ig lambda chain pr	832	6	1.4	154	2	AH0704	probable lipoprote

833	6	1.4	154	2	F86437	protein F28K20.12	906	6	1.4	178	1	LGBO	beta-lactoglobulin
834	6	1.4	154	2	E96728	hypothetical prote	907	6	1.4	178	2	G97359	fxsA protein (WC26
835	6	1.4	155	2	T00844	hypothetical prote	908	6	1.4	178	2	AH2577	conserved hypochet
836	6	1.4	155	2	T35626	probable membrane	909	6	1.4	178	2	E83025	conserved hypochet
837	6	1.4	155	2	G72580	hypothetical prote	910	6	1.4	178	2	E88637	protein W09G12.6 l
838	6	1.4	156	2	S41771	glycine-rich RNA-b	911	6	1.4	178	2	F87408	hypothetical prote
839	6	1.4	156	2	B36905	conserved hypochet	912	6	1.4	179	2	T05810	hypothetical prote
840	6	1.4	156	2	T16066	hypothetical prote	913	6	1.4	180	1	LWRZ1	H+-transporting tw
841	6	1.4	156	2	C84688	probable C2H2-type	914	6	1.4	180	1	LGST	beta-lactoglobulin
842	6	1.4	157	2	S18651	variant surface an	915	6	1.4	180	1	LGSH	hypothetical prote
843	6	1.4	157	2	AH1070	probable membrane	916	6	1.4	180	2	E69024	hypothetical prote
844	6	1.4	157	2	S57603	hypothetical prote	917	6	1.4	180	2	S43791	PBX protein - hum
845	6	1.4	157	2	G97402	hypothetical prote	918	6	1.4	181	2	D81450	aminocacyl-tRNA hyd
846	6	1.4	157	2	A70058	conserved hypochet	919	6	1.4	181	2	E84775	hypothetical prote
847	6	1.4	158	2	S74928	ribosomal protein-	920	6	1.4	181	2	T48241	hypothetical prote
848	6	1.4	158	2	S61953	hrpK protein - Pse	921	6	1.4	181	2	H95863	hypothetical prote
849	6	1.4	158	2	S77877	hypothetical prote	922	6	1.4	181	2	E86819	hypothetical prote
850	6	1.4	159	2	AC1103	7,8-dihydro-6-hydr	923	6	1.4	181	2	C85354	RNase L inhibitor-
851	6	1.4	159	2	AC1465	7,8-dihydro-6-hydr	924	6	1.4	182	1	KRBO2A	keratin, 68K type
852	6	1.4	159	2	F86429	protein F26G16.9 l	925	6	1.4	183	1	PWMT1	H+-transporting tw
853	6	1.4	159	2	T04173	heat shock protein	926	6	1.4	183	1	KNRZG2	glycine-rich cell
854	6	1.4	159	2	T31598	hypothetical prote	927	6	1.4	183	2	S57772	early nodulin GRP3
855	6	1.4	159	2	D87658	hypothetical prote	928	6	1.4	183	2	D45392	orf4 protein - por
856	6	1.4	159	2	T48209	hypothetical prote	929	6	1.4	183	2	E36861	orf4 protein - bel
857	6	1.4	160	2	S30056	major allergen Cor	930	6	1.4	183	2	D71828	hypothetical prote
858	6	1.4	160	2	C83048	hypothetical prote	931	6	1.4	183	2	G64689	hypothetical prote
859	6	1.4	161	2	T07639	pEARL1 1 protein h	932	6	1.4	183	2	AC2632	hypothetical prote
860	6	1.4	161	2	T46048	hypothetical prote	933	6	1.4	183	2	G97414	hypothetical prote
861	6	1.4	161	2	F86303	hypothetical prote	934	6	1.4	183	2	A11562	B. subtilis Ydfe p
862	6	1.4	161	2	E43719	ureg protein - Pro	935	6	1.4	184	1	LMNT1	H+-transporting tw
863	6	1.4	162	2	C85356	hypothetical prote	936	6	1.4	184	1	PWSP1	H+-transporting tw
864	6	1.4	162	2	F75339	hypothetical prote	937	6	1.4	184	2	JC2429	activin-A protein
865	6	1.4	162	2	B87656	hypothetical prote	938	6	1.4	184	2	AB2503	hypothetical prote
866	6	1.4	163	2	JC6571	cold-inducible RNA	939	6	1.4	184	2	AB1206	B. subtilis Ydfe p
867	6	1.4	163	2	T23076	hypothetical prote	940	6	1.4	185	2	B97156	probable membrane
868	6	1.4	163	2	KNRZG1	glycine-rich cell	941	6	1.4	185	2	G84671	hypothetical prote
869	6	1.4	166	1	KRBO2B	keratin, 68K type	942	6	1.4	187	2	T45176	conserved hypochet
870	6	1.4	166	2	T10463	glycine-rich prote	943	6	1.4	187	2	G70769	precorrin-6B methy
871	6	1.4	166	2	A33637	Xtvi protein - Afr	944	6	1.4	188	1	G70955	probable 2-amino-4
872	6	1.4	167	2	D87431	single-strand bind	945	6	1.4	188	2	AF1295	phosphoribosylglyc
873	6	1.4	167	2	A87150	tuberculin related	946	6	1.4	188	2	F89876	phosphoribosylglyc
874	6	1.4	167	2	S76890	hypothetical prote	947	6	1.4	188	2	S18956	fix23-4 protein -
875	6	1.4	167	2	H72579	hypothetical prote	948	6	1.4	189	2	JC4072	virulence-associat
876	6	1.4	168	2	F84459	hypothetical prote	949	6	1.4	189	2	T28092	hypothetical prote
877	6	1.4	169	1	S38331	glycine-rich RNA-b	950	6	1.4	189	2	T06555	blue copper-bindin
878	6	1.4	169	2	S30148	glycine-rich prote	951	6	1.4	189	2	A86369	hypothetical prote
879	6	1.4	169	2	F84259	hypothetical prote	952	6	1.4	190	2	S25740	Ig lambda chain -
880	6	1.4	170	2	D87707	hypothetical prote	953	6	1.4	190	2	S12674	ribosomal protein
881	6	1.4	171	2	T27371	peptidylprolyl iso	954	6	1.4	190	2	T00735	hypothetical prote
882	6	1.4	171	2	H84709	probable glycine-r	955	6	1.4	190	2	T46985	hypothetical prote
883	6	1.4	171	2	A11280	hypothetical prote	956	6	1.4	190	2	AI0240	conserved hypochet
884	6	1.4	171	2	H84923	hypothetical prote	957	6	1.4	190	2	H85357	hypothetical prote
885	6	1.4	171	2	S57894	laminin - Hydra vu	958	6	1.4	190	2	A87263	hypothetical prote
886	6	1.4	172	2	S66014	single-stranded DN	959	6	1.4	191	2	S56012	XS-2 protein (homo
887	6	1.4	172	2	T39026	conserved hypochet	960	6	1.4	191	2	H87330	hypothetical prote
888	6	1.4	173	2	JQ1064	glycine-rich prote	961	6	1.4	191	2	F75340	conserved hypochet
889	6	1.4	173	2	H82149	crossover junction	962	6	1.4	192	2	S16572	plastoquinol-plast
890	6	1.4	173	2	A47303	FTZ-F1 steroid rec	963	6	1.4	192	2	AH3643	cytochrome b561 [i
891	6	1.4	174	2	S54379	pancreatitis-aseoc	964	6	1.4	192	2	S15930	hypothetical 21.5K
892	6	1.4	174	2	E88274	inositol 1,4,5-tri	965	6	1.4	192	2	E71917	hypothetical prote
893	6	1.4	174	2	E84868	hypothetical prote	966	6	1.4	192	2	D64594	hypothetical prote
894	6	1.4	175	2	T01215	protein kinase hom	967	6	1.4	192	2	F72805	gp49 protein - Myc
895	6	1.4	175	2	PH0261	hypothetical 17.8K	968	6	1.4	193	2	C86334	hypothetical prote
896	6	1.4	176	1	A46606	platelet glycoprot	969	6	1.4	193	2	H90364	hypothetical prote
897	6	1.4	176	2	F81098	endopeptidase Clp	970	6	1.4	194	2	D83175	hypothetical prote
898	6	1.4	176	2	S30147	glycine-rich RNA b	971	6	1.4	194	2	AG3177	Mg(2+) transport A
899	6	1.4	176	2	I40121	outer surface prot	972	6	1.4	195	2	A83031	conserved hypochet
900	6	1.4	176	2	G83369	hypothetical prote	973	6	1.4	195	2	E81903	hypothetical prote
901	6	1.4	176	2	D84369	hypothetical prote	974	6	1.4	195	2	B84603	AtRer1B [imported]
902	6	1.4	177	2	H86710	hypothetical prote	975	6	1.4	195	2	T51628	endoplasmatic reti
903	6	1.4	177	2	F81442	hypothetical prote	976	6	1.4	195	2	AD2782	hypothetical prote
904	6	1.4	177	2	A12177	hypothetical prote	977	6	1.4	195	2	G83170	hypothetical prote
905	6	1.4	177	2	I49069	A+U-rich RNA-bind	978	6	1.4	195	2	T03245	G-box binding fact

979	6	1.4	196	2	B28964	platelet-derived g	1052	6	1.4	215	2	C95352	hypothetical prote
980	6	1.4	196	2	A40623	heat shock protein	1053	6	1.4	215	2	G87554	hypothetical prote
981	6	1.4	196	2	E97561	hypothetical prote	1054	6	1.4	216	1	TLBPX2	tail fiber protein
982	6	1.4	197	2	S46928	phycochrome - Char	1055	6	1.4	216	2	S61545	transferrin bindin
983	6	1.4	197	2	T03442	glycine-rich prote	1056	6	1.4	216	2	S61544	transferrin bindin
984	6	1.4	197	2	F96799	Similar to 'MADS b	1057	6	1.4	216	2	AD1118	dihydroxyacetone k
985	6	1.4	198	2	T49955	40S ribosomal prot	1058	6	1.4	216	2	AF1478	dihydroxyacetone k
986	6	1.4	199	2	T36594	probable single-st	1059	6	1.4	216	2	F70073	hypothetical prote
987	6	1.4	199	2	S41316	coat protein - cuc	1060	6	1.4	216	2	T25025	hypothetical prote
988	6	1.4	200	2	D82698	DNA repair system	1061	6	1.4	216	2	G82532	outer membrane lip
989	6	1.4	200	2	D83997	hypothetical prote	1062	6	1.4	217	2	S74394	phosphoribosylglyc
990	6	1.4	200	2	G86214	protein T6D22.4 [i	1063	6	1.4	217	2	T45364	ribosomal protein
991	6	1.4	200	2	C49529	RNA-directed RNA p	1064	6	1.4	217	2	H70641	probable ribosomal
992	6	1.4	200	2	AD3220	conserved hypotet	1065	6	1.4	217	2	T27524	hypothetical prote
993	6	1.4	201	2	F84596	glycine-rich prote	1066	6	1.4	217	2	H85433	homeodomain protei
994	6	1.4	201	2	D82779	hypothetical prote	1067	6	1.4	218	2	A87142	50S ribosomal prot
995	6	1.4	201	2	T46295	hypothetical prote	1068	6	1.4	218	2	A97237	uncharacterized co
996	6	1.4	201	2	G01204	twist protein homo	1069	6	1.4	218	2	T47889	hypothetical prote
997	6	1.4	201	2	G95852	conserved hypotet	1070	6	1.4	219	2	S71472	endo-1,4-beta-xyla
998	6	1.4	201	2	F95270	hypothetical prote	1071	6	1.4	219	2	A64864	probable 2-hydroxy
999	6	1.4	202	2	E72466	hypothetical prote	1072	6	1.4	219	2	C85696	probable isomerase
1000	6	1.4	203	1	JQ1061	hypothetical prote	1073	6	1.4	219	2	C90838	probable isomerase
1001	6	1.4	203	2	I40890	sarcosine oxidase	1074	6	1.4	219	2	T06302	hypothetical prote
1002	6	1.4	204	2	A81844	endopeptidase Clp	1075	6	1.4	219	2	AH2953	conserved hypotet
1003	6	1.4	204	2	G70029	hypothetical prote	1076	6	1.4	220	2	I55963	Lyt-2.1 lymphocyte
1004	6	1.4	204	2	S50723	hypothetical prote	1077	6	1.4	220	2	B49736	collagen alpha 3(I
1005	6	1.4	204	2	T29489	hypothetical prote	1078	6	1.4	220	2	T50624	hypothetical prote
1006	6	1.4	204	2	T13208	minor capsid prote	1079	6	1.4	220	2	S30977	gene 32 protein -
1007	6	1.4	205	2	T31489	hypothetical prote	1080	6	1.4	221	2	T52622	probable peptidylp
1008	6	1.4	205	2	AF3046	hypothetical prote	1081	6	1.4	221	2	E97834	ABC transporter AT
1009	6	1.4	205	2	D90455	hypothetical prote	1082	6	1.4	221	2	F71676	glutamine transpor
1010	6	1.4	206	2	D85481	hypothetical prote	1083	6	1.4	222	1	C83CFE	cell division ATP-
1011	6	1.4	206	2	D90630	hypothetical prote	1084	6	1.4	222	2	H83528	phosphoribosylamin
1012	6	1.4	206	2	T34979	probable lipoprote	1085	6	1.4	222	2	A27270	myosin light chain
1013	6	1.4	206	2	F84459	hypothetical prote	1086	6	1.4	222	2	AH0991	cell division ATP-
1014	6	1.4	206	2	I53066	gene M-twist prote	1087	6	1.4	222	2	H86013	cell division ATP-
1015	6	1.4	206	2	C71032	hypothetical prote	1088	6	1.4	222	2	H91167	cell division ATP-
1016	6	1.4	207	2	A51925	cytochrome c oxida	1089	6	1.4	222	2	AD0464	cell division ATP-
1017	6	1.4	207	2	T51296	phosphoribosylglyc	1090	6	1.4	222	2	T29457	probable two-compo
1018	6	1.4	207	2	T07381	glycine-rich prote	1091	6	1.4	223	1	CSNCM	peptidylprolyl iso
1019	6	1.4	207	2	F84563	hypothetical prote	1092	6	1.4	223	2	T21646	hypothetical prote
1020	6	1.4	208	2	T04884	hypothetical prote	1093	6	1.4	223	2	F98239	hypothetical prote
1021	6	1.4	209	2	T35041	hypothetical prote	1094	6	1.4	224	2	G72746	hypothetical prote
1022	6	1.4	209	2	T17551	methytransferase-	1095	6	1.4	225	2	T35127	hypothetical prote
1023	6	1.4	209	2	B82501	hypothetical prote	1096	6	1.4	225	2	S54391	prohead proteinase
1024	6	1.4	209	2	T20155	hypothetical prote	1097	6	1.4	225	2	F6742	hypothetical prote
1025	6	1.4	209	2	C70630	hypothetical prote	1098	6	1.4	225	2	C85475	hypothetical prote
1026	6	1.4	209	2	JE0154	mitochondrial inne	1099	6	1.4	226	2	A69904	hypothetical prote
1027	6	1.4	210	2	G95228	ABC transporter, A	1100	6	1.4	226	2	C97488	hypothetical 21.6K
1028	6	1.4	210	2	F83450	hypothetical prote.	1101	6	1.4	226	2	T43814	conserved hypotet
1029	6	1.4	210	2	E75315	probable c-type cy	1102	6	1.4	227	2	A64129	probable ABC-type
1030	6	1.4	210	2	C98093	hypothetical prote	1103	6	1.4	227	2	E83288	probable ATP-bind
1031	6	1.4	210	2	A97693	probable acetyltra	1104	6	1.4	227	2	D83271	probable ABC-trans
1032	6	1.4	210	2	AE2970	conserved hypotet	1105	6	1.4	227	2	F96964	ABC transporter, A
1033	6	1.4	210	2	AF2918	acetyltransferase	1106	6	1.4	228	2	S25312	plastoquinol-plast
1034	6	1.4	210	2	F98312	hypothetical prote	1107	6	1.4	228	2	C26599	clathrin light cha
1035	6	1.4	211	1	FFHUG1	platelet-derived g	1108	6	1.4	228	2	JC7761	dendritic cell-der
1036	6	1.4	211	2	D96507	hypothetical prote	1109	6	1.4	228	2	G64856	probable ABC-type
1037	6	1.4	212	1	E71111	hypothetical prote	1110	6	1.4	228	2	B90815	hypothetical prote
1038	6	1.4	212	2	A40047	peptidylprolyl iso	1111	6	1.4	228	2	C85675	hypothetical prote
1039	6	1.4	212	2	B95140	uridine kinase [im	1112	6	1.4	228	2	A82147	ABC transporter, A
1040	6	1.4	212	2	A99008	uridine kinase (EC	1113	6	1.4	229	2	S37101	ATAF1 protein - Ar
1041	6	1.4	212	2	AC0074	probable tellurium	1114	6	1.4	231	2	C81107	ABC transporter, A
1042	6	1.4	212	2	I40603	hypothetical prote	1115	6	1.4	231	2	B86154	T6A9.7 protein - A
1043	6	1.4	212	2	AG1050	conserved hypotet	1116	6	1.4	231	2	C81909	probable ABC-trans
1044	6	1.4	213	2	B83420	endopeptidase Clp	1117	6	1.4	231	2	A11262	ABC transporter, A
1045	6	1.4	213	2	S68213	Ig heavy chain (Ma	1118	6	1.4	231	2	AC1625	ABC transporter, A
1046	6	1.4	213	2	H83552	conserved hypotet	1119	6	1.4	232	2	S17399	Ig lambda chain pr
1047	6	1.4	214	1	KNNT2S	glycine-rich prote	1120	6	1.4	232	2	D72037	macromolecule tran
1048	6	1.4	214	1	ABBYD	ADE8 protein - yea	1121	6	1.4	232	2	G86588	macromolecule tran
1049	6	1.4	214	2	G84361	hypothetical prote	1122	6	1.4	232	2	F84798	hypothetical prote
1050	6	1.4	214	2	T23593	hypothetical prote	1123	6	1.4	233	2	S25748	Ig lambda chain -
1051	6	1.4	215	2	A86437	F28K20.7 protein -	1124	6	1.4	233	2	S62063	H+-exporting ATPas



1125	6	1.4	233	2	T00566	hypothenical prote	1198	6	1.4	249	1	R3RTS6	ribosomal protein
1126	6	1.4	233	2	E71515	hypothenical prote	1199	6	1.4	249	2	T09297	topoplast intrinsi
1127	6	1.4	233	2	C64412	hypothenical prote	1200	6	1.4	249	2	T25643	hypothenical prote
1128	6	1.4	233	2	F72542	hypothenical prote	1201	6	1.4	249	2	S41374	single chain Fv an
1129	6	1.4	233	2	AC0645	hypothenical prote	1202	6	1.4	249	2	S76327	hypothenical prote
1130	6	1.4	234	1	S15102	ABC transporter At	1203	6	1.4	249	2	A41497	36k antigen pra -
1131	6	1.4	234	2	A39956	eosinophil major b	1204	6	1.4	249	2	T20790	hypothenical prote
1132	6	1.4	234	2	C75639	ig lambda chain pr	1205	6	1.4	250	2	T45893	hypothenical prote
1133	6	1.4	234	2	T46203	transcription fact	1206	6	1.4	251	1	B60492	homeotic protein H
1134	6	1.4	234	2	T49448	hypothenical prote	1207	6	1.4	251	2	S25186	probable dehydroge
1135	6	1.4	234	2	AF0198	lipoprotein releas	1208	6	1.4	251	2	D70215	hypothenical prote
1136	6	1.4	235	2	S25749	ig lambda chain -	1209	6	1.4	251	2	T32200	hypothenical prote
1137	6	1.4	235	2	C64744	yeaB protein - Esc	1210	6	1.4	252	1	S01821	glycine-rich prote
1138	6	1.4	235	2	E90653	hypothenical prote	1211	6	1.4	252	2	S50217	multidrug resistan
1139	6	1.4	235	2	R85504	hypothenical prote	1212	6	1.4	252	2	F84607	hypothenical prote
1140	6	1.4	235	2	AG0532	conserved hypotet	1213	6	1.4	252	2	T45737	hypothenical prote
1141	6	1.4	235	2	AD3274	uroporphyrinogen-I	1214	6	1.4	252	2	S31022	gene 77 protein -
1142	6	1.4	236	2	B65088	hypothenical prote	1215	6	1.4	252	2	T03160	capsid protein - a
1143	6	1.4	236	2	H91115	2,5-diketo-D-gluco	1216	6	1.4	253	2	AH3280	hypothenical membr
1144	6	1.4	236	2	H85960	probable enzyme yq	1217	6	1.4	254	2	T44458	histidine/ornithin
1145	6	1.4	236	2	C75516	hypothenical prote	1218	6	1.4	254	2	H84017	hypothenical prote
1146	6	1.4	236	2	F75443	probable hydrolase	1219	6	1.4	254	2	E98329	hypothenical prote
1147	6	1.4	236	2	F75375	nodulin 21-related	1220	6	1.4	254	2	T41477	hypothenical prote
1148	6	1.4	237	2	A45587	lectin - Dioclea l	1221	6	1.4	254	2	H97081	proline/glycine be
1149	6	1.4	237	2	JU0176	lectin alpha chain	1222	6	1.4	254	2	A31488	filaggrin - mouse
1150	6	1.4	238	2	T40820	proline-rich prote	1223	6	1.4	255	2	B84777	hypothenical prote
1151	6	1.4	238	2	T34710	hypothenical prote	1224	6	1.4	255	2	F69962	amino acid ABC tra
1152	6	1.4	239	2	T40555	hypothenical prote	1225	6	1.4	255	2	E95931	probable amino aci
1153	6	1.4	239	2	AC0811	hypothenical prote	1226	6	1.4	255	2	D83281	histidine transpor
1154	6	1.4	239	2	D85073	probable amidotran	1227	6	1.4	255	2	C89936	hypothenical prote
1155	6	1.4	240	2	AB1905	phosphoribosylglyc	1228	6	1.4	255	2	A86457	probable peptide c
1156	6	1.4	240	2	B24264	proline-rich prote	1229	6	1.4	255	2	A35026	filaggrin A - mous
1157	6	1.4	240	2	S36797	lectin BMA - Bowri	1230	6	1.4	256	1	TRPF	trypsin-like prote
1158	6	1.4	240	2	D71272	hypothenical prote	1231	6	1.4	256	2	D82147	amino acid ABC tra
1159	6	1.4	240	2	A81837	probable dnaJ-fami	1232	6	1.4	256	2	T46871	C-8 sterol isomera
1160	6	1.4	240	2	T20791	hypothenical prote	1233	6	1.4	256	2	S13338	hypothenical prote
1161	6	1.4	240	2	B40357	homeotic protein 1	1234	6	1.4	256	2	B83612	hypothenical prote
1162	6	1.4	241	2	H86719	hypothenical prote	1235	6	1.4	256	2	AC1561	conserved hypotet
1163	6	1.4	241	2	G69899	transcription regu	1236	6	1.4	257	2	G42600	ABC-type transport
1164	6	1.4	242	2	B81719	conserved hypotet	1237	6	1.4	257	2	AB3231	hypothenical prote
1165	6	1.4	242	2	T34767	hypothenical prote	1238	6	1.4	257	2	H65002	histidine transpor
1166	6	1.4	243	2	A53381	hypothenical prote	1239	6	1.4	257	2	G85871	ATP-binding compon
1167	6	1.4	243	2	G97161	conserved membrane	1240	6	1.4	257	2	F91027	ATP-binding compon
1168	6	1.4	243	2	G95928	hypothenical prote	1241	6	1.4	257	2	B69213	protein-export mem
1169	6	1.4	244	2	F64247	triose-phosphate 1	1242	6	1.4	257	2	C84890	hypothenical prote
1170	6	1.4	244	2	AD1225	cobalamin biosynth	1243	6	1.4	257	2	T21029	hypothenical prote
1171	6	1.4	244	2	AF1578	cobalamin biosynth	1244	6	1.4	257	2	E83001	probable ATP-bindi
1172	6	1.4	245	1	H71873	hypothenical prote	1245	6	1.4	257	2	A96908	ABC transporter, A
1173	6	1.4	245	1	KYBOB	chymotrypsin (SC 3	1246	6	1.4	258	1	QREBPT	histidine transpor
1174	6	1.4	245	1	KYBOB	chymotrypsin (SC 3	1247	6	1.4	258	2	C70885	probable dehydroge
1175	6	1.4	245	2	AB0499	ABC transporter pe	1248	6	1.4	258	2	AE0800	histidine transpor
1176	6	1.4	245	2	C65206	thiF protein - Esc	1249	6	1.4	258	2	AD2867	hypothenical prote
1177	6	1.4	245	2	A86091	thiamin biosynthes	1250	6	1.4	258	2	A97644	hypothenical prote
1178	6	1.4	245	2	C91243	thiamin biosynthes	1251	6	1.4	259	1	WMMS28	complement factor
1179	6	1.4	246	2	A29523	T-cell surface gly	1252	6	1.4	259	2	T15126	hypothenical prote
1180	6	1.4	246	2	T46446	hypothenical prote	1253	6	1.4	259	2	T35284	hypothenical prote
1181	6	1.4	246	2	H97922	glutamine ABC tran	1254	6	1.4	259	2	T49291	hypothenical prote
1182	6	1.4	246	2	D95052	amino acid ABC tra	1255	6	1.4	259	2	S55884	CCHH finger protei
1183	6	1.4	246	2	S37959	hypothenical prote	1256	6	1.4	259	2	S01704	merozoite surface
1184	6	1.4	246	2	B96707	hypothenical prote	1257	6	1.4	260	2	H97357	stage 0 sporulatio
1185	6	1.4	246	2	T49305	hypothenical prote	1258	6	1.4	260	2	B96686	probable C2H2-type
1186	6	1.4	246	2	T20792	hypothenical prote	1259	6	1.4	261	2	C84584	probable cAMP-depe
1187	6	1.4	247	1	RWM572	T-cell surface gly	1260	6	1.4	261	2	E75335	conserved hypotet
1188	6	1.4	247	1	JQ1550	coat protein - Pan	1261	6	1.4	261	2	T40482	apoptosis specific
1189	6	1.4	247	2	T32198	hypothenical prote	1262	6	1.4	261	2	D97334	metallo-beta-lacta
1190	6	1.4	247	2	A34954	T-cell surface gly	1263	6	1.4	261	2	E86354	hypothenical prote
1191	6	1.4	247	2	G64341	hypothenical prote	1264	6	1.4	262	2	AD1239	phosphatidate cyti
1192	6	1.4	247	2	D84448	probable ankryrin I	1265	6	1.4	262	2	AH1601	phosphatidate cyti
1193	6	1.4	248	2	C83431	type III export pr	1266	6	1.4	262	2	F87484	indole-3-glycerol
1194	6	1.4	248	2	B95334	probable transcrip	1267	6	1.4	262	2	C41044	octopine transpor
1195	6	1.4	249	1	S05398	granaticin polyket	1268	6	1.4	262	2	T27381	hypothenical prote
1196	6	1.4	249	1	R3H06	ribosomal protein	1269	6	1.4	263	2	B83025	probable enoyl-CoA
1197	6	1.4	249	1	R3M56	ribosomal protein	1270	6	1.4	263	2	E70215	hypothenical prote

1271	6	1.4	263	2	S72978	hypothetical prote	1344	6	1.4	275	2	D70737	hypothetical prote
1272	6	1.4	263	2	S64857	hypothetical prote	1345	6	1.4	275	2	T43004	hypothetical prote
1273	6	1.4	264	2	B89980	hypothetical prote	1346	6	1.4	275	2	T00710	thioredoxin homolo
1274	6	1.4	264	2	T52104	GATA-binding trans	1347	6	1.4	276	2	G83304	chloroperoxidase P
1275	6	1.4	264	2	F86628	prophage p81 prote	1348	6	1.4	276	2	AF0402	transketolase (EC
1276	6	1.4	264	2	T10637	hypothetical prote	1349	6	1.4	276	2	F90063	hypothetical prote
1277	6	1.4	265	2	AI0338	histidine transpor	1350	6	1.4	277	2	T24048	hypothetical prote
1278	6	1.4	265	2	D82871	conserved hypothet	1351	6	1.4	277	2	G83473	probable short-cha
1279	6	1.4	265	2	T05085	hypothetical prote	1352	6	1.4	277	2	AF0083	probable aldo/keto
1280	6	1.4	265	2	H83139	conserved hypothet	1353	6	1.4	277	2	B85354	hypothetical prote
1281	6	1.4	265	2	S74282	hypothetical prote	1354	6	1.4	277	2	S71222	xyloglucan endo-1,
1282	6	1.4	266	2	G87308	hypothetical prote	1355	6	1.4	277	2	S47216	transcription anti
1283	6	1.4	266	2	T31217	transcription regu	1356	6	1.4	277	2	H87213	conserved hypothet
1284	6	1.4	266	2	G89797	conserved hypothet	1357	6	1.4	277	2	D84596	hypothetical prote
1285	6	1.4	267	1	CTHUP	corticotropin / 11	1358	6	1.4	277	2	D97067	probable xylanase/
1286	6	1.4	267	2	S38373	interleukin-1 beta	1359	6	1.4	278	1	C35114	indole-3-glycerol-
1287	6	1.4	267	2	B86313	hypothetical prote	1360	6	1.4	278	2	T20490	hypothetical prote
1288	6	1.4	267	2	B90486	ABC transporter, A	1361	6	1.4	278	2	S25189	hypothetical prote
1289	6	1.4	268	2	E86962	probable oxidoredu	1362	6	1.4	278	2	A49067	transcription init
1290	6	1.4	268	2	D42424	chitinase (EC 3.2.	1363	6	1.4	278	2	AH1168	a probable haloace
1291	6	1.4	268	2	T51678	myb-related transc	1364	6	1.4	279	2	T32196	hypothetical prote
1292	6	1.4	268	2	S22201	tonoplast intrinsi	1365	6	1.4	279	2	B86402	hypothetical prote
1293	6	1.4	268	2	D81807	phosphomethylpyrim	1366	6	1.4	279	2	E96586	hypothetical prote
1294	6	1.4	268	2	A70379	conserved hypothet	1367	6	1.4	279	2	T27734	hypothetical prote
1295	6	1.4	268	2	A56446	Ig heavy chain V r	1368	6	1.4	280	2	H71320	hypothetical prote
1296	6	1.4	268	2	T35568	probable lipoprote	1369	6	1.4	280	2	A35872	steroid hormone re
1297	6	1.4	268	2	T04660	hypothetical prote	1370	6	1.4	281	2	C84868	probable endochiti
1298	6	1.4	268	2	T17319	hypothetical prote	1371	6	1.4	281	2	JQ2226	middle surface pro
1299	6	1.4	268	2	T16544	hypothetical prote	1372	6	1.4	281	2	A83477	hypothetical cytos
1300	6	1.4	269	1	JQ2127	tryptophan synthas	1373	6	1.4	281	2	G86956	conserved hypothet
1301	6	1.4	269	2	T35068	indole-3-glycerol-	1374	6	1.4	281	2	T04522	hypothetical prote
1302	6	1.4	269	2	S61555	xyloglucan endo-1,	1375	6	1.4	281	2	D70845	hypothetical prote
1303	6	1.4	269	2	B95142	vicX protein limpo	1376	6	1.4	281	2	S26052	hypothetical prote
1304	6	1.4	269	2	H98009	vicX protein limpo	1377	6	1.4	282	2	T02354	xyloglucan endo-1,
1305	6	1.4	269	2	A47822	A+U-rich RNA-bind	1378	6	1.4	282	2	A85354	hypothetical prote
1306	6	1.4	270	2	H83441	probable hydrolase	1379	6	1.4	283	1	C47755	pectic enzyme secr
1307	6	1.4	270	2	D64625	thiamin biosynthes	1380	6	1.4	283	2	JC7338	carbonyl reductase
1308	6	1.4	270	2	T06118	hypothetical prote	1381	6	1.4	283	2	C84321	hypothetical prote
1309	6	1.4	270	2	F84293	hypothetical prote	1382	6	1.4	283	2	G69844	hypothetical prote
1310	6	1.4	270	2	F86177	protein F19P19.1 l	1383	6	1.4	283	2	F85700	isopentenyl monoph
1311	6	1.4	270	2	T02955	probable cytochrom	1384	6	1.4	283	2	AE0720	ychB protein (saim
1312	6	1.4	271	2	D97154	purine nucleoside	1385	6	1.4	283	2	A90843	ychB protein - Esc
1313	6	1.4	271	2	F81381	2-dehydro-3-deoxy-	1386	6	1.4	283	2	B47706	conserved hypothet
1314	6	1.4	271	2	AB2784	indole-3-glycerol-	1387	6	1.4	283	2	S27732	heat shock transcr
1315	6	1.4	271	2	S34666	glycine-rich prote	1388	6	1.4	284	1	S71851	heat shock transcr
1316	6	1.4	271	2	G90699	repressor of allan	1389	6	1.4	284	2	H85436	hypothetical prote
1317	6	1.4	271	2	A64782	probable transcrip	1390	6	1.4	284	2	T23158	hypothetical prote
1318	6	1.4	271	2	B85550	probable regulator	1391	6	1.4	284	2	E52097	homoeotic protein s
1319	6	1.4	271	2	H72261	conserved hypothet	1392	6	1.4	284	2	S74256	hypothetical prote
1320	6	1.4	271	2	T26640	hypothetical prote	1393	6	1.4	285	2	T31503	hypothetical prote
1321	6	1.4	272	1	A26936	NAD synthase (EC 6	1394	6	1.4	285	2	H86212	hypothetical prote
1322	6	1.4	272	2	C83841	purine nucleoside	1395	6	1.4	285	2	E75317	glycerophosphoryl
1323	6	1.4	272	2	AG0566	negative regulator	1396	6	1.4	285	2	T18689	hypothetical prote
1324	6	1.4	272	2	F87351	hypothetical prote	1397	6	1.4	285	2	T18689	hypothetical prote
1325	6	1.4	272	2	B71618	merozoite surface	1398	6	1.4	286	1	LRRTA1	clathrin light cha
1326	6	1.4	272	2	T30959	hypothetical prote	1399	6	1.4	286	2	A70667	hypothetical prote
1327	6	1.4	273	2	T46959	indole-3-glycerol-	1400	6	1.4	286	2	AE1200	3-hydroxyisobutyr
1328	6	1.4	273	2	B28928	pregnancy-specific	1401	6	1.4	286	2	AC1558	xyloglucan endo-1,
1329	6	1.4	273	2	S04125	chlorophyll a/b-bi	1402	6	1.4	286	2	T06202	hypothetical prote
1330	6	1.4	273	2	H81177	conserved hypothet	1403	6	1.4	286	2	A70854	hypothetical prote
1331	6	1.4	273	2	H81927	hypothetical prote	1404	6	1.4	286	2	T51008	related to antifre
1332	6	1.4	273	2	F91083	hypothetical membr	1405	6	1.4	286	2	C61615	sericin MG-2 - gre
1333	6	1.4	273	2	AC3277	transposase BME102	1406	6	1.4	287	1	A47697	probable methyltra
1334	6	1.4	274	1	SUBSD	subtilisin (EC 3.4	1407	6	1.4	287	1	I39885	RNA methylase erm
1335	6	1.4	274	2	JT0873	purine-nucleoside	1408	6	1.4	287	2	A69151	NADH dehydrogenase
1336	6	1.4	274	2	T25404	hypothetical prote	1409	6	1.4	287	2	S77770	xyloglucan endo-1,
1337	6	1.4	274	2	A72241	endoglucanase - Th	1410	6	1.4	288	2	E82978	conserved hypothet
1338	6	1.4	274	2	A82032	probable periplasm	1411	6	1.4	288	2	T05954	transcription fact
1339	6	1.4	274	2	AB0041	rihamulose-1-phosp	1412	6	1.4	288	2	A81009	hypothetical prote
1340	6	1.4	275	2	JC1085	subtilisin (EC 3.4	1413	6	1.4	288	2	D84370	halocyanin precurs
1341	6	1.4	275	2	F71714	2-dehydro-3-deoxyp	1414	6	1.4	288	2	S75502	hypothetical prote
1342	6	1.4	275	2	E81413	probable lipoprote	1415	6	1.4	289	2	A89824	hypothetical prote
1343	6	1.4	275	2	A82578	glycerol uptake fa	1416	6	1.4	289	2	S49812	xyloglucan endo-1,

1417 6 1.4 289 2 T49154 DNA-binding WRKY-1  
1418 6 1.4 289 2 G83029 hypothetical prote  
1419 6 1.4 289 2 G64105 transferrin-bindin  
1420 6 1.4 289 2 JC5938 thioredoxin-like p  
1421 6 1.4 289 2 E86148 TING-12 protein -  
1422 6 1.4 289 2 A98217 hemK protein homol  
1423 6 1.4 289 2 A13069 protoporphyriinogen  
1424 6 1.4 289 2 A84790 probable RNA-bindi  
1425 6 1.4 290 2 D82233 conserved hypothet  
1426 6 1.4 290 2 T21846 hypothetical prote  
1427 6 1.4 290 2 T21198 hypothetical prote  
1428 6 1.4 291 1 S31435 glycine-rich prote  
1429 6 1.4 291 2 AH3074 short-chain dehydr  
1430 6 1.4 291 2 A96212 probable short-cha  
1431 6 1.4 291 2 B70337 aspartate carbamoy  
1432 6 1.4 291 2 S73501 probable UTP-gluco  
1433 6 1.4 291 2 F75172 hypothetical prote  
1434 6 1.4 292 2 T06201 xyloglucan endo-1,  
1435 6 1.4 292 2 T04514 xyloglucan endo-1,  
1436 6 1.4 292 2 T34997 lysR-type transcri  
1437 6 1.4 292 2 F98340 hypothetical prote  
1438 6 1.4 292 2 AD2942 conserved hypothet  
1439 6 1.4 292 2 AE0419 probable ABC trans  
1440 6 1.4 293 1 WMBP11 gene 11 protein -  
1441 6 1.4 293 1 WMBP19 succinyl-CoA synth  
1442 6 1.4 293 2 AB2295 hypothetical prote  
1443 6 1.4 293 2 F70724 hypothetical prote  
1444 6 1.4 293 2 AF0475 lysR-family transc  
1445 6 1.4 293 2 B82988 hypothetical prote.  
1446 6 1.4 294 2 S72897 pyrroline-5-carbox  
1447 6 1.4 294 2 G84949 hypothetical prote  
1448 6 1.4 294 2 T46195 hypothetical prote  
1449 6 1.4 294 2 D70525 hypothetical beta-1 -  
1450 6 1.4 294 2 T31946 hypothetical prote  
1451 6 1.4 294 2 A55477 survival motor neu  
1452 6 1.4 294 2 E81420 probable flagellar  
1453 6 1.4 295 2 G70745 probable proc prot  
1454 6 1.4 295 2 S49261 ornithine carbamoy  
1455 6 1.4 295 2 B82109 kinase, GHMP famil  
1456 6 1.4 295 2 T02575 adenylate kinase h  
1457 6 1.4 295 2 E84962 hypothetical prote  
1458 6 1.4 296 2 A36366 enhancer-binding p  
1459 6 1.4 296 2 H83480 cytochrome o ubiq  
1460 6 1.4 296 2 T48401 histone deacetylase  
1461 6 1.4 296 2 AH1173 conserved hypothet  
1462 6 1.4 297 2 A35914 transcription fact  
1463 6 1.4 297 2 T51005 hypothetical prote  
1464 6 1.4 298 2 S49934 hypothetical prote  
1465 6 1.4 298 2 B87134 conserved hypothet  
1466 6 1.4 298 2 C96690 unknown protein F2  
1467 6 1.4 299 2 I46690 CD80 precursor - r  
1468 6 1.4 299 2 E82116 flagellar biosynth  
1469 6 1.4 299 2 AH0245 probable 4-diphosp  
1470 6 1.4 299 2 F96554 hypothetical prote  
1471 6 1.4 299 2 T47989 RAV-like protein -  
1472 6 1.4 299 2 F97089 probable permease,  
1473 6 1.4 300 1 WMLJB1 bel-1 protein - hu  
1474 6 1.4 300 2 D83158 hypothetical prote  
1475 6 1.4 300 2 S75558 cytochrome-c oxida  
1476 6 1.4 300 2 A96351 heterodisulfide re  
1477 6 1.4 301 1 Q6C3R transcription acti  
1478 6 1.4 301 2 D82997 ribosomal protein  
1479 6 1.4 301 2 B82096 ribosomal protein  
1480 6 1.4 301 2 B85482 transcription acti  
1481 6 1.4 301 2 B90631 transcription acti  
1482 6 1.4 301 2 JQ1663 hybrid proline-ric  
1483 6 1.4 301 2 A70787 hypothetical prote  
1484 6 1.4 301 2 G85928 hypothetical prote  
1485 6 1.4 302 1 S31818 myb-related protei  
1486 6 1.4 302 2 S69188 probable flavonol  
1487 6 1.4 302 2 F83492 conserved hypothet  
1488 6 1.4 302 2 D83479 probable transcrip  
1489 6 1.4 302 2 C84470 hypothetical prote

1490 6 1.4 303 2 B69160 mevalonate kinase  
1491 6 1.4 303 2 A81215 transcription regu  
1492 6 1.4 303 2 H81792 probable LysR-fami  
1493 6 1.4 303 2 D83503 probable transcrip  
1494 6 1.4 303 2 T29321 hypothetical prote  
1495 6 1.4 303 2 B84744 hypothetical prote  
1496 6 1.4 303 2 C69897 hypothetical prote  
1497 6 1.4 303 2 T02606 hypothetical prote  
1498 6 1.4 304 2 B96009 probable dihydrotol  
1499 6 1.4 304 2 E71823 DNA transfer prote  
1500 6 1.4 304 2 E64697 conjugative trans

## ALIGNMENTS

## RESULT 1

T08852

lustrin A - California red abalone

C/Species: Haliotis rufescens (California red abalone)

C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C/Accession: T08852

R/Shen, X.; Belcher, A.M.; Hansma, P.K.; Stucky, G.D.; Morse, D.E.

J. Biol. Chem. 272, 32472-32481, 1997

A/Title: Molecular cloning and characterization of lustrin A, a matrix protein from shell

A/Reference number: Z16496; MUID:98070424; PMID:9405458

A/Accession: T08852

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1428 &lt;SHE&gt;

A/Cross-references: UNIPROT:O44341; EMBL:AF023459; NID:G2723361; PIDN:AAB95154.1; PID:G2723361

A/Experimental source: tissue type mantle (shell and pearl nacre); cell type pallial

A/Keywords: extracellular matrix; extracellular protein

F;I382-1436/Domain: antileukoproteinase repeat homology &lt;ALP&gt;

Query Match 3.0%; Score 13; DB 2; Length 1428;

Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GSSSGSSSGSSSG 283

Db 1027 GSSSGSSSGSSSG 1039

## RESULT 2

A82704

1,4-beta-cellobiosidase XP1267 [imported] - Xylella fastidiosa (strain 9a5c)

C/Species: Xylella fastidiosa

C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C/Accession: A82704

R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc

Nature 406, 151-157, 2000

A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A/Reference number: A82515; MUID:20365717; PMID:10910347

A/Note: for a complete list of authors see reference number A59328 below

A/Accession: A82704

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-683 &lt;SIM&gt;

A/Cross-references: UNIPROT:Q9PDW2; GB:AE003849; NID:g9106242; PIDN:AAP84076

A/Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.; Al

Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Prohm

J.D.; Junqueira, M.B.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigri

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.

A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328  
A;Contents: annotation  
C;Genetics:  
A;Gene: XF1267

Query Match 2.7% Score 12; DB 2; Length 683;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 SSSGSSGSSGSSG 283  
Db 557 SSSGSSGSSGSSG 568

RESULT 3  
S39356  
transcription factor btd - fruit fly (Drosophila sp.)  
C;Species: Drosophila sp.  
C;Date: 18-Feb-1994 #sequence\_revision 01-Dec-1995 #text\_change 07-May-1999  
C;Accession: S39356  
R;Wimmer, E.A.; Jaeckle, H.; Pfeifle, C.; Cohen, S.M.  
Nature 366, 690-694, 1993  
A;Title: A Drosophila homologue of human Spi1 is a head-specific segmentation gene.  
A;Reference number: S39356; MUID:94081952; PMID:8259212  
A;Accession: S39356  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-644 <WIM>  
A;Cross-references: EMBL:Z29361; NID:g4411283; PID:g4411284  
C;Genetics:  
A;Gene: FlyBase:btd  
A;Cross-references: FlyBase:FBgn0000233  
A;Introns: 245/2

Query Match 2.5% Score 11; DB 2; Length 644;  
Best Local Similarity 100.0%; Pred. No. 0.097;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GSSGSSGSSGSS 281  
Db 107 GSSGSSGSSGSS 117

RESULT 4  
S68178  
mixed-lineage protein kinase 2 (EC 2.7.1.-) - human  
C;Species: Homo sapiens (man)  
C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S68178; I38044; S32468  
R;Dorow, D.S.; Devereux, L.; Tu, G.F.; Price, G.; Nicholl, J.K.; Sutherland, G.R.; Simpson, J. J. Biochem. 234, 492-500, 1995  
A;Title: Complete nucleotide sequence, expression, and chromosomal localisation of human mixed-lineage protein kinase 2.  
A;Reference number: S68178; MUID:96128179; PMID:8536694  
A;Accession: S68178  
A;Molecule type: mRNA  
A;Residues: 1-954 <DOR>  
A;Cross-references: UNIPROT:Q02779; EMBL:X90846; NID:g971419; PIDN:CAA62351.1; PID:g971419  
R;Katoh, M.; Hirai, M.; Sugimura, T.; Terada, M.  
Oncogene 10, 1447-1451, 1995  
A;Title: Cloning and characterization of MST, a novel (putative) serine/threonine kinase from human placenta.  
A;Reference number: I38044; MUID:95249256; PMID:7731697  
A;Accession: I38044  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-461, 'A', 'V', '465-470, 'S', '472-806, 'R', '808-817, 'A', '819-954 <RES>  
A;Cross-references: EMBL:Z48615; NID:g758592; PIDN:CAA88531.1; PID:g758593  
R;Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kreter, T.  
Eur. J. Biochem. 213, 701-710, 1993  
A;Title: Identification of a new family of human epithelial protein kinases containing a conserved catalytic domain.  
A;Reference number: S32467; MUID:93238756; PMID:8477742  
A;Accession: S32468  
A;Molecule type: mRNA  
A;Residues: 244-464, 'AQAQRQHPQALWL' <DO2>

C;Genetics:  
A;Gene: GDB:MLK2; GDB:MST  
A;Cross-references: GDB:362654; GDB:624810; OMIM:600137  
A;Map position: 19q13.1-19q13.2  
C;Superfamily: mixed-lineage protein kinase 2; protein kinase homology; SH3 homology  
C;Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein kinase  
F;23-76/Domain: SH3 homology <SH3>  
F;96-364/Domain: protein kinase homology <KIN>  
F;104-112/Region: protein kinase ATP-binding motif  
F;384-405/Region: leucine zipper motif  
F;419-440/Region: leucine zipper motif  
F;449-463/Region: basic  
F;125,145,222,224/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 2.5% Score 11; DB 1; Length 954;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GSSGSSGSSGSS 285  
Db 525 GSSGSSGSSGSS 535

RESULT 5  
T18272  
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) - slime mold (Dictyostelium discoideum)  
C;Species: Dictyostelium discoideum  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T18272  
R;Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.  
Mol. Cell. Biol. 15, 5645-5656, 1995  
A;Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: BioI  
A;Reference number: Z06411  
A;Accession: T18272  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1570 <ZHO>  
A;Cross-references: UNIPROT:P54673; EMBL:U23476; NID:g733519; PID:g733520; PIDN:AAA85721.  
C;Genetics:  
A;Gene: PIK1  
C;Keywords: phosphotransferase

Query Match 2.5% Score 11; DB 2; Length 1570;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GSSGSSGSSGSS 285  
Db 171 GSSGSSGSSGSS 181

RESULT 6  
G01758  
transcription factor SOX11 - human  
N;Alternate names: Aip-1  
C;Species: Homo sapiens (man)  
C;Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 16-Aug-2004  
C;Accession: G01758; JCT156  
R;Jay, P.  
submitted to the EMBL Data Library, March 1995  
A;Reference number: G08331  
A;Accession: G01758  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-441 <JAY>  
A;Cross-references: UNIPROT:P35716; EMBL:U23752; NID:g974247; PIDN:AAB08518.1; PID:g974247  
R;Azuma, T.; Ao, S.; Saito, Y.; Yano, K.; Seki, N.; Wakao, H.; Masuho, Y.; Muramatsu, M.  
DNA Res. 6, 357-360, 1999  
A;Title: Human SOX11, an upregulated gene during the neural differentiation, has a long 3'  
A;Reference number: JCT156; MUID:20039622; PMID:10574465  
A;Accession: JCT156  
A;Status: preliminary  
A;Molecule type: DNA

A;Residues: 1-441 <AZU>  
A;Cross-references: DDBJ:AB028641; NID:G6527111; PIDN:BAA88122.1; PID:G6527112  
C;Genetics:  
A;Gene: GDB:SOX11; SOX-11  
A;Cross-references: GDB:677487; OMIM:600898  
A;Map position: 2p25-2p25  
C;Superfamily: HMG box homology  
F;46-121/Domain: HMG box homology <HMG1>

Query Match 2.3%; Score 10; DB 2; Length 441;  
Best Local Similarity 100.0%; Pred. No. 0.57;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 SSGSSSGSS 281  
Db 345 SSGSSSGSS 354  
|||||

RESULT 7  
T37541  
probable glycolipid anchored surface protein - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T37541  
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
submitted to the EMBL Data Library, August 1997  
A;Reference number: Z21721  
A;Accession: T37541  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-510 <MUR>  
A;Cross-references: UNIPROT:O13692; EMBL:298595; PIDN:CAB11192.1; GSPDB:GN00066; SPDB:SF  
A;Experimental source: strain 972h-; cosmid c11E3  
C;Genetics:  
A;Gene: SPDB:SPAC11E3.13c  
A;Map position: 1  
C;Superfamily: glycopospholipid-anchored surface glycoprotein GAS1

Query Match 2.3%; Score 10; DB 2; Length 510;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 SSGSSSGSS 282  
Db 473 SSGSSSGSS 482  
|||||

RESULT 8  
T06728  
pectate lyase (EC 4.2.2.2) F28P10.100 - Arabidopsis thaliana  
N;Alternate names: protein F28P10.100  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 23-Jul-1999  
C;Accession: T06728  
R;Quettier, F.; Choise, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artig  
submitted to the Protein Sequence Database, April 1999  
A;Reference number: Z15793  
A;Accession: T06728  
A;Molecule type: DNA  
A;Residues: 1-542 <QUE>  
A;Cross-references: EMBL:AL049655  
A;Experimental source: cultivar Columbia; BAC clone F28P10  
C;Genetics:  
A;Map position: 3  
A;Introns: 46/2; 346/3; 413/2; 480/2  
A;Note: F28P10.100  
C;Superfamily: pectate lyase LAT59  
C;Keywords: carbon-oxygen lyase

Query Match 2.3%; Score 10; DB 2; Length 542;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 GSGSSSGSSG 292  
Db 433 GSGSSSGSSG 442  
|||||

RESULT 9  
KRHU2  
keratin 1, type II, cytoskeletal - human  
N;Alternate names: 67K type II epidermal keratin; cytokeratin 1  
C;Species: Homo sapiens (man)  
C;Date: 04-Dec-1986 #sequence\_revision 22-Oct-1999 #text\_change 10-Dec-1999  
C;Accession: A22940; A02950; A43342  
R;Johnson, L.D.; Idler, W.W.; Zhou, X.M.; Roop, D.R.; Steinert, P.M.  
Proc. Natl. Acad. Sci. U.S.A. 82, 1896-1900, 1985  
A;Reference number: A22940; MUID:85166239; PMID:2580302  
A;Accession: A22940  
A;Molecule type: DNA  
A;Residues: 1-643 <JOH>  
A;Cross-references: GB:M98776; GB:M11215; GB:M11845; GB:M11846; NID:G1843461  
A;Note: translation of initiator Met is not shown  
R;Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.  
J. Biol. Chem. 260, 7142-7149, 1985  
A;Title: Amino acid sequences of mouse and human epidermal type II keratins of Mr 67,000  
late filament subunits.  
A;Reference number: A92535; MUID:85207740; PMID:2581964  
A;Accession: A02950  
A;Molecule type: mRNA  
A;Residues: 151-183, 'K', 185-199, 'M', 201-204, 'K', 206-236, 'S', 238-239, 'R', 241-356, 'Y', 358-  
'S', 638-643 <STE>  
A;Cross-references: GB:M10938; NID:G186787; PIDN:AAA36153.1; PID:G386854  
A;Experimental source: tissue neonatal foreskin  
A;Note: the authors translated the codon CUG for residue 476 as Met  
R;Chipev, C.C.; Korge, B.P.; Markova, N.; Bale, S.J.; DiGiovanna, J.J.; Compton, J.G.; S  
Cell 70, 821-828, 1992  
A;Title: A leucine---proline mutation in the H1 subdomain of keratin 1 causes epidermol  
A;Reference number: A43342; MUID:92386601; PMID:1381288  
A;Accession: A43342  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 144-146, 'P', 148-159, 'P', 161-183, 'K', 185-186 <CHI>  
A;Cross-references: GB:M98776; GB:M11215; GB:M11845; GB:M11846; NID:G1843461  
A;Note: sequence extracted from NCBI backbone (NCBIP:112784)  
C;Comment: The cytoskeletal and microfibrillar keratins are classified into two types, t  
atin IF protein subunit appears to be a heterotetramer of two type I and two type II prot  
C;Comment: Keratin 1 is expressed in terminally differentiating epidermis.  
C;Genetics:  
A;Gene: GDB:KRT1  
A;Cross-references: GDB:128198; OMIM:139350  
A;Map position: 12q11-12q13  
A;Note: defects in this gene may result in epidermolytic hyperkeratosis  
C;Complex: heterotetramer of two type I, usually keratin 10 (see PIR:KRHU0), and two type  
C;Superfamily: cytoskeletal keratin  
C;Keywords: coiled coil; heterotetramer; intermediate filament  
F;4-179/Domain: head <HED>  
F;4-143/Region: E1 and V1 subdomains  
F;14-179/Region: H1 subdomain  
F;180-492/Domain: rod <ROD>  
F;180-214/Region: coil 1A  
F;215-226/Region: linker 1  
F;227-327/Region: coil 1B  
F;328-344/Region: linker 12  
F;345-363/Region: coil 2A  
F;364-371/Region: linker 2  
F;372-492/Region: coil 2B  
F;430/Region: stutter  
F;493-643/Domain: tail <END>  
F;493-512/Region: H2 subdomain  
F;513-643/Region: V2 and E2 subdomains

Query Match 2.3%; Score 10; DB 1; Length 643;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 GGSSGGSSGG 292  
Db 605 GGSSGGSSGG 614

## RESULT 10

outD protein - *Erwinia chrysanthemi*  
 C:Species: *Erwinia chrysanthemi*  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
 C:Accession: S28014; S23886  
 R:Condemine, G.; Dorel, C.; Hugouvieux-Cotte-Pattat, N.; Robert-Baudouy, J.  
 Mol. Microbiol. 6, 3199-3211, 1992  
 A:Title: Some of the out genes involved in the secretion of pectate lyases in *Erwinia chrysanthemi*  
 A:Reference number: S28011; MUID:93086427; PMID:1453958  
 A:Accession: S28014  
 A:Molecule type: DNA  
 A:Residues: 1-710 <CON>  
 A:Cross-references: UNIPROT:Q01565; EMBL:X65265; NID:g3152953; PIDN:CAA46370.1; PID:g50111  
 C:Genetics:  
 A:Gene: outD  
 A:Start codon: GTG

Query Match	Best Local Similarity	Matches	10; Conservative
QY	273	SSGSSSGSSS	282
Db	322	SSGSSSGSSS	331

## RESULT 11

T09219  
basal transcription factor SNAPc large chain SNAP190 - human  
C:Species: Homo sapiens (man)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 16-Aug-2004  
C:Accession: T09219  
R:Mong, M.W.; Henry, R.W.; Ma, B.; Kobayashi, R.; Klages, N.; Matthias, P.; Strubin, M.;  
Mol. Cell. Biol. 18, 368-377, 1998  
A:Title: The large subunit of basal transcription factor SNAPc is a Myb domain protein  
A:Reference number: Z16616; MUID:98078693; PMID:9418884  
A:Accession: T09219  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1469 <N>  
A:Cross-references: UNIPROT:Q916P7; EMBL:AF032387; NID:G92641556; PIDN:AAC02972.1; PID:G92641556  
A:Experimental source: tissue type fetal cell teratocarcinoma  
C:Genetics:  
A:Gene: SNAP190

A;Description: transcription factor; required for transcription of snRNA genes  
C;Function:  
C;Superfamily: myb DNA-binding repeat homology  
C;Keywords: RNA binding; RNA biosynthesis; transcription factor  
F:396-447/Domain: myb DNA-binding repeat homology <MYB>

Query Match	2
Best Local Similarity	10
Matches	10; Conservative
Qy	272 SSSGSSSSSS 281
Db	522 SSSGSSSSSS 531

## RESULT 12

Tl3594  
 Hypothetical protein pib - fruit fly (*Drosophila melanogaster*)  
 C:Species: *Drosophila melanogaster*  
 C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
 C:Accession: Tl3594  
 R:Ferriaz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.  
 submitted to the EMBL Data Library. October 1998

A:Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.  
A:Reference number: Z17692  
A:Accession: T13594  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1891 <FER>  
A:Cross-references: UNIPROT:O77275; EMBL:AL031227; NID:e1330103; PID:e1316856  
C:Genetics:  
A:Gene: peb  
A:Cross-References: FlyBase:FBgn003053  
A:Introns: 289/3

	Query Match	2.3%	Score 10;	DB 2;	Length 1891;
	Best Local Similarity	100.0%;	Pred. No. 2;		
	Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	276	SSSSSSSSSS	285		
Db	215	SSSSSSSSSS	224		

RESULT 13

Gene hindsight protein - fruit fly (*Drosophila melanogaster*)  
 TI3893  
 C:Species: *Drosophila melanogaster*  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: T13893  
 R:Yip, M.L.R.; Lamka, M.L.; Lipshitz, H.D.  
 Development 124, 2129-2141, 1997  
 A:Title: Control of germ-band retraction in *Drosophila* by the zinc-finger p  
 A:Reference number: T17807; MUID:97330681; PMID:9187140

A:Accession: J13953  
A:Status: preliminary; translated from GB/EMBL/DDBB  
A:Molecule type: mRNA  
A:Residues: 1-1920 <YIP>  
A:Cross-references: UNIPROT:O46205; EMBL:U86010; N  
C:Genetics:  
A:Gene: hindsight  
A:Cross-references: FlyBase:FBgn0003053  
C:Function:  
A:Description: probably function as a transcription  
C:Keywords: nucleus; zinc finger

Query Match	2.3%;	Scores 10;	DB 2;	Length 1920;
Best Local Similarity	100.0%;	Pred. No. 2;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	276	SSGSSSSGGG	285	
Db	215	SSGSSSSGGG	224	

## RESULT 14

D87278  
DNA-binding response regulator [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #seqblu\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: D87278  
E:Ernerman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; H  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt  
n, J.; Ermlaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.;  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.  
A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: D6/278  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-235 <STO>  
A:Cross-references: UNIPROT:Q9ABJ0; GB:AE005673; NID:g13  
C:Genetics:  
A:Gene: CC0237  
C:Superfamily: ompR protein; response regulator homology

Query Match 2.0%; Score 9; DB 2; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 2.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AGGAAGSKV 67  
 |||||  
 Db 129 AGGAAGSKV 137

RESULT 15  
 F84088  
 N-acetylmuramoyl-L-alanine amidase (sporulation mother cell wall hydrolase) BH3510 [impo  
 C;Species: Bacillus halodurans  
 C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C;Accession: F84088  
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A;Reference number: A83650; MUID:20512582; PMID:11058132  
 A;Accession: F84088  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-275 <STO>  
 A;Cross-references: UNIPROT:Q9K763; GB:AF001519; GB:BA000004; NID:g10176109; PIDN:BAB072  
 A;Experimental source: strain C-125  
 C;Genetics:  
 A;Gene: BH3510

Query Match 2.0%; Score 9; DB 2; Length 275;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 SSGSGSGGS 289  
 |||||  
 Db 184 SSGSGSGGS 192

Search completed: April 7, 2005, 00:41:20  
 Job time : 62 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 7, 2005, 00:23:07 ; Search time 178 Seconds  
(without alignments)  
1265.814 Million cell updates/sec

Title: US-10-063-561-52  
Perfect score: 440  
Sequence: 1 MKPQGLACLLALCLGSGE.....KLGFINDAINKQDRSSRIP 440

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Uniprot\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	440	100.0	440	2	Q6UXC7
2	178	40.5	476	2	Q6E0U4
3	25	5.7	137	2	Q96EW8
4	16	3.6	182	2	Q9CR91
5	15	3.4	319	2	Q6C4B0
6	15	3.4	417	2	Q693B5
7	15	3.4	456	2	Q7UJ76
8	14	3.2	792	2	Q8PZV5
9	13	3.0	120	2	Q6ZUH6
10	13	3.0	199	2	Q94476
11	13	3.0	202	2	Q8WML4
12	13	3.0	282	2	Q8MYJ1
13	13	3.0	297	2	Q86HE5
14	13	3.0	375	2	Q8TI63
15	13	3.0	418	2	Q9GRU6
16	13	3.0	476	2	Q18453
17	13	3.0	770	2	Q6BIY3
18	13	3.0	1428	2	Q44341
19	12	2.7	283	2	Q6NZV7
20	12	2.7	283	2	Q6PG31
21	12	2.7	411	2	Q8LW55
22	12	2.7	484	2	Q75WB9
23	12	2.7	487	2	Q75WB8
24	12	2.7	683	2	Q9PDW2
25	12	2.7	708	2	Q8SX98
26	12	2.7	751	2	Q8MLU0
27	12	2.7	761	2	Q7KVL6
28	12	2.7	1690	2	Q76P31
29	11	2.5	90	2	Q7RWL2
30	11	2.5	158	2	Q9EWB3
31	11	2.5	161	1	TATB_STRCO

32	11	2.5	167	2	Q6EP11	Q6ep11 oryza sativ
33	11	2.5	202	1	SSBI_STRAW	Q82fg5 streptomyce
34	11	2.5	252	2	Q9WJ70	Q9w3t0 drosophila
35	11	2.5	270	1	CIT2_HUMAN	Q9967 homo sapien
36	11	2.5	315	2	Q8SX83	Q8ex3 drosophila
37	11	2.5	473	1	CHIA_MOUSE	Q9ix39 mus musculu
38	11	2.5	493	2	Q6SZJ9	Q6szj9 mus musculu
39	11	2.5	508	2	Q6P253	Q6p253 mus musculu
40	11	2.5	517	2	Q6E0U6	Q6e0u6 mus musculu
41	11	2.5	525	2	Q693B7	Q693b7 microbulbif
42	11	2.5	530	2	Q693B6	Q693b6 microbulbif
43	11	2.5	607	2	Q693B4	Q693b4 debaryomyce
44	11	2.5	644	1	BTB_DROME	Q24266 drosophila
45	11	2.5	718	2	Q73619	Q73619 xenopus lae
46	11	2.5	766	2	Q6CV63	Q6cv63 kluyveromyc
47	11	2.5	954	1	M3KA_HUMAN	Q02779 homo sapien
48	11	2.5	1570	1	P3K1_DICDI	P54673 dictyosteli
49	10	2.3	100	2	Q964C3	Q964c3 encephalito
50	10	2.3	102	2	Q964C0	Q964c0 encephalito
51	10	2.3	117	2	Q964C2	Q964c2 encephalito
52	10	2.3	121	2	Q964C5	Q964c5 encephalito
53	10	2.3	125	2	Q964C1	Q964c1 encephalito
54	10	2.3	138	2	Q964C4	Q964c4 encephalito
55	10	2.3	185	2	Q827Z8	Q827z8 streptomyce
56	10	2.3	174	2	Q6BNH9	Q6bnh9 debaryomyce
57	10	2.3	230	2	Q8TCV1	Q8tcv1 plasmodium
58	10	2.3	232	2	Q8TGU2	Q8tgu2 plasmodium
59	10	2.3	251	2	Q9UVE7	Q9uve7 varrowia li
60	10	2.3	273	2	Q898T3	Q898t3 clostridium
61	10	2.3	407	2	Q8C4L6	Q8c4l6 mus musculu
62	10	2.3	441	1	SL11_HUMAN	F35716 homo sapien
63	10	2.3	450	1	SWP1_ENCCU	Q9xzv1 encephalito
64	10	2.3	454	2	Q7X8B6	Q7x8b6 oryza sativ
65	10	2.3	476	1	CHIA_HUMAN	Q9bzp6 homo sapien
66	10	2.3	476	2	Q80890	Q80890 herpesvirus
67	10	2.3	480	2	Q8T2I5	Q8t2i5 dictyosteli
68	10	2.3	501	1	PLI3_ARATH	Q93z04 arabidopsis
69	10	2.3	508	2	Q8DA23	Q8da23 vibrio vuln
70	10	2.3	510	1	YDYD_SCHPO	O13692 schizosacch
71	10	2.3	542	2	Q7MK56	Q7mk56 vibrio vuln
72	10	2.3	561	2	Q7TFC1	Q7tpc1 mus musculu
73	10	2.3	572	2	Q88NL2	Q88nl2 pseudomonas
74	10	2.3	641	1	GSQD_ERWCH	Q7pfh8 anopheles g
75	10	2.3	710	1	Q01565	Q01565 erwinia chr
76	10	2.3	732	2	Q7RYT2	Q7ryt2 neuropeptora
77	10	2.3	952	2	Q9V4V0	Q9v4v0 drosophila
78	10	2.3	1028	2	Q86P35	Q86p35 drosophila
79	10	2.3	1398	2	Q6E2N4	Q6e2n4 brachydanio
80	10	2.3	1398	2	Q6UV33	Q6uv33 brachydanio
81	10	2.3	1469	2	Q9Y6P7	Q9y6p7 homo sapien
82	10	2.3	1562	2	Q7YY78	Q7yy78 cryptospori
83	10	2.3	1891	2	Q77275	Q77275 drosophila
84	10	2.3	1893	2	Q9W4J1	Q9w4j1 drosophila
85	10	2.3	1920	2	Q46205	Q46205 drosophila
86	10	2.3	2090	2	Q9W2T1	Q9w2t1 drosophila
87	10	2.3	3122	2	Q8B3T9	Q8b3t9 citrullus tris
88	9	2.0	109	2	Q71D57	Q71d57 drosophila
89	9	2.0	152	2	Q8B571	Q8b571 pseudocowpo
90	9	2.0	167	2	Q9D428	Q9d428 mus musculu
91	9	2.0	197	2	Q9CRD9	Q9crd9 mus musculu
92	9	2.0	207	2	Q7Z4M7	Q7z4m7 homo sapien
93	9	2.0	208	2	Q7PFN9	Q7pf9 anopheles g
94	9	2.0	227	2	Q6Z8R3	Q6z8r3 oryza sativ
95	9	2.0	230	2	Q9N9X2	Q9n9x2 geodia cydo
96	9	2.0	235	2	Q9ABJ0	Q9abj0 caulobacter
97	9	2.0	260	2	Q86U74	Q86u74 dictyosteli
98	9	2.0	262	2	Q767M8	Q767m8 sus scrofa
99	9	2.0	275	2	Q9K763	Q9k763 bacillus ha
100	9	2.0	280	2	Q9VI07	Q9vi07 drosophila
101	9	2.0	322	2	Q8G4E5	Q8g4e5 bifidobacte
102	9	2.0	324	2	Q7X6C5	Q7x6c5 oryza sativ
103	9	2.0	326	2	Q9C9A0	Q9c9a0 arabidopsis
104	9	2.0	328	2	Q6BK18	Q6bk18 debaryomyce

105	9	2.0	343	2	Q7S729	Q7S729	neurospora	178	9	2.0	1427	2	Q9KGX8	Q9kgx8	mycoplasma
106	9	2.0	347	2	Q8C9F3	Q8c9f3	mus musculus	179	9	2.0	1436	2	Q8C523	Q8c523	bifidobacte
107	9	2.0	360	2	Q8MSN0	Q8msn0	drosoephila	180	9	2.0	1478	2	Q8TLD5	Q8tld5	methanosarc
108	9	2.0	361	2	Q8C9Q5	Q8c9q5	mus musculus	181	9	2.0	1486	2	Q95RES	Q95res	drosoephila
109	9	2.0	388	2	Q8IR08	Q8ir08	drosoephila	182	9	2.0	1486	2	Q967Y2	Q967y2	drosoephila
110	9	2.0	389	2	Q7PT82	Q7pt82	anopheles g	183	9	2.0	1486	2	Q7KR7	Q7krp7	drosoephila
111	9	2.0	394	2	Q8TQ10	Q8tq10	methanosarc	184	9	2.0	1582	2	Q7KR6	Q7krp6	drosoephila
112	9	2.0	395	1	QX11_MOUSE	Qx11_MOUSE	mus musculus	185	9	2.0	1709	1	CHD1_HUMAN	Chd1_HUMAN	homo sapien
113	9	2.0	395	2	Q7M6Y2	Q7m6y2	mus musculus	186	9	2.0	1711	1	CHD1_MOUSE	Chd1_MOUSE	mus musculus
114	9	2.0	395	2	Q80XF0	Q80xf0	mus musculus	187	9	2.0	1786	2	Q7ZT34	Q7zt34	poephila gu
115	9	2.0	402	1	QPS4_CANAL	P46596	candida alb	188	9	2.0	1806	2	Q800S6	Q800s6	poephila gu
116	9	2.0	406	2	Q8YH69	Q8yh69	bradyrhizob	189	9	2.0	1808	2	Q42142	Q42142	gallus gall
117	9	2.0	417	2	Q7PS00	Q7ps00	anopheles g	190	9	2.0	1815	2	Q6CF66	Q6cf66	yarrowia li
118	9	2.0	420	2	Q82HS1	Q82hs1	streptomyce	191	9	2.0	1840	2	Q6PD15	Q6pd15	mus musculus
119	9	2.0	432	2	Q9BLJ0	Q9blj0	halocynthia	192	9	2.0	3099	2	Q6EB12	Q6eb12	dictyosteli
120	9	2.0	486	1	CDSN_HUMAN	Q15517	homo sapien	193	9	2.0	3409	2	Q6SSE6	Q6sse6	chlamydomon
121	9	2.0	499	2	Q9NRH4	Q9nrh4	homo sapien	194	8	1.8	67	1	YI05_STRRP6	Yi05_STRRP6	streptococc
122	9	2.0	499	2	Q9NRH5	Q9nrh5	homo sapien	195	8	1.8	67	1	YI05_STRPN	Yi05_STRPN	streptococc
123	9	2.0	500	2	Q9NP52	Q9np52	homo sapien	196	8	1.8	78	2	Q6W067	Q6w067	mus musculus
124	9	2.0	500	2	Q9NPE0	Q9npe0	homo sapien	197	8	1.8	97	2	Q49407	Q49407	mycoplasma
125	9	2.0	500	2	Q9NPF5	Q9npf5	homo sapien	198	8	1.8	99	2	Q9CD66	Q9cd66	mycobacteri
126	9	2.0	500	2	Q9NRH6	Q9nrh6	homo sapien	199	8	1.8	102	2	Q86EM7	Q86em7	schistosoma
127	9	2.0	500	2	Q9NRH7	Q9nrh7	homo sapien	200	8	1.8	114	2	Q9JG72	Q9jg72	tt virus . o
128	9	2.0	500	2	Q9NRH8	Q9nrh8	homo sapien	201	8	1.8	115	1	SER1_GALME	Ser1_GALME	galleria me
129	9	2.0	503	2	Q6FLN7	Q6fln7	candida gla	202	8	1.8	118	2	Q949R3	Q949r3	arabidopsis
130	9	2.0	513	2	Q95IF9	Q95if9	homo sapien	203	8	1.8	120	2	Q925G3	Q925g3	mycobacteri
131	9	2.0	517	1	Y652_HUMAN	Q75143	homo sapien	204	8	1.8	130	2	Q8S5Q1	Q8s5q1	oryza sativ
132	9	2.0	518	2	Q67WR0	Q67wr0	oryza sativ	205	8	1.8	133	2	Q9D731	Q9d731	mus musculus
133	9	2.0	528	2	Q81ZU5	Q81zu5	homo sapien	206	8	1.8	136	2	Q6W031	Q6w031	mus musculus
134	9	2.0	528	2	Q81ZU6	Q81zu6	homo sapien	207	8	1.8	137	2	Q8NN75	Q8nn75	corynebacte
135	9	2.0	528	2	Q8NSP3	Q8nsp3	homo sapien	208	8	1.8	137	2	Q9D149	Q9d149	mus musculus
136	9	2.0	529	2	Q43509	Q43509	homo sapien	209	8	1.8	139	2	Q9W2M0	Q9w2m0	drosoephila
137	9	2.0	529	2	Q81ZU4	Q81zu4	homo sapien	210	8	1.8	139	2	Q9D0X3	Q9d0x3	mus musculus
138	9	2.0	529	2	Q7YR44	Q7yr44	pan troglod	211	8	1.8	139	2	Q9D195	Q9d195	mus musculus
139	9	2.0	535	2	Q24455	Q24455	drosoephila	212	8	1.8	140	2	Q9D6R3	Q9d6r3	mus musculus
140	9	2.0	549	2	Q19318	Q19318	caenorhabdi	213	8	1.8	143	2	Q9CQH5	Q9cqh5	m mus muscu
141	9	2.0	595	2	Q7SFY1	Q7sfy1	neurospora	214	8	1.8	143	2	Q9D139	Q9d139	mus musculus
142	9	2.0	596	2	Q8MZ04	Q8mz04	drosoephila	215	8	1.8	147	2	Q9D1C5	Q9dic5	mus musculus
143	9	2.0	596	2	Q9VB83	Q9vb83	drosoephila	216	8	1.8	147	2	Q9D1I4	Q9di14	mus musculus
144	9	2.0	604	2	Q87XD4	Q87xd4	pseudomonas	217	8	1.8	149	2	Q9D1K4	Q9dik4	mus musculus
145	9	2.0	610	2	Q7KTN9	Q7ktn9	drosoephila	218	8	1.8	149	2	Q9D6P5	Q9d6p5	mus musculus
146	9	2.0	624	1	RN12_HUMAN	Q9nvw2	homo sapien	219	8	1.8	156	2	Q6W073	Q6w073	mus musculus
147	9	2.0	624	2	Q96D38	Q96d38	homo sapien	220	8	1.8	160	2	Q7X8K1	Q7x8k1	oryza sativ
148	9	2.0	633	2	Q96GF2	Q96gf2	homo sapien	221	8	1.8	161	2	Q8W007	Q8w007	oryza sativ
149	9	2.0	660	2	Q75J88	Q75j88	dictyosteli	222	8	1.8	161	2	Q84Q77	Q84q77	oryza sativ
150	9	2.0	668	2	Q48297	Q48297	halobacteri	223	8	1.8	164	2	Q9NSJ2	Q9nsj2	homo sapien
151	9	2.0	668	2	Q9HQW7	Q9hqw7	halobacteri	224	8	1.8	164	2	Q9PN76	Q9pn76	anopheles g
152	9	2.0	668	2	Q9ZKJ0	Q9zkj0	helicobacte	225	8	1.8	179	2	Q9HQS3	Q9hq83	halobacteri
153	9	2.0	675	1	HS7M_PHAVU	Q01899	phaseolus v	226	8	1.8	180	2	Q72GQ6	Q72gq6	thermus the
154	9	2.0	677	1	SP87_DICDI	P54643	dictyosteli	227	8	1.8	185	2	Q7XDV1	Q7xdv1	oryza sativ
155	9	2.0	712	1	GSPD_ERWCH	P31700	erwinia chr	228	8	1.8	185	2	Q9LVB5	Q9llb5	arabidopsis
156	9	2.0	717	2	Q6MTA9	Q6mta9	mycoplasma	229	8	1.8	190	2	Q8LBE9	Q8lbe9	arabidopsis
157	9	2.0	718	2	Q94HG1	Q94hg1	oryza sativ	230	8	1.8	194	2	Q8LBE9	Q8lbe9	arabidopsis
158	9	2.0	729	2	Q18660	Q18660	drosoephila	231	8	1.8	199	2	Q944V7	Q944v7	phytophthor
159	9	2.0	729	2	Q9VMS4	Q9vms4	drosoephila	232	8	1.8	202	2	Q9WA49	Q9wa49	porcine ade
160	9	2.0	768	2	Q7Q394	Q7q394	anopheles g	233	8	1.8	204	2	Q8MYL3	Q8myl3	drosoephila
161	9	2.0	868	2	Q8SX72	Q8sx72	drosoephila	234	8	1.8	211	1	PEM_RAT	P63630	rattus norv
162	9	2.0	879	2	Q6CXL0	Q6cx10	kluvereromyc	235	8	1.8	214	2	Q922H8	Q922h8	mus musculus
163	9	2.0	923	2	Q8TTE9	Q8tte9	methanosarc	236	8	1.8	216	2	Q70Z58	Q70z58	canis famill
164	9	2.0	942	2	Q8CAH0	Q8cah0	mus musculus	237	8	1.8	216	2	Q70Z60	Q70z60	canis famill
165	9	2.0	973	2	Q6ZR04	Q6zr04	homo sapien	238	8	1.8	216	2	Q70Z13	Q70z13	canis famill
166	9	2.0	1046	2	Q7KQZ6	Q7kqz6	drosoephila	239	8	1.8	217	2	Q8MYL2	Q8myl2	drosoephila
167	9	2.0	1064	2	Q7KQZ5	Q7kqz5	drosoephila	240	8	1.8	224	2	Q7PF45	Q7pf45	anopheles g
168	9	2.0	1065	2	Q9V5N1	Q9v5n1	drosoephila	241	8	1.8	228	2	Q9NYG3	Q9nyg3	homo sapien
169	9	2.0	1081	2	Q8C7Q2	Q8c7q2	mus musculus	242	8	1.8	232	1	DJB8_HUMAN	Q8nhs0	homo sapien
170	9	2.0	1085	2	Q7JN04	Q7jñ04	drosoephila	243	8	1.8	239	2	Q69T79	Q69t79	oryza sativ
171	9	2.0	1097	1	CCT_DRONE	Q96433	drosoephila	244	8	1.8	247	2	Q6ARC8	Q6arc8	desulfotale
172	9	2.0	1173	2	Q9VFC2	Q9vfc2	drosoephila	245	8	1.8	251	2	Q92TZ5	Q92tz5	rhizobium m
173	9	2.0	1266	2	Q6BXJ1	Q6bxj1	debaromyce	246	8	1.8	254	2	Q8BEN1	Q8ben1	callitrichi
174	9	2.0	1306	1	MSB2_YEAST	F32334	saccharomyc	247	8	1.8	260	2	Q7Q616	Q7q616	anopheles g
175	9	2.0	1333	2	Q70JAB	Q70jab	butyrivibri	248	8	1.8	262	2	Q94115	Q94115	sorghum bic
176	9	2.0	1357	2	Q9W4M4	Q9w4m4	drosoephila	249	8	1.8	273	2	Q9VY58	Q9vy58	drosoephila
177	9	2.0	1410	2	Q9KGY0	Q9kgy0	mycoplasma	250	8	1.8	275	2	Q6C2G8	Q6c2g8	yarrowia li

251	8	1.8	276	1	SLEB_OCEIH	P59105 oceanobacil	324	8	1.8	392	2	Q7U3X2	Q7u3x2 synechococc
252	8	1.8	276	2	Q9W5C7	Q9w5c7 drosophila	325	8	1.8	393	2	Q18880	Q18880 caenorhabdi
253	8	1.8	277	2	Q9AE60	Q9ae60 rhodococcus	326	8	1.8	393	2	Q6VYN1	Q6vyn1 drosophila
254	8	1.8	282	2	Q8WY42	Q8wy42 homo sapien	327	8	1.8	396	2	Q975D0	Q975d0 sulfolobus
255	8	1.8	288	2	Q9VRL6	Q9vrl6 drosophila	328	8	1.8	396	2	Q7R271	Q7r271 giardia lam
256	8	1.8	290	2	Q91P07	Q91p07 cynomolgus	329	8	1.8	396	2	Q65450	Q65450 arabidopsis
257	8	1.8	293	2	Q7EZ23	Q7ez23 oryza sativ	330	8	1.8	396	2	Q6YTH3	Q6yth3 oryza sativ
258	8	1.8	295	2	Q6ERH9	Q6erh9 oryza sativ	331	8	1.8	397	2	Q6CG83	Q6cg83 yarrowia li
259	8	1.8	296	2	Q6P9D8	Q6p9d8 homo sapien	332	8	1.8	398	2	Q9UXP2	Q9uxf2 sulfolobus
260	8	1.8	296	2	Q6LTX0	Q6ltx0 photobacter	333	8	1.8	399	2	Q82PG5	Q82pg5 streptomyce
261	8	1.8	305	2	Q75308	Q75308 homo sapien	334	8	1.8	406	2	Q8NAC5	Q8nac5 homo sapien
262	8	1.8	305	2	Q15287	Q15287 homo sapien	335	8	1.8	407	2	Q75DT6	Q75dt6 ashyba goos
263	8	1.8	305	2	Q15844	Q15844 leishmania	336	8	1.8	408	2	Q96WQ9	Q96wq9 aspergillus
264	8	1.8	305	2	Q6AYK1	Q6ayk1 rattus norv	337	8	1.8	410	2	Q7S340	Q7s340 neurospora
265	8	1.8	305	2	Q99M28	Q99m28 mus musculu	338	8	1.8	410	2	Q9W1W2	Q9w1w2 drosophila
266	8	1.8	309	2	Q8IMV1	Q8imv1 drosophila	339	8	1.8	414	2	Q876J8	Q876j8 saccharomyc
267	8	1.8	311	1	OSAN_HUMAN	Q8ang18 homo sapien	340	8	1.8	415	2	Q9VHX2	Q9vhx2 drosophila
268	8	1.8	311	2	Q6CA40	Q6ca40 yarrowia li	341	8	1.8	415	2	Q6AYU4	Q6ayu4 rattus norv
269	8	1.8	311	2	Q8RKT7	Q8rkt7 pseudomonas	342	8	1.8	416	2	Q9DBF7	Q9dbf7 mus musculu
270	8	1.8	312	2	Q8VFW5	Q8vfw5 mus musculu	343	8	1.8	417	2	Q9KWC4	Q9kwc4 agrobacteri
271	8	1.8	312	2	Q8VFW6	Q8vfw6 mus musculu	344	8	1.8	418	2	Q7RL88	Q7rl88 plasmodium
272	8	1.8	312	2	Q8VFW8	Q8vfw8 mus musculu	345	8	1.8	421	2	Q7M984	Q7m984 wolinnella s
273	8	1.8	312	2	Q7TQR7	Q7tqr7 mus musculu	346	8	1.8	422	2	Q95YL3	Q95yl3 ciona savig
274	8	1.8	312	2	Q7TQR8	Q7tqr8 mus musculu	347	8	1.8	423	2	Q9ST79	Q9st79 oryza sativ
275	8	1.8	312	2	Q7TQR9	Q7tqr9 mus musculu	348	8	1.8	425	2	Q8DW34	Q8dw34 streptococc
276	8	1.8	314	2	Q7S8K9	Q7s8k9 neurospora	349	8	1.8	427	1	AROA_ABRSA	Q93321 aeromonas s
277	8	1.8	315	1	SOL2_YEAST	P37262 saccharomyc	350	8	1.8	430	1	PIF4_ARATH	Q8w2f3 arabidopsis
278	8	1.8	315	2	Q8VFW7	Q8vfw7 mus musculu	351	8	1.8	431	2	Q692G4	Q692g4 nephila cla
279	8	1.8	316	1	LORI_HUMAN	P23490 homo sapien	352	8	1.8	431	2	Q6LBN1	Q6lbn1 canis famli
280	8	1.8	316	2	Q6PHT3	Q6phy3 homo sapien	353	8	1.8	434	2	Q87CW9	Q87cw9 xylella fae
281	8	1.8	319	2	Q9NF33	Q9nf33 drosophila	354	8	1.8	435	2	Q65IH0	Q65ih0 bacillus li
282	8	1.8	319	2	Q9WSB4	Q9wsb4 drosophila	355	8	1.8	436	2	Q7QDL5	Q7qdl5 anopheles g
283	8	1.8	319	2	Q38926	Q38926 arabidopsis	356	8	1.8	441	2	Q9LX71	Q9lxl71 arabidopsis
284	8	1.8	325	2	Q6AXH2	Q6axh2 mus musculu	357	8	1.8	442	1	CYS4_DICDI	P54639 dictyosteli
285	8	1.8	326	2	Q62010	Q62010 ceratitidis c	358	8	1.8	442	1	UFO_ARATH	Q39090 arabidopsis
286	8	1.8	326	2	Q9NFX5	Q9nfx5 ceratitidis c	359	8	1.8	447	2	Q9SIA8	Q9sia8 arabidopsis
287	8	1.8	326	2	Q6GQX6	Q6gqx6 mus musculu	360	8	1.8	458	2	Q89VK4	Q89vk4 bradyrhizob
288	8	1.8	329	2	Q8SV52	Q8sv52 drosophila	361	8	1.8	459	2	Q89Q42	Q89q42 bradyrhizob
289	8	1.8	329	2	Q80ZE8	Q80ze8 rattus norv	362	8	1.8	460	2	Q72NI1	Q72ni1 leptospira
290	8	1.8	329	2	Q80ZK5	Q80zk5 mus musculu	363	8	1.8	460	2	Q9XD16	Q9xd16 leptospira
291	8	1.8	330	2	Q7PPK2	Q7ppx2 anopheles g	364	8	1.8	461	2	Q89I33	Q89i33 bradyrhizob
292	8	1.8	331	2	Q692G6	Q692g6 nephila cla	365	8	1.8	463	1	CD4_CANPA	P33705 canis famli
293	8	1.8	332	1	SIX3_HUMAN	Q95343 homo sapien	366	8	1.8	466	2	Q7PSE1	Q7pse1 anopheles g
294	8	1.8	332	2	Q6C1Z7	Q6c1z7 yarrowia li	367	8	1.8	469	2	Q6DVF4	Q6dvf4 oryzias lat
295	8	1.8	333	1	AMR1_HUMAN	Q9y4x0 homo sapien	368	8	1.8	471	1	SIR2_SCHPO	Q94640 schizosacch
296	8	1.8	334	2	Q8N9L6	Q8n9l6 homo sapien	369	8	1.8	471	2	Q6P2R2	Q6p2r2 homo sapien
297	8	1.8	336	2	Q98321	Q98321 molluscum c	370	8	1.8	471	2	Q9ZWB3	Q9zbw3 arabidopsis
298	8	1.8	338	2	Q60354	Q60354 homo sapien	371	8	1.8	472	1	POU2_BRARE	Q90270 brachydanio
299	8	1.8	340	2	Q8VJ24	Q8vj24 mycobacteri	372	8	1.8	472	2	Q7ZU11	Q7zu11 brachydanio
300	8	1.8	340	2	Q9KY73	Q9ky73 streptomyce	373	8	1.8	473	1	CHIA_RAT	Q6ry07 rattus norv
301	8	1.8	344	1	AMR1_MOUSE	Q9jht5 mus musculu	374	8	1.8	475	2	Q9P8U4	Q9ph8 s transcrip
302	8	1.8	347	2	Q8MT45	Q8mt45 drosophila	375	8	1.8	475	2	Q880G7	Q880g7 pseudomonas
303	8	1.8	347	2	Q9V518	Q9v518 drosophila	376	8	1.8	475	2	Q880Q1	Q880q1 bradyrhizob
304	8	1.8	351	2	Q86M55	Q86m55 drosophila	377	8	1.8	475	2	Q89QA1	Q89qa1 arabidopsis
305	8	1.8	355	2	Q9VCW9	Q9vcw9 drosophila	378	8	1.8	476	2	Q8W0Z0	Q8w0z0 arabidopsis
306	8	1.8	356	2	Q8T0P0	Q8t0p0 drosophila	379	8	1.8	476	2	Q9FFH8	Q9ffh8 arabidopsis
307	8	1.8	356	2	Q67QB2	Q67qb2 symbiobacte	380	8	1.8	476	2	Q6N5K0	Q6nsk0 rhodopseudo
308	8	1.8	359	2	Q6ZUZ0	Q6zuz0 homo sapien	381	8	1.8	477	2	Q9PPU5	Q9ppu5 ureaplasma
309	8	1.8	360	2	P77853	P77853 dictyoglomu	382	8	1.8	482	1	GATA_SYNEL	Q8dk65 synechococc
310	8	1.8	361	2	Q52375	Q52375 caldicellul	383	8	1.8	482	2	Q8RYL5	Q8ryl5 oryza sativ
311	8	1.8	369	2	Q9AV13	Q9av13 oryza sativ	384	8	1.8	484	2	Q6MWY1	Q6mwy1 mycobacteri
312	8	1.8	370	2	Q6CVD1	Q6cvd1 kluyveromyc	385	8	1.8	486	1	LORI_MOUSE	P18165 mus musculu
313	8	1.8	371	2	Q8QC02	Q8qc02 methanosaar	386	8	1.8	486	2	Q7Q3X8	Q7q3x8 anopheles g
314	8	1.8	371	2	Q8MKV0	Q8mkv0 drosophila	387	8	1.8	490	2	Q89CA1	Q89ca1 bradyrhizob
315	8	1.8	380	2	Q9HKR5	Q9hkr5 thermoplas	388	8	1.8	492	2	Q6IA44	Q6ia44 homo sapien
316	8	1.8	380	2	Q9VHL7	Q9vhl7 drosophila	389	8	1.8	492	2	Q6IAZ3	Q6iaz3 homo sapien
317	8	1.8	381	2	Q8NFJ8	Q8nfj8 homo sapien	390	8	1.8	496	2	Q62MR4	Q62mr4 burkholderi
318	8	1.8	382	2	Q6LKC2	Q6lkc2 photobacter	391	8	1.8	496	2	Q63YJ9	Q63yj9 burkholderi
319	8	1.8	384	2	Q6BU29	Q6bu29 debaryomyce	392	8	1.8	498	2	Q6PUU6	Q6puu6 methanosaar
320	8	1.8	386	2	Q62003	Q62003 branchiost	393	8	1.8	500	2	Q6N950	Q6n950 rhodopseudo
321	8	1.8	387	2	Q692G3	Q692g3 nephila cla	394	8	1.8	505	1	AMID_PSECL	P27765 pseudomonas
322	8	1.8	389	2	Q8BKH6	Q8bkh6 mus musculu	395	8	1.8	506	1	GATA_TREPA	Q83983 treponema p
323	8	1.8	392	1	HME1_HUMAN	Q05925 homo sapien	396	8	1.8	508	2	Q9LLF2	Q9llf2 lycopersico

397	8	1.8	512	2	Q95KP5	Q95KP5 canis famil	470	8	1.8	671	2	Q7ZXV4	Q7zxv4 xenopus lae
398	8	1.8	521	2	Q8TS45	Q8ta45 methanosarc	471	8	1.8	672	2	Q6FK03	Q6fk03 candida gla
399	8	1.8	521	2	Q9ABN0	Q9abn0 caulobacter	472	8	1.8	673	2	Q7PPD2	Q7ppd2 anopheles g
400	8	1.8	522	2	Q9P9G7	Q9p9g7 methanococc	473	8	1.8	673	2	Q8II79	Q8ii79 drosophila
401	8	1.8	523	2	Q8C774	Q8c774 mus musculus	474	8	1.8	677	2	Q7V0U5	Q7v0u5 mus musculus
402	8	1.8	527	2	Q01894	Q01894 caenorhabdi	475	8	1.8	689	2	Q70UR5	Q70ur5 mus musculus
403	8	1.8	527	2	Q95Q27	Q95q27 caenorhabdi	476	8	1.8	694	1	FR22_DROME	Q9vvx3 drosophila
404	8	1.8	529	2	Q95Q28	Q95q28 caenorhabdi	477	8	1.8	695	2	Q8N568	Q8n568 homo sapien
405	8	1.8	529	2	Q95Q29	Q95q29 caenorhabdi	478	8	1.8	703	2	Q7S2G5	Q7s2g5 neurospora
406	8	1.8	535	2	Q8UZG3	Q8uzg3 aspergillus	479	8	1.8	707	2	Q9ASH4	Q9ash4 oryza sativ
407	8	1.8	536	2	Q9UVS8	Q9uvs8 cercoptithec	480	8	1.8	710	2	Q7CTV9	Q7ctv9 agrobacteri
408	8	1.8	544	2	Q46171	Q46171 nephila cla	481	8	1.8	716	2	Q8U8R8	Q8u8r8 agrobacteri
409	8	1.8	547	2	Q8TFE9	Q8tfef9 schizosacch	482	8	1.8	718	2	Q9NKS6	Q9nks6 leishmania
410	8	1.8	548	1	ERF_HUMAN	P50548 homo sapien	483	8	1.8	721	2	Q7QLG4	Q7qlg4 anopheles g
411	8	1.8	549	1	AMDY_YEAST	P22580 saccharomyc	484	8	1.8	727	1	BRCL_DROME	Q0195 drosophila
412	8	1.8	550	2	Q6F379	Q6f379 oryza sativ	485	8	1.8	728	2	Q8QZ68	Q8qz68 tomato mild
413	8	1.8	551	1	ERF_MOUSE	P70459 mus musculus	486	8	1.8	730	1	CCT2_HUMAN	Q60583 homo sapien
414	8	1.8	551	2	Q6P544	Q6p544 mus musculus	487	8	1.8	733	2	Q6AWZ0	Q6awz0 homo sapien
415	8	1.8	552	2	Q6CA43	Q6ca43 yarrowia li	488	8	1.8	747	1	SPD1_NBPCL	P19837 nephila cla
416	8	1.8	552	2	Q6IFZ8	Q6ifz8 mus musculus	489	8	1.8	749	2	Q8LPD9	Q8lpd9 chlamydomon
417	8	1.8	553	2	Q8HXE2	Q8hxe2 macaca fasc	490	8	1.8	750	2	Q8LPE0	Q8lep0 chlamydomon
418	8	1.8	556	2	Q8LM88	Q8lm88 photobacter	491	8	1.8	750	2	Q68DC1	Q68dc1 mus musculus
419	8	1.8	558	2	Q8JKR4	Q8jkr4 heliothis z	492	8	1.8	756	2	Q68DC2	Q68dc2 homo sapien
420	8	1.8	561	2	Q6C873	Q6c873 yarrowia li	493	8	1.8	756	2	Q8JG32	Q8jg32 gallus gall
421	8	1.8	562	2	Q80WS6	Q80ws6 mus musculus	494	8	1.8	763	1	DYRA_HUMAN	Q13627 homo sapien
422	8	1.8	570	2	Q8IQC5	Q8iqc5 drosophila	495	8	1.8	763	1	DYRA_MOUSE	Q61214 mus musculus
423	8	1.8	570	2	Q95TF7	Q95tf7 drosophila	496	8	1.8	763	1	DYRA_RAT	Q63470 rattus norv
424	8	1.8	570	2	Q95G65	Q95g65 cellvibrio	497	8	1.8	766	2	Q9DWF7	Q9dwf7 rat cytoMeg
425	8	1.8	575	2	Q6BVD6	Q6bvd6 debaryomyce	498	8	1.8	772	2	Q21492	Q21492 caenorhabdi
426	8	1.8	579	2	Q16901	Q16901 caenorhabdi	499	8	1.8	772	2	P79149	P79149 canis famil
427	8	1.8	581	2	Q18349	Q18349 drosophila	500	8	1.8	774	2	Q868B4	Q868b4 caenorhabdi
428	8	1.8	582	2	Q9VUH2	Q9vuh2 drosophila	501	8	1.8	775	2	Q21493	Q21493 caenorhabdi
429	8	1.8	584	2	Q68DB8	Q68db8 homo sapien	502	8	1.8	777	2	Q8MQ04	Q8mq04 caenorhabdi
430	8	1.8	588	2	Q9IP08	Q9ipq8 cynomolgus	503	8	1.8	778	1	PG46_MYCTU	P71333 mycobacteri
431	8	1.8	589	1	DYR_MOUSE	Q9zi88 mus musculus	504	8	1.8	786	2	O18740	O18740 canis famil
432	8	1.8	589	2	Q7Y214	Q7y214 arabadopsis	505	8	1.8	791	2	Q9GRX2	Q9grx2 drosophila
433	8	1.8	590	2	Q7Y214	Q7y214 arabadopsis	506	8	1.8	791	2	Q9NFS1	Q9nfs1 drosophila
434	8	1.8	592	2	Q7V676	Q7v676 prochloroco	507	8	1.8	791	2	Q9VSY7	Q9vsy7 drosophila
435	8	1.8	593	2	Q8K006	Q8k006 mus musculus	508	8	1.8	805	1	E2F_DROME	Q21368 drosophila
436	8	1.8	594	2	Q9A796	Q9a796 caulobacter	509	8	1.8	805	2	Q8XU01	Q8xua1 raltostonia s
437	8	1.8	595	2	Q8FRP9	Q8frp9 corynebacte	510	8	1.8	806	2	Q7K9G4	Q7k9g4 drosophila
438	8	1.8	599	2	Q8PEM1	Q8pem1 xanthomonas	511	8	1.8	815	2	Q96JS2	Q96js2 homo sapien
439	8	1.8	600	2	Q8TJW3	Q8tjw3 methanosarc	512	8	1.8	816	1	NEL2_HUMAN	Q99435 homo sapien
440	8	1.8	600	2	Q75RY3	Q75ry3 oleomonas s	513	8	1.8	821	2	Q9W1J9	Q9w1j9 drosophila
441	8	1.8	600	2	Q6D599	Q6d599 erwinnia car	514	8	1.8	831	2	Q7RWM6	Q7rmw6 neurospora
442	8	1.8	601	2	Q887D5	Q887d5 pseudomonas	515	8	1.8	833	2	Q9U2S8	Q9u2s8 caenorhabdi
443	8	1.8	603	2	Q897G7	Q897g7 clostridium	516	8	1.8	838	2	Q9Y0C9	Q9y0c9 dictyosteli
444	8	1.8	604	2	Q9ALV2	Q9alv2 enterobacte	517	8	1.8	847	2	Q96N13	Q96n13 mus musculus
445	8	1.8	605	2	Q936X2	Q936x2 pseudomonas	518	8	1.8	849	2	Q8CCE4	Q8cge4 mus musculus
446	8	1.8	607	2	Q7QJ60	Q7qj60 anopheles g	519	8	1.8	858	2	Q9XV70	Q9xv70 dictyosteli
447	8	1.8	608	1	SAV_DROME	Q9vcr6 drosophila	520	8	1.8	858	2	Q9XXV8	Q9xxv8 dictyosteli
448	8	1.8	609	2	Q96E25	Q96e25 homo sapien	521	8	1.8	859	2	Q7PRJ1	Q7prj1 anopheles g
449	8	1.8	614	2	Q80220	Q80220 brachydanio	522	8	1.8	866	2	Q962I0	Q962i0 drosophila
450	8	1.8	617	2	Q46172	Q46172 nephila cla	523	8	1.8	867	2	Q7ZVU1	Q7zvu1 brachydanio
451	8	1.8	618	2	Q6CB69	Q6cb69 yarrowia li	524	8	1.8	877	2	Q9UE51	Q9uf51 homo sapien
452	8	1.8	619	2	Q9IPQ9	Q9ipq9 cynomolgus	525	8	1.8	881	2	Q9NE42	Q9ne42 leishmania
453	8	1.8	629	1	DYR_HUMAN	Q9y463 homo sapien	526	8	1.8	883	2	Q8TTT9	Q8ttt9 methanosarc
454	8	1.8	629	2	Q9EPM2	Q9epm2 mus musculus	527	8	1.8	890	1	BCN5_CLOPE	P08596 clostridium
455	8	1.8	633	2	Q9ZKQ8	Q9zq8 arabadopsis	528	8	1.8	893	2	Q7XNW2	Q7xmw2 oryza sativ
456	8	1.8	638	2	Q8EAU4	Q8eau4 shewanella	529	8	1.8	894	2	Q9GYB4	Q9gyb4 leishmania
457	8	1.8	643	2	Q9LSL2	Q9ls12 arabadopsis	530	8	1.8	903	2	Q8TLY6	Q8tly6 methanosarc
458	8	1.8	643	2	Q87800	Q87e00 xylolla fas	531	8	1.8	908	2	Q86J00	Q86j00 dictyosteli
459	8	1.8	644	2	Q8WSW4	Q8wew4 nephila cla	532	8	1.8	913	2	Q6C979	Q6c979 yarrowia li
460	8	1.8	644	2	Q8BKB2	Q8bkb2 mus musculus	533	8	1.8	918	2	Q7SGE4	Q7sges4 neurospora
461	8	1.8	645	2	Q84965	Q84965 anaplasm p	534	8	1.8	918	2	Q8ML49	Q8ml49 drosophila
462	8	1.8	645	2	Q6PG69	Q6pg69 mus musculus	535	8	1.8	918	2	Q86NR8	Q86nr8 drosophila
463	8	1.8	646	2	Q96F45	Q96f45 homo sapien	536	8	1.8	927	2	Q7QBA4	Q7qba4 anopheles g
464	8	1.8	650	2	Q9N013	Q9n013 macaca fasc	537	8	1.8	934	1	IP3L_RAT	P42335 rattus norv
465	8	1.8	656	1	UL25_HCMVA	P16761 human cytom	538	8	1.8	937	1	HYR1_CANAL	P46591 candida alb
466	8	1.8	656	2	Q7MGQ8	Q7mgq8 human cytom	539	8	1.8	948	2	Q8T065	Q8t065 drosophila
467	8	1.8	660	2	Q23832	Q23832 cryptospori	540	8	1.8	950	2	Q9ULL2	Q9ull2 homo sapien
468	8	1.8	661	2	Q59674	Q59674 cellvibrio	541	8	1.8	957	2	Q8TR89	Q8tr89 methanosarc
469	8	1.8	663	2	Q8CHT4	Q8cht4 mus musculus	542	8	1.8	965	2	Q66665	Q66665 equid herpe

543	8	1.8	968	2	Q9VKL0	Q9vk10 drosophila	616	8	1.8	2761	2	Q18447	Q18447
544	8	1.8	970	2	Q6MTA8	Q6mta8 mycoplasma	617	8	1.8	2850	1	HORN HUMAN	Q86y33 caenorhabdi
545	8	1.8	973	2	Q7PMX5	Q7pmx5 anopheles g	618	8	1.8	3080	1	Q9V602	Q86y33 homo sapien
546	8	1.8	977	1	KFMS MOUSE	P09581 mus musculus	619	8	1.8	3109	2	Q9BMO0	Q9v602 drosophila
547	8	1.8	977	1	Q6NXV8	Q6nxv8 mus musculus	620	8	1.8	3446	2	Q86AC8	Q9bmo0 drosophila
548	8	1.8	978	1	KFMS RAT	Q00495 rattus norv	621	8	1.8	3726	1	TRX_DROME	Q86ac8 dictyosteli
549	8	1.8	1007	2	Q8C8T6	Q8c8t6 mus musculus	622	8	1.8	3726	2	Q8VFL1	P20659 drosophila
550	8	1.8	1009	2	Q8PME3	Q8pme3 xanthomonas	623	8	1.8	10	2	Q8BHN2	Q8vfl1 drosophila
551	8	1.8	1024	1	U203 ARATH	Q9m2g4 arabidopsis	624	7	1.6	14	2	Q8CJA8	Q8bhn2 mus musculus
552	8	1.8	1029	1	RIP3 RAT	Q9ere6 rattus norv	625	7	1.6	15	2	Q8CJA9	Q8cja8 mus musculus
553	8	1.8	1031	2	Q7SRN6	Q7srn6 neurospora	626	7	1.6	16	2	Q86UF7	Q8cja9 mus musculus
554	8	1.8	1033	2	Q8D6V3	Q8d6v3 vibrio vuln	627	7	1.6	16	2	Q86UF7	Q86uf7 homo sapien
555	8	1.8	1037	2	Q6P559	Q6p559 mus musculus	628	7	1.6	38	2	Q96850	Q96uf7 bombyx mori
556	8	1.8	1040	2	Q7MDU0	Q7mdu0 vibrio vuln	629	7	1.6	38	2	Q96851	Q96851 bombyx mori
557	8	1.8	1052	2	Q8Q0S0	Q8q0s0 methanosaarc	630	7	1.6	46	2	Q6MQF4	Q96851 drosophila
558	8	1.8	1087	2	Q7UUE7	Q7uu67 rhodopirell	631	7	1.6	51	2	Q8CIW7	Q8ciw7 mus musculus
559	8	1.8	1108	2	Q7YU81	Q7yu81 drosophila	632	7	1.6	52	2	Q67U08	Q67u08 oryza sativ
560	8	1.8	1108	2	Q9V788	Q9v788 drosophila	633	7	1.6	54	2	Q85513	Q85513 feline earc
561	8	1.8	1119	2	Q6ZQ66	Q6zq66 mus musculus	634	7	1.6	57	2	Q6YRP3	Q6yrp3 oryza sativ
562	8	1.8	1141	1	SRE2 HUMAN	Q12772 homo sapien	635	7	1.6	57	2	Q92K72	Q92k72 rhizobium m
563	8	1.8	1193	2	Q86V36	Q86v36 homo sapien	636	7	1.6	61	2	Q65285	Q65285 african swi
564	8	1.8	1198	2	Q7PKP4	Q7pkp4 anopheles g	637	7	1.6	62	1	PA2S AUSSU	P59067 austrelaps
565	8	1.8	1229	2	Q68H99	Q68h99 sus scrofa	638	7	1.6	62	2	Q6X1B8	Q6xib8 drosophila
566	8	1.8	1230	1	ST20 CANAL	Q92212 candida alb	639	7	1.6	63	2	Q25832	Q25832 plasmodium
567	8	1.8	1230	2	Q13431	Q13431 candida alb	640	7	1.6	66	1	PER_DROSA	Q04536 drosophila
568	8	1.8	1233	1	M4K4 MOUSE	P97820 mus musculus	641	7	1.6	66	2	Q9XZQ8	Q9xzz8 caenorhabdi
569	8	1.8	1235	2	Q8T250	Q8t250 dictyosteli	642	7	1.6	69	2	Q86JP8	Q86jp8 dictyosteli
570	8	1.8	1239	1	M4K4 HUMAN	Q95819 homo sapien	643	7	1.6	71	2	Q8H442	Q8h442 oryza sativ
571	8	1.8	1255	2	Q6ZQ68	Q6zq68 mus musculus	644	7	1.6	72	2	Q7YTK1	Q7ytk1 caenorhabdi
572	8	1.8	1258	2	Q8R457	Q8r457 mus musculus	645	7	1.6	72	2	Q6Z4A6	Q6z4a6 oryza sativ
573	8	1.8	1258	2	Q8R458	Q8r458 rattus norv	646	7	1.6	72	2	Q8H7A9	Q8h7a9 arabidopsis
574	8	1.8	1263	2	Q7R1D0	Q7r1d0 giardia lam	647	7	1.6	72	2	Q8UUQ2	Q8uuq2 oncorhynch
575	8	1.8	1265	2	Q8EV72	Q8ev72 mycoplasma	648	7	1.6	73	2	Q64M28	Q64m28 bacteroides
576	8	1.8	1266	2	Q800D9	Q800d9 gallus gall	649	7	1.6	74	2	Q6TLV4	Q6tlv4 macaca fasc
577	8	1.8	1278	2	Q9AV65	Q9av65 oryza sativ	650	7	1.6	74	2	Q6LS49	Q6ls49 oryza sativ
578	8	1.8	1281	2	Q82KW0	Q82kw0 streptomyce	651	7	1.6	75	2	Q6YWA4	Q6ywa4 oryza sativ
579	8	1.8	1287	2	Q68DW9	Q68dw9 homo sapien	652	7	1.6	77	2	Q7SEB9	Q7seb9 neurospora
580	8	1.8	1317	1	GAP CAEEL	F34288 caenorhabdi	653	7	1.6	78	2	Q63082	Q63082 rattus norv
581	8	1.8	1349	2	Q9B272	Q9b272 homo sapien	654	7	1.6	79	2	Q6YTA1	Q6yta1 oryza sativ
582	8	1.8	1359	2	Q9P271	Q9p271 homo sapien	655	7	1.6	80	2	Q6ASQ3	Q6asq3 oryza sativ
583	8	1.8	1359	2	Q8CHH0	Q8chh0 mus musculus	656	7	1.6	82	2	Q9FYR0	Q9fyro arabidopsis
584	8	1.8	1404	2	Q86180	Q86180 dictyosteli	657	7	1.6	84	2	Q7X182	Q7x182 oryza sativ
585	8	1.8	1422	2	Q95KU4	Q95ku4 canis famli	658	7	1.6	86	2	Q8CJA5	Q8cjas mus musculus
586	8	1.8	1456	2	Q6PDJ8	Q6pdj8 mus musculus	659	7	1.6	87	2	Q9GC22	Q9gc22 oceanodroma
587	8	1.8	1474	2	Q86G87	Q86g87 pseudoplusi	660	7	1.6	87	2	Q9DUC6	Q9duc6 tt virus. o
588	8	1.8	1476	2	Q8ST66	Q8st66 dictyosteli	661	7	1.6	88	2	Q84MS9	Q84ms9 oryza sativ
589	8	1.8	1476	2	Q965D3	Q965d3 dictyosteli	662	7	1.6	90	2	Q8HAN9	Q8han9 oryza sativ
590	8	1.8	1479	2	Q7Q1C2	Q7q1c2 anopheles g	663	7	1.6	90	2	Q6NTS2	Q6nte2 xenopus lae
591	8	1.8	1490	1	CRK7 HUMAN	Q9nyv4 homo sapien	664	7	1.6	91	2	Q92G67	Q92g67 rickettsia
592	8	1.8	1523	2	Q86L99	Q86l99 dictyosteli	665	7	1.6	91	2	Q8XBR6	Q8xbre escherichia
593	8	1.8	1583	2	Q6C398	Q6c398 yarrowia li	666	7	1.6	94	2	Q8BAY8	Q8bay8 canis famli
594	8	1.8	1606	2	Q924A2	Q924a2 mus musculus	667	7	1.6	95	2	Q6DGJ3	Q6dgt3 brachydanio
595	8	1.8	1693	2	Q86J17	Q86j17 dictyosteli	668	7	1.6	96	2	Q88DT1	Q88dt1 pseudomonas
596	8	1.8	1723	1	FW20 CHLPN	Q92812 chlamydia p	669	7	1.6	97	2	Q8AGE5	Q8age5 leifsonia x
597	8	1.8	1751	2	Q6C3G1	Q6c3g1 yarrowia li	670	7	1.6	99	2	Q8C9S1	Q8c9s1 mus musculus
598	8	1.8	1796	2	Q6NNW7	Q6nnw7 drosophila	671	7	1.6	99	2	Q95P64	Q95p64 penaeus van
599	8	1.8	1851	2	Q7KV98	Q7kv98 drosophila	672	7	1.6	99	2	Q8PLF4	Q8plf4 xanthomonas
600	8	1.8	1889	2	Q7Q138	Q7q138 anopheles g	673	7	1.6	100	2	Q6NZ39	Q6nz39 homo sapien
601	8	1.8	1934	2	Q7QDG9	Q7qdg9 anopheles g	674	7	1.6	100	2	Q8QGB6	Q8qgb6 oncorhynch
602	8	1.8	1960	1	TF20 HUMAN	Q9ugu0 homo sapien	675	7	1.6	100	2	Q8QGB7	Q8qgb7 oncorhynch
603	8	1.8	1960	2	Q7R4L8	Q7r4l8 giardia lam	676	7	1.6	100	2	Q710Q6	Q710q6 oncorhynch
604	8	1.8	2142	1	B4634	B4634 homo sapien	677	7	1.6	102	1	MIH PENVA	P55322 penaeus van
605	8	1.8	2148	2	Q8IR53	Q8ir53 drosophila	678	7	1.6	102	2	Q816N5	Q8i6n5 penaeus van
606	8	1.8	2157	2	Q95875	Q95875 homo sapien	679	7	1.6	102	2	Q817Y6	Q8i7y6 penaeus van
607	8	1.8	2157	2	Q96QC6	Q96qc6 homo sapien	680	7	1.6	103	2	Q810H5	Q8i0h5 penaeus van
608	8	1.8	2157	2	Q6P9P7	Q6p9p7 homo sapien	681	7	1.6	105	2	Q9FW42	Q9fw42 oryza sativ
609	8	1.8	2167	1	SHK1 RAT	Q9wv48 rattus norv	682	7	1.6	106	2	Q9NR52	Q9nr52 homo sapien
610	8	1.8	2196	2	Q9VY40	Q9vy40 drosophila	683	7	1.6	107	2	Q52119	Q52119 plasmid psw
611	8	1.8	2197	2	Q9W016	Q9w016 drosophila	684	7	1.6	109	2	Q9VTF2	Q9vtf2 drosophila
612	8	1.8	2223	2	Q7Q1V0	Q7qv10 anopheles g	685	7	1.6	110	2	Q24333	Q24333 drosophila
613	8	1.8	2228	2	Q9VN58	Q9vn58 drosophila	686	7	1.6	110	2	Q9KYV8	Q9kyv8 streptomyce
614	8	1.8	2254	2	Q75J05	Q75ju5 dictyosteli	687	7	1.6	111	2	Q9VE31	Q9ve31 drosophila
615	8	1.8	2517	2	Q7QL19	Q7ql19 anopheles g	688	7	1.6	113	2	Q82H68	Q82h68 streptomyce

689	7	1.6	114	2	Q9LB87	Q9LB87 helicobacte	762	7	1.6	157	2	Q8CJA7	Q8CJA7 mus musculu
690	7	1.6	116	2	Q9LB77	Q9LB77 helicobacte	763	7	1.6	158	2	Q6X757	Q6X757 neurospora
691	7	1.6	118	2	CRYP_CRYPA	F52753 cryptonectr	764	7	1.6	159	2	Q6X752	Q6X752 anopheles g
692	7	1.6	118	1	NLTI_ARATH	Q42589 arabidopsis	765	7	1.6	159	2	Q7QK59	Q7QK59 xylella fas
693	7	1.6	118	2	Q6IKB2	Q6IKB2 drosophila	766	7	1.6	159	2	Q87BU9	Q87BU9 astatotilap
694	7	1.6	118	2	Q9S1B5	Q9S1B5 arthrobacte	767	7	1.6	159	2	Q8JIL5	Q8JIL5 astatoeoch
695	7	1.6	119	2	Q998G5	Q998G5 cynoscion a	768	7	1.6	159	2	Q8JIL6	Q8JIL7 tropheus du
696	7	1.6	119	2	Q998G5	Q998G5 cynoscion a	769	7	1.6	159	2	Q8JIL7	Q8JIL8 labidochrom
697	7	1.6	120	2	Q8BSC1	Q8BSC1 mus musculu	770	7	1.6	159	2	Q8JIL8	Q8JIL8 labidochrom
698	7	1.6	120	2	Q648Z3	Q648Z3 uncultured	771	7	1.6	160	2	Q8UKJ6	Q8UKJ6 heliothis z
699	7	1.6	120	2	Q82HT6	Q82HT6 streptomyce	772	7	1.6	161	2	Q6X751	Q6X751 neurospora
700	7	1.6	121	2	Q9LB62	Q9LB62 helicobacte	773	7	1.6	161	2	Q6X754	Q6X754 neurospora
701	7	1.6	124	2	Q9VO84	Q9VQ84 drosophila	774	7	1.6	161	2	Q6X755	Q6X755 neurospora
702	7	1.6	125	2	Q8LP38	Q8LP38 pueraria lo	775	7	1.6	161	2	Q43472	Q43472 hordeum vul
703	7	1.6	125	2	Q655T4	Q655T4 oryza sativ	776	7	1.6	161	2	Q8ZCP1	Q8ZCP1 yersinia pe
704	7	1.6	125	2	Q73282	Q73282 human immu	777	7	1.6	162	2	Q8RMH6	Q8RMH6 chloroflexu
705	7	1.6	128	2	Q6MWK9	Q6MWK9 oryza sativ	778	7	1.6	162	2	Q6X749	Q6X749 neurospora
706	7	1.6	129	2	Q9LB75	Q9LB75 helicobacte	779	7	1.6	163	2	Q8IQW8	Q8IQW8 drosophila
707	7	1.6	129	2	Q9LB87	Q9LB87 helicobacte	780	7	1.6	163	2	Q7XM11	Q7XM11 oryza sativ
708	7	1.6	129	2	Q8JAH6	Q8JAH6 chimpanzee	781	7	1.6	163	2	Q6X763	Q6X763 neurospora
709	7	1.6	131	2	Q8TW52	Q8TW52 methanopyru	782	7	1.6	164	2	Q6XQF0	Q6XQF0 enterobacte
710	7	1.6	131	2	Q84N67	Q84N67 swartzia jo	783	7	1.6	164	2	Q6XQF0	Q6XQF0 enterobacte
711	7	1.6	132	2	Q7YTS2	Q7YTS2 caenorhabdi	784	7	1.6	165	2	Q6X759	Q6X759 neurospora
712	7	1.6	132	2	Q9LBB9	Q9LBB9 helicobacte	785	7	1.6	166	2	Q8GQX0	Q8GQX0 plasmodium
713	7	1.6	133	1	VEGH_OREN2	P52584 orf virus (	786	7	1.6	166	2	Q8RYF2	Q8RYF2 avena strig
714	7	1.6	133	2	Q8DA19	Q8DA19 vibrio vuln	787	7	1.6	167	2	Q6X753	Q6X753 neurospora
715	7	1.6	133	2	Q8FMP5	Q8FMP5 corynebacte	788	7	1.6	167	2	Q7X683	Q7X683 oryza sativ
716	7	1.6	134	2	Q7MFJ0	Q7MFJ0 vibrio vuln	789	7	1.6	167	2	Q7P724	Q7P724 fusobacteri
717	7	1.6	136	2	Q6BKU5	Q6BKU5 debaryomyce	790	7	1.6	167	2	Q9JXT9	Q9JXT9 neisseria m
718	7	1.6	136	2	Q8CIU7	Q8CIU7 mus musculu	791	7	1.6	168	2	Q63115	Q63115 rattus norv
719	7	1.6	137	2	Q7RAW9	Q7RAW9 plasmodium	792	7	1.6	168	2	Q711H0	Q711H0 lactobacill
720	7	1.6	138	2	Q8AXY1	Q8AXY1 bothrops ja	793	7	1.6	169	2	Q7KR54	Q7KR54 drosophila
721	7	1.6	139	2	Q7Q2R6	Q7Q2R6 anopheles g	794	7	1.6	170	2	Q43539	Q43539 lilium long
722	7	1.6	139	2	Q9V556	Q9V556 drosophila	795	7	1.6	172	2	Q8LJQ4	Q8LJQ4 prunus peis
723	7	1.6	139	2	Q9MA77	Q9MA77 arabidopsis	796	7	1.6	172	2	Q8B0U5	Q8B0U5 mus musculu
724	7	1.6	140	1	EXB1_XANCP	Q34259 xanthomonas	797	7	1.6	173	2	Q876E9	Q876E9 saccharomyc
725	7	1.6	140	2	Q9LB71	Q9LB71 helicobacte	798	7	1.6	173	2	Q6Z7U4	Q6Z7U4 oryza sativ
726	7	1.6	140	2	Q8PRF3	Q8PRF3 xanthomonas	799	7	1.6	173	2	Q7N8T0	Q7N8T0 photorhabdu
727	7	1.6	143	2	Q6IKU8	Q6IKU8 drosophila	800	7	1.6	173	2	Q7N8T1	Q7N8T1 photorhabdu
728	7	1.6	143	2	Q6IL10	Q6IL10 drosophila	801	7	1.6	175	2	Q7KLE9	Q7KLE9 drosophila
729	7	1.6	143	2	Q9QZD3	Q9QZD3 rattus ever	802	7	1.6	175	2	Q8GWW9	Q8GWW9 arabidopsis
730	7	1.6	144	2	Q7M4U6	Q7M4U6 pleurotus c	803	7	1.6	175	2	Q9LSN6	Q9LSN6 arabidopsis
731	7	1.6	145	1	HB2_XENBO	P07433 xenopus bor	804	7	1.6	175	2	Q9M1T6	Q9M1T6 arabidopsis
732	7	1.6	145	2	Q23606	Q23606 caenorhabdi	805	7	1.6	175	2	Q66639	Q66639 aquifex aeo
733	7	1.6	146	2	Q9NWA0	Q9NWA0 homo sapien	806	7	1.6	175	2	Q8F508	Q8F508 corynebacte
734	7	1.6	146	2	Q6ZLH9	Q6ZLH9 oryza sativ	807	7	1.6	175	2	Q9JW30	Q9JW30 neisseria m
735	7	1.6	146	2	Q6DKM5	Q6DKM5 xenopus lae	808	7	1.6	177	2	Q6ACZ4	Q6ACZ4 xenopus lae
736	7	1.6	147	2	Q7LHH0	Q7LHH0 saccharomyc	809	7	1.6	177	2	Q6C8X6	Q6C8X6 yarrowia li
737	7	1.6	148	2	Q6X748	Q6X748 neurospora	810	7	1.6	177	2	Q6CBT3	Q6CBT3 yarrowia li
738	7	1.6	148	2	Q7Q8C1	Q7Q8C1 anopheles g	811	7	1.6	177	2	Q6CFK5	Q6CFK5 yarrowia li
739	7	1.6	148	2	Q9UB93	Q9UB93 helicoverpa	812	7	1.6	177	2	Q8SKF6	Q8SKF6 macrodon an
740	7	1.6	149	2	Q6X747	Q6X747 neurospora	813	7	1.6	177	2	Q9M9H3	Q9M9H3 arabidopsis
741	7	1.6	149	2	Q6X758	Q6X758 neurospora	814	7	1.6	177	2	Q9M9H3	Q9M9H3 arabidopsis
742	7	1.6	150	2	Q8O490	Q8O490 arabidopsis	815	7	1.6	177	2	Q92F29	Q92F29 listeria in
743	7	1.6	151	2	Q8RYF3	Q8RYF3 avena strig	816	7	1.6	177	2	Q73FB0	Q73FB0 bacillus ce
744	7	1.6	151	2	Q6X756	Q6X756 neurospora	817	7	1.6	177	2	Q81J54	Q81J54 bacillus ce
745	7	1.6	151	2	Q7QHH5	Q7QHH5 anopheles g	818	7	1.6	177	2	Q81VU4	Q81VU4 bacillus an
746	7	1.6	151	2	Q9LB65	Q9LB65 helicobacte	819	7	1.6	177	2	Q6HPS2	Q6HPS2 bacillus th
747	7	1.6	151	2	Q8B0U5	Q8B0U5 mus musculu	820	7	1.6	177	2	Q6KYJ3	Q6KYJ3 bacillus an
748	7	1.6	152	2	Q86EL6	Q86EL6 schistosoma	821	7	1.6	178	2	Q9C7W1	Q9C7W1 arabidopsis
749	7	1.6	152	2	Q73VH4	Q73VH4 mycobacteri	822	7	1.6	179	2	Q7R2J4	Q7R2J4 giardia lam
750	7	1.6	153	2	Q6K8J6	Q6K8J6 oryza sativ	823	7	1.6	180	2	Q9LR35	Q9LR35 arabidopsis
751	7	1.6	153	2	Q8K064	Q8K064 mus musculu	824	7	1.6	181	2	Q61KG1	Q61KG1 drosophila
752	7	1.6	154	2	Q6X750	Q6X750 neurospora	825	7	1.6	181	2	Q864S4	Q864S4 ovis aries
753	7	1.6	154	2	Q6X761	Q6X761 neurospora	826	7	1.6	181	2	Q69QA5	Q69QA5 oryza sativ
754	7	1.6	154	2	Q6B877	Q6B877 ixodes paci	827	7	1.6	181	2	Q82K97	Q82K97 streptomyce
755	7	1.6	154	2	Q79FQ8	Q79FQ8 mycobacteri	828	7	1.6	181	2	Q8EKA9	Q8EKA9 shewanella
756	7	1.6	154	2	Q7U0C8	Q7U0C8 mycobacteri	829	7	1.6	182	1	K2C3_BOVIN	P04261 bos taurus
757	7	1.6	155	1	YFH3_YEAST	P43587 saccharomyc	830	7	1.6	182	2	K2C4_BOVIN	P04260 bos taurus
758	7	1.6	155	2	Q8SVU8	Q8SVU8 encephalito	831	7	1.6	182	2	Q6ZP96	Q6ZP96 homo sapien
759	7	1.6	155	2	Q6XHY3	Q6XHY3 drosophila	832	7	1.6	182	2	Q86MQ9	Q86MQ9 drosophila
760	7	1.6	157	2	Q6X760	Q6X760 neurospora	833	7	1.6	182	2	Q948F5	Q948F5 oryza sativ
761	7	1.6	157	2	Q6X762	Q6X762 neurospora	834	7	1.6	183	2	Q6K846	Q6K846 oryza sativ
					Q96DN7	Q96DN7 homo sapien						Q86QX1	Q86QX1 plasmodium

835	7	1.6	183	2	Q69886	Q69886 oryza sativ	908	7	1.6	218	2	Q6K5T4	Q6K5T4 oryza sativ
836	7	1.6	183	2	Q6Y7H2	Q6Y7H2 anaplasm p	909	7	1.6	218	2	Q8UVD4	Q8UVD4 gallus gall
837	7	1.6	183	2	Q8P912	Q8P912 xanthomonas	910	7	1.6	219	2	Q7SEB3	Q7SEB3 neurospora
838	7	1.6	183	2	Q8BGF8	Q8BGF8 mus musculus	911	7	1.6	219	2	Q9NG66	Q9NG66 speleonecte
839	7	1.6	184	2	Q9C2X0	Q9C2X0 cladosporiu	912	7	1.6	219	2	Q8VK50	Q8VK50 mycobacteri
840	7	1.6	184	2	Q83FUI	Q83FUI tropheryma	913	7	1.6	219	2	Q7VW56	Q7VW56 bordetella
841	7	1.6	185	2	Q9NAB4	Q9NAB4 caenorhabdi	914	7	1.6	220	2	Q8MVP0	Q8MVP0 bolitenia vi
842	7	1.6	185	2	Q8L8M5	Q8L8M5 arabidopsis	915	7	1.6	220	2	Q7PVU8	Q7PVU8 anopheles g
843	7	1.6	185	2	Q705U8	Q705U8 arena strig	916	7	1.6	220	2	Q6ZGC4	Q6ZGC4 oryza sativ
844	7	1.6	185	2	Q8H2M5	Q8H2M5 arena strig	917	7	1.6	220	2	Q6NPF4	Q6NPF4 corynebacte
845	7	1.6	185	2	Q8C5Y9	Q8C5Y9 mus musculus	918	7	1.6	221	2	Q7RYB1	Q7RYB1 neurospora
846	7	1.6	186	2	Q7QT36	Q7QT36 giardia lam	919	7	1.6	221	2	Q6SEW8	Q6SEW8 bacillus li
847	7	1.6	186	2	Q85KG5	Q85KG5 macrodon an	920	7	1.6	221	2	Q8YXH1	Q8YXH1 anabaena sp
848	7	1.6	186	2	Q705D8	Q705D8 arena strig	921	7	1.6	221	2	Q6MP72	Q6MP72 bdellovibri
849	7	1.6	188	2	Q9VVD0	Q9VVD0 drosophila	922	7	1.6	222	2	Q867E3	Q867E3 drosophila
850	7	1.6	188	2	Q72NE3	Q72NE3 leptospira	923	7	1.6	222	2	Q868B5	Q868B5 drosophila
851	7	1.6	188	2	Q8F844	Q8F844 leptospira	924	7	1.6	222	2	Q86ML2	Q86ML2 drosophila
852	7	1.6	189	2	Q668S3	Q668S3 yersinia ps	925	7	1.6	222	2	Q7YRX1	Q7YRX1 procyn loc
853	7	1.6	189	2	Q8CLE0	Q8CLE0 yersinia pe	926	7	1.6	222	2	Q69K36	Q69K36 oryza sativ
854	7	1.6	190	2	Q9BX21	Q9BX21 homo sapien	927	7	1.6	222	2	Q7W5L3	Q7W5L3 bordetella
855	7	1.6	191	2	Q46029	Q46029 chironomus	928	7	1.6	222	2	Q7WD49	Q7WD49 bordetella
856	7	1.6	191	2	Q93JB5	Q93JB5 streptomyc	929	7	1.6	222	2	Q82RK8	Q82RK8 streptomyc
857	7	1.6	192	2	Q7YV80	Q7YV80 cryptospori	930	7	1.6	223	1	COAT_TRVCA	COAT_TRVCA
858	7	1.6	192	2	Q7XDT3	Q7XDT3 oryza sativ	931	7	1.6	224	2	Q17668	Q17668 caenorhabdi
859	7	1.6	192	2	Q8DYK7	Q8DYK7 streptococc	932	7	1.6	224	2	Q6ZIG9	Q6ZIG9 oryza sativ
860	7	1.6	192	2	Q8E463	Q8E463 streptococc	933	7	1.6	225	2	Q866V9	Q866V9 macrotus ca
861	7	1.6	193	1	CIT1_HUMAN	Q99966 homo sapien	934	7	1.6	225	2	Q7SHQ2	Q7SHQ2 oryza sativ
862	7	1.6	193	2	Q06290	Q06290 mycobacteri	935	7	1.6	225	2	Q90XZ3	Q90XZ3 erpatoichth
863	7	1.6	193	2	Q8NFP9	Q8NFP9 corynebacte	936	7	1.6	226	2	Q7QCJ2	Q7QCJ2 anopheles g
864	7	1.6	193	2	Q88FP9	Q88FP9 pseudomonas	937	7	1.6	226	2	Q22684	Q22684 arabidopsis
865	7	1.6	195	2	Q7PUD3	Q7PUD3 anopheles g	938	7	1.6	226	2	Q9LK95	Q9LK95 arabidopsis
866	7	1.6	196	2	Q6LAV1	Q6LAV1 oryza sativ	939	7	1.6	227	2	Q84W21	Q84W21 arabidopsis
867	7	1.6	196	2	Q9A726	Q9A726 caulobacter	940	7	1.6	228	2	Q6YW05	Q6YW05 oryza sativ
868	7	1.6	197	2	Q93103	Q93103 aedes aegypt	941	7	1.6	230	2	Q9HLZ9	Q9HLZ9 thermoplasm
869	7	1.6	197	2	Q9WM61	Q9WM61 streptococc	942	7	1.6	230	2	Q69GY7	Q69GY7 solanum tub
870	7	1.6	198	2	Q9CRS6	Q9CRS6 mus musculus	943	7	1.6	231	1	YC9G_SCHPO	YC9G_SCHPO
871	7	1.6	199	2	Q8T1B2	Q8T1B2 dictyostelli	944	7	1.6	231	2	Q94F39	Q94F39 arabidopsis
872	7	1.6	199	2	Q82GT5	Q82GT5 streptomyc	945	7	1.6	233	2	Q9NZ86	Q9NZ86 homo sapien
873	7	1.6	200	1	SP24_BOVIN	Q27967 bos taurus	946	7	1.6	233	2	Q9BIT6	Q9BIT6 nephila ina
874	7	1.6	200	2	Q7TTE1	Q7TTE1 bordetella	947	7	1.6	233	2	Q9XUQ2	Q9XUQ2 caenorhabdi
875	7	1.6	200	2	Q72087	Q72087 human immun	948	7	1.6	234	2	Q9XRE4	Q9XRE4 brachydanio
876	7	1.6	201	2	Q8WSQ6	Q8WSQ6 penaeus jap	949	7	1.6	234	2	Q76KU9	Q76KU9 pisum sativ
877	7	1.6	202	2	Q754L2	Q754L2 ashbya goss	950	7	1.6	234	2	Q03538	Q03538 plasmodi rp4
878	7	1.6	202	2	Q9SII2	Q9SII2 arabidopsis	951	7	1.6	234	2	Q62IB0	Q62IB0 burkholderi
879	7	1.6	202	2	Q7WMF1	Q7WMF1 bordetella	952	7	1.6	234	2	Q6DHH2	Q6DHH2 brachydanio
880	7	1.6	202	2	Q9A699	Q9A699 caulobacter	953	7	1.6	234	2	Q8AXN7	Q8AXN7 cyprinus ca
881	7	1.6	203	2	Q70TH4	Q70TH4 ovis aries	954	7	1.6	235	2	Q8IGN6	Q8IGN6 drosophila
882	7	1.6	203	2	Q6GX94	Q6GX94 streptococc	955	7	1.6	236	2	Q6GLZ6	Q6GLZ6 xenopus lae
883	7	1.6	204	2	Q84J58	Q84J58 arabidopsis	956	7	1.6	236	2	Q9W6H2	Q9W6H2 xenopus lae
884	7	1.6	204	2	Q9AV63	Q9AV63 oryza sativ	957	7	1.6	237	2	Q38004	Q38004 bacterioph
885	7	1.6	204	2	Q9AXJ0	Q9AXJ0 oryza sativ	958	7	1.6	237	2	Q7XLA1	Q7XLA1 oryza sativ
886	7	1.6	204	2	Q9SHH9	Q9SHH9 arabidopsis	959	7	1.6	237	2	Q674Y1	Q674Y1 gymmarchus
887	7	1.6	204	2	Q6QWB0	Q6QWB0 azospirillum	960	7	1.6	237	2	Q9PUT2	Q9PUT2 brachydanio
888	7	1.6	204	2	Q7V6G4	Q7V6G4 prochloroco	961	7	1.6	238	2	Q63WG5	Q63WG5 burkholderi
889	7	1.6	205	2	Q8LCZ7	Q8LCZ7 arabidopsis	962	7	1.6	239	2	Q6ZJE7	Q6ZJE7 oryza sativ
890	7	1.6	205	2	Q7XUD3	Q7XUD3 oryza sativ	963	7	1.6	239	2	Q8G6R1	Q8G6R1 bifidobacte
891	7	1.6	207	2	Q8WYX6	Q8WYX6 homo sapien	964	7	1.6	240	2	Q6BNL7	Q6BNL7 debaryomyce
892	7	1.6	208	2	Q9W2Z9	Q9W2Z9 drosophila	965	7	1.6	240	2	Q6B8G7	Q6B8G7 ixodes paci
893	7	1.6	208	2	Q70614	Q70614 rattus sp.	966	7	1.6	240	2	Q8RU62	Q8RU62 oryza sativ
894	7	1.6	208	2	Q9QYQ9	Q9QYQ9 rattus exul	967	7	1.6	240	2	Q6UUL3	Q6UUL3 oryza sativ
895	7	1.6	209	2	Q7X7I0	Q7X7I0 oryza sativ	968	7	1.6	240	2	Q87YL4	Q87YL4 pseudomonas
896	7	1.6	209	2	Q83UE0	Q83UE0 cloning vec	969	7	1.6	241	2	Q8LM66	Q8LM66 oryza sativ
897	7	1.6	210	2	Q8XTO7	Q8XTO7 ralstonia s	970	7	1.6	243	2	Q67WQ9	Q67WQ9 oryza sativ
898	7	1.6	211	1	ZEP5_ARATH	Q39264 arabidopsis	971	7	1.6	245	2	Q863J4	Q863J4 ovis aries
899	7	1.6	211	2	Q8H5B5	Q8H5B5 oryza sativ	972	7	1.6	245	2	Q849T3	Q849T3 haemophilus
900	7	1.6	213	2	Q7VUD5	Q7VUD5 prochloroco	973	7	1.6	246	2	Q8XGK1	Q8XGK1 salmonella
901	7	1.6	214	2	Q8JFN4	Q8JFN4 oncorhynch	974	7	1.6	246	2	Q7CQX7	Q7CQX7 salmonella
902	7	1.6	216	1	FLGH_AQUAE	Q67609 aquifex aeo	975	7	1.6	247	2	Q41616	Q41616 trifolium r
903	7	1.6	216	2	Q7XW20	Q7XW20 oryza sativ	976	7	1.6	247	2	Q89LL9	Q89LL9 bradyrhizob
904	7	1.6	216	2	Q67QM3	Q67QM3 symbiobacte	977	7	1.6	247	2	Q8X116	Q8X116 mus musculu
905	7	1.6	216	2	Q7WAY7	Q7WAY7 bordetella	978	7	1.6	248	1	ATPDD_TOBAC	ATPDD_TOBAC
906	7	1.6	217	1	RIT2_MOUSE	P70425 mus musculu	979	7	1.6	248	2	Q9USS9	Q9USS9 schizosacch
907	7	1.6	218	2	Q759N0	Q759N0 ashbya goss	980	7	1.6	248	2	Q9FH54	Q9FH54 arabidopsis

981	7	1.6	248	2	O6GMF7	O6gmf7 brachydanio	1054	7	1.6	267	2	O6I417	O6i417 bacillus an
982	7	1.6	249	2	O6GUG5	O6gug5 pterocarpus	1055	7	1.6	267	2	O8UYU8	O8uyy8 sugarcane m
983	7	1.6	249	2	O8GTR8	O8gtr8 arabisopsis	1056	7	1.6	267	2	O8UYU9	O8uyy9 sugarcane m
984	7	1.6	249	2	O8XVNA	O8xvna ralstonia s	1057	7	1.6	267	2	O8UYV0	O8uyv0 sugarcane m
985	7	1.6	250	2	O84PD9	O84pd9 oryza sativ	1058	7	1.6	267	2	O8UYV1	O8uyv1 sugarcane m
986	7	1.6	250	2	O8K2K5	O8k2k5 mus musculu	1059	7	1.6	267	2	O8UYV2	O8uyv2 sugarcane m
987	7	1.6	250	2	O7S2T0	O7s2t0 xenopus lae	1060	7	1.6	267	2	O8UYV3	O8uyv3 sugarcane m
988	7	1.6	250	2	O9PUY6	O9puy6 anguilla sp	1061	7	1.6	267	2	O8UYV4	O8uyv4 sugarcane m
989	7	1.6	251	2	O9LWR2	O9lwr2 oryza sativ	1062	7	1.6	267	2	O8UYV5	O8uyv5 sugarcane m
990	7	1.6	251	2	O8COC5	O8coc5 m mus muscu	1063	7	1.6	267	2	O8UYV6	O8uyv6 sugarcane m
991	7	1.6	251	2	O9DW88	O9dw88 rat cytomeg	1064	7	1.6	267	2	O8UYV7	O8uyv7 sugarcane m
992	7	1.6	252	2	O75T55	O75t55 prunus pers	1065	7	1.6	267	2	O7T3J3	O7t3j3 oreochromis
993	7	1.6	252	2	O9ATL3	O9atl3 zea mays (m	1066	7	1.6	267	2	PSB4	PSb4 drosophila
994	7	1.6	252	2	O67E15	O67e15 zenopsis co	1067	7	1.6	268	2	O8IW10	O8iw10 homo sapien
995	7	1.6	253	2	O7SBQ0	O7sbq0 neurospora	1068	7	1.6	268	2	O96JC9	O96jc9 homo sapien
996	7	1.6	253	2	O9BIT4	O9bit4 nephila sen	1069	7	1.6	268	2	O6ZN62	O6zn62 homo sapien
997	7	1.6	253	2	O49388	O49388 arabisopsis	1070	7	1.6	268	2	O7FNQ5	O7fnq5 anopheles g
998	7	1.6	253	2	O6IQD2	O6iqd2 brachydanio	1071	7	1.6	268	2	O8NKZ1	O8nkz1 xanthomonas
999	7	1.6	254	1	PRIO_SIGHI	O9z0t3 sigmodon hi	1072	7	1.6	268	2	O8PJ80	O8pj80 xanthomonas
1000	7	1.6	254	2	O05777	O05777 saccharomyc	1073	7	1.6	268	2	O9D4C5	O9d4c5 m mus muscu
1001	7	1.6	254	2	O18434	O18434 helicoverpa	1074	7	1.6	269	2	O7OHS8	O7ohs8 leishmania
1002	7	1.6	254	2	O18436	O18436 helicoverpa	1075	7	1.6	269	2	O8SKF1	O8skf1 macrodon an
1003	7	1.6	254	2	O6YJN7	O6ynj7 oryza sativ	1076	7	1.6	269	2	O8SKF2	O8skf2 macrodon an
1004	7	1.6	254	2	O6ZFM9	O6zfm9 oryza sativ	1077	7	1.6	269	2	O8SKF3	O8skf3 macrodon an
1005	7	1.6	254	2	O84N51	O84n51 oryza sativ	1078	7	1.6	269	2	O8SKG2	O8skg2 macrodon an
1006	7	1.6	254	2	O9ZOT4	O9zot4 sigmodon fu	1079	7	1.6	270	1	PLJN_RAT	PLjn84 rattus norv
1007	7	1.6	254	2	O9COC5	O9coc5 m mus muscu	1080	7	1.6	270	2	O8SA27	O8sa27 macrodon an
1008	7	1.6	254	2	O9PUY4	O9puy4 chanos chan	1081	7	1.6	270	2	O8SB79	O8sb79 macrodon an
1009	7	1.6	255	2	O7S567	O7s567 neurospora	1082	7	1.6	270	2	O8SBU3	O8sbu3 macrodon an
1010	7	1.6	255	2	O692G5	O692g5 nephila cia	1083	7	1.6	270	2	O8SBW7	O8sbw7 macrodon an
1011	7	1.6	255	2	O8LFS7	O8lfs7 arabisopsis	1084	7	1.6	270	2	O8SBW8	O8sbw8 macrodon an
1012	7	1.6	255	2	O9ASY3	O9asy3 arabisopsis	1085	7	1.6	270	2	O8SKE9	O8ske9 macrodon an
1013	7	1.6	255	2	O9SJW8	O9sjw8 arabisopsis	1086	7	1.6	270	2	O8SKF0	O8skf0 macrodon an
1014	7	1.6	256	2	O9XUQ3	O9xug3 caenorhabdi	1087	7	1.6	270	2	O8SKF4	O8skf4 macrodon an
1015	7	1.6	256	2	O24568	O24568 zea mays (m	1088	7	1.6	270	2	O8SKF5	O8skf5 macrodon an
1016	7	1.6	256	2	O82F25	O82f25 streptomyce	1089	7	1.6	270	2	O8SKF8	O8skf8 macrodon an
1017	7	1.6	256	2	O7ZGM1	O7zgm1 human immun	1090	7	1.6	270	2	O8SKF9	O8skf9 macrodon an
1018	7	1.6	256	2	O7ZGP3	O7zgp3 human immun	1091	7	1.6	270	2	O8SKG0	O8skg0 macrodon an
1019	7	1.6	257	2	O6YX12	O6yx12 oryza sativ	1092	7	1.6	270	2	O8SKG1	O8skg1 macrodon an
1020	7	1.6	257	2	O9XIL1	O9xil1 arabisopsis	1093	7	1.6	270	2	O8SKG3	O8skg3 macrodon an
1021	7	1.6	257	2	O81275	O81275 bacillus an	1094	7	1.6	270	2	O8SKG4	O8skg4 macrodon an
1022	7	1.6	258	2	O49284	O49284 arabisopsis	1095	7	1.6	270	2	O8SKG6	O8skg6 macrodon an
1023	7	1.6	258	2	O9M0J2	O9m0j2 arabisopsis	1096	7	1.6	270	2	O9R8B0	O9r8b0 mycobacteri
1024	7	1.6	258	2	O83VA1	O83va1 western x p	1097	7	1.6	270	2	O61764	O61764 mus musculu
1025	7	1.6	259	2	O9C8P8	O9c8p8 arabisopsis	1098	7	1.6	271	2	O81793	O81793 arabisopsis
1026	7	1.6	260	2	O6IHY8	O6ihy8 drosophila	1099	7	1.6	271	2	YD66_MYCPN	Yd66 mycoplasma
1027	7	1.6	260	2	O8GS50	O8gs50 pterocarpus	1100	7	1.6	272	1	YD66_MYCPN	Yd66 mycoplasma
1028	7	1.6	260	2	O8GSD2	O8gsd2 pterocarpus	1101	7	1.6	272	2	O7QG03	O7qg03 anopheles g
1029	7	1.6	260	2	O8GU50	O8gu50 pterocarpus	1102	7	1.6	272	2	O69SG3	O69sg3 oryza sativ
1030	7	1.6	261	2	O6C0J1	O6c0j1 yarrowiala li	1103	7	1.6	272	2	O6YT06	O6yt06 oryza sativ
1031	7	1.6	261	2	O8NG19	O8ng19 homo sapien	1104	7	1.6	272	2	O8GRS1	O8grs1 pterocarpus
1032	7	1.6	261	2	O9LH16	O9lh16 arabisopsis	1105	7	1.6	272	2	O97M20	O97m20 clostridium
1033	7	1.6	261	2	O78279	O78279 human immun	1106	7	1.6	273	2	O04032	O04032 arabisopsis
1034	7	1.6	262	2	O95RY2	O95ry2 drosophila	1107	7	1.6	273	2	O75I35	O75i35 oryza sativ
1035	7	1.6	262	2	O95289	O95289 leishmania	1108	7	1.6	273	2	O8PQG6	O8pgq6 xanthomonas
1036	7	1.6	262	2	O9VIX5	O9vix5 drosophila	1109	7	1.6	274	2	O871T9	O871t9 neurospora
1037	7	1.6	262	2	O8W2Q2	O8w2q2 oryza sativ	1110	7	1.6	274	2	O8PDB9	O8pdb9 xanthomonas
1038	7	1.6	262	2	O9M3C1	O9m3c1 arabisopsis	1111	7	1.6	275	1	Z339_HUMAN	Z339 homo sapien
1039	7	1.6	262	2	O9F945	O9f945 rhodobacter	1112	7	1.6	275	2	O9B850	O9b850 aspergillus
1040	7	1.6	263	2	O9TH24	O9th24 aspergillus	1113	7	1.6	275	2	O9XLX5	O9xlx5 aspergillus
1041	7	1.6	263	2	O8RXV5	O8rxv5 arabisopsis	1114	7	1.6	276	2	O8TUR9	O8tur9 methanopyru
1042	7	1.6	263	2	O9LY29	O9ly29 arabisopsis	1115	7	1.6	276	2	O9KAX8	O9kax8 bacillus ha
1043	7	1.6	263	2	O67KZ5	O67kz5 symbiobacte	1116	7	1.6	276	2	O9DAU1	O9dau1 m mus muscu
1044	7	1.6	264	2	O85KF7	O85kf7 macrodon an	1117	7	1.6	277	2	O17376	O17376 caenorhabdi
1045	7	1.6	264	2	O8BQT2	O8bqt2 mus musculu	1118	7	1.6	277	2	O61297	O61297 haemaphysal
1046	7	1.6	265	2	O7SSK4	O7ssk4 neurospora	1119	7	1.6	277	2	O6H500	O6h500 oryza sativ
1047	7	1.6	265	2	O69PC6	O69pc6 oryza sativ	1120	7	1.6	277	2	O90Z61	O90z61 scophthalmu
1048	7	1.6	265	2	O97L09	O97l09 clostridium	1121	7	1.6	278	2	O6FSF5	O6fsf5 candida gla
1049	7	1.6	265	2	O6ML35	O6ml35 bdellovibri	1122	7	1.6	278	2	O8JFN5	O8jfn5 oncorhynch
1050	7	1.6	265	2	O72C40	O72c40 desulfovibr	1123	7	1.6	278	2	O9AVD0	O9avd0 oryza sativ
1051	7	1.6	266	2	O86G55	O86g55 glomeris ma	1124	7	1.6	278	2	O7UNE9	O7une9 rhodopirell
1052	7	1.6	267	1	COLI_PIG	P01192 s corticotr	1125	7	1.6	279	2	O86I28	O86i28 dictyosteli
1053	7	1.6	267	1	PANB_SULTO	O974y0 sulfolobus	1126	7	1.6	280	2	O6JBP9	O6jbp9 zea mays (s



1127	7	1.6	280	2	Q6R7P4	Q6r7p4 streptomyce	1200	7	1.6	302	2	Q9VQH5	Q9vqh5 drosophila
1128	7	1.6	281	2	Q6C8B5	Q6c8e5 yarrowia li	1201	7	1.6	302	2	Q7Y4N4	Q7y4n4 bacterioph
1129	7	1.6	281	2	Q717A4	Q71ta4 bacterioph	1202	7	1.6	302	2	Q93Y00	Q93y00 arabidopsi
1130	7	1.6	281	2	Q6JBR1	Q6jbr1 zea mays (s	1203	7	1.6	303	2	Q8NC24	Q8nc24 homo sapien
1131	7	1.6	282	1	KPRS_PYRAB	Q9uy08 pyrococcus	1204	7	1.6	303	2	Q9HA60	Q9ha60 homo sapien
1132	7	1.6	282	2	Q8MG1	Q8mng1 drosophila	1205	7	1.6	303	2	Q8W5G1	Q8w5g1 oryza sativ
1133	7	1.6	283	2	Q7SFO1	Q7sfq1 neurospora	1206	7	1.6	303	2	Q8BRJ3	Q8brj3 mus musculu
1134	7	1.6	284	2	Q99331	Q99331 sus scrofa	1207	7	1.6	304	2	Q631F9	Q631f9 burkholderi
1135	7	1.6	284	2	Q8L9D1	Q8l9d1 arabidopsi	1208	7	1.6	304	2	Q8A394	Q8a394 bacteroides
1136	7	1.6	284	2	Q69WN1	Q69wn1 oryza sativ	1209	7	1.6	305	1	PYRD_LACPL	P77887 lactobacill
1137	7	1.6	285	2	Q9BSD6	Q9bsd6 homo sapien	1210	7	1.6	305	2	Q7PRF9	Q7prf9 anopheles g
1138	7	1.6	285	2	Q9BVF4	Q9bvf4 homo sapien	1211	7	1.6	305	2	Q7QEB6	Q7qeb6 xanthomonas
1139	7	1.6	285	2	Q9NW55	Q9nw55 homo sapien	1212	7	1.6	305	2	Q8PDN7	Q8pdn7 xanthomonas
1140	7	1.6	285	2	Q9NEF0	Q9nef0 leishmania	1213	7	1.6	305	2	Q8QND6	Q8qnd6 ectocarpus
1141	7	1.6	285	2	Q8GUN3	Q8gun3 arabidopsi	1214	7	1.6	306	2	Q8W0D0	Q8w0d0 oryza sativ
1142	7	1.6	286	2	Q7KN81	Q7kn81 drosophila	1215	7	1.6	307	1	DF54_ARATH	Q81d10 arabidopsi
1143	7	1.6	286	2	Q9LVU0	Q9lvu0 arabidopsi	1216	7	1.6	307	2	Q6AVL6	Q6avl6 oryza sativ
1144	7	1.6	287	1	CAP2_DICD1	P34122 dictyosteli	1217	7	1.6	307	2	Q6K5Q4	Q6k5q4 oryza sativ
1145	7	1.6	287	2	Q8N358	Q8n358 homo sapien	1218	7	1.6	308	2	Q76762	Q76762 anopheles g
1146	7	1.6	287	2	Q9VIX6	Q9vix6 drosophila	1219	7	1.6	308	2	Q8BP15	Q8bp15 mus musculu
1147	7	1.6	287	2	Q8RUI9	Q8rui9 oryza sativ	1220	7	1.6	309	2	Q95PQ4	Q95pq4 oikopleura
1148	7	1.6	287	2	Q69PU4	Q69pu4 oryza sativ	1221	7	1.6	310	2	Q8NIY9	Q8niy9 neurospora
1149	7	1.6	287	2	Q8PBU3	Q8pbu3 xanthomonas	1222	7	1.6	310	2	Q817E6	Q817e6 bacillus ce
1150	7	1.6	288	2	Q846S8	Q846s8 myxococcus	1223	7	1.6	310	2	Q88198	Q88198 sugarcane m
1151	7	1.6	289	2	Q21155	Q21155 caenorhabdi	1224	7	1.6	311	2	Q6CL53	Q6cl53 kluyveromyc
1152	7	1.6	290	2	Q7SAF2	Q7saf2 neurospora	1225	7	1.6	312	1	RALY_MOUSE	Q9x215 mus musculu
1153	7	1.6	290	2	Q81G11	Q81g11 drosophila	1226	7	1.6	312	2	Q9XZ15	Q9xz15 drosophila
1154	7	1.6	290	2	Q7PP09	Q7pp09 anopheles g	1227	7	1.6	312	2	Q82HK0	Q82hk0 streptomyce
1155	7	1.6	290	2	Q8E154	Q8e154 streptococc	1228	7	1.6	312	2	Q82HR2	Q82hr2 streptomyce
1156	7	1.6	290	2	Q8E6L9	Q8e6l9 streptococc	1229	7	1.6	312	2	Q9RX31	Q9rx31 deinococcus
1157	7	1.6	291	2	Q9FK36	Q9fk36 arabidopsi	1230	7	1.6	312	2	Q8VF59	Q8vf59 mus musculu
1158	7	1.6	292	2	Q75MR7	Q75mr7 homo sapien	1231	7	1.6	313	1	KRE1_YEAST	P17260 saccharomyc
1159	7	1.6	292	2	Q23620	Q23620 arabidopsi	1232	7	1.6	313	2	Q8RVW3	Q8rvw3 lycopersico
1160	7	1.6	292	2	Q94H41	Q94h41 oryza sativ	1233	7	1.6	313	2	Q9RCW7	Q9rcw7 streptomyce
1161	7	1.6	292	2	Q9D4F2	Q9d4f2 mus musculu	1234	7	1.6	313	2	Q80PW8	Q80pw8 sugarcane m
1162	7	1.6	293	1	VHED_BPT2	P09035 bacterioph	1235	7	1.6	313	2	Q88194	Q88194 sugarcane m
1163	7	1.6	293	1	VHED_BPT6	P09797 bacterioph	1236	7	1.6	313	2	Q88195	Q88195 sugarcane m
1164	7	1.6	293	2	Q7S3Z7	Q7s3z7 neurospora	1237	7	1.6	313	2	Q88197	Q88197 sugarcane m
1165	7	1.6	293	2	Q7Q3D6	Q7q3d6 anopheles g	1238	7	1.6	313	2	Q88199	Q88199 sugarcane m
1166	7	1.6	293	2	Q87973	Q87973 mycobacteri	1239	7	1.6	314	2	Q9VVP2	Q9vvp2 drosophila
1167	7	1.6	293	2	Q9R3P7	Q9r3p7 mycobacteri	1240	7	1.6	314	2	Q7XXC8	Q7xxc8 oryza sativ
1168	7	1.6	293	2	Q6NCM5	Q6ncm5 rhodospseudo	1241	7	1.6	315	1	SL12_HUMAN	Q15370 homo sapien
1169	7	1.6	293	2	Q66H88	Q66h88 rattus norv	1242	7	1.6	315	2	Q8BKE4	Q8bke4 mus musculu
1170	7	1.6	293	2	Q90Y65	Q90y65 paralichthy	1243	7	1.6	316	1	CC12_CABEL	P20630 caenorhabdi
1171	7	1.6	293	2	Q6GND1	Q6gnd1 xenopus lae	1244	7	1.6	316	1	CC13_CABEL	P20631 caenorhabdi
1172	7	1.6	294	2	Q8N144	Q8n144 homo sapien	1245	7	1.6	316	2	Q9VOB3	Q9vob3 drosophila
1173	7	1.6	294	2	Q8YB41	Q8yb41 brucella me	1246	7	1.6	316	2	Q87972	Q87972 mycobacteri
1174	7	1.6	294	2	Q6MG73	Q6mg73 bdellovibri	1247	7	1.6	316	2	Q825C9	Q829c9 streptomyce
1175	7	1.6	294	2	Q8FEG9	Q8feg9 escherichia	1248	7	1.6	316	2	Q9F3K6	Q9f3k6 streptomyce
1176	7	1.6	294	2	Q8CFT0	Q8cft0 mus musculu	1249	7	1.6	317	1	V35K_RCNMV	P10838 red clover
1177	7	1.6	295	2	Q6ZUM6	Q6zum6 homo sapien	1250	7	1.6	317	2	Q9WLK3	Q9wlk3 drosophila
1178	7	1.6	295	2	Q76407	Q76407 caenorhabdi	1251	7	1.6	318	2	Q9V8Z9	Q9v8z9 drosophila
1179	7	1.6	295	2	Q9VNN2	Q9vnn2 drosophila	1252	7	1.6	318	2	Q6KAR2	Q6kar2 mus musculu
1180	7	1.6	295	2	Q94GG7	Q94gg7 oryza sativ	1253	7	1.6	319	2	Q7SEB9	Q7seb9 aahya goss
1181	7	1.6	295	2	Q7XGA2	Q7xga2 oryza sativ	1254	7	1.6	319	2	Q8LJL5	Q8lj15 oryza sativ
1182	7	1.6	296	2	Q95PQ3	Q95pq3 oikopleura	1255	7	1.6	319	2	Q82HH3	Q82hh3 streptomyce
1183	7	1.6	296	2	Q94CN4	Q94cn4 oryza sativ	1256	7	1.6	320	2	Q692U7	Q692u7 ixodes scap
1184	7	1.6	296	2	Q9ADH8	Q9adh8 ehrlichia c	1257	7	1.6	320	2	Q7QDF2	Q7qdf2 anopheles g
1185	7	1.6	296	2	Q982J9	Q982j9 rhizobium l	1258	7	1.6	320	2	Q8V6R9	Q8v6r9 halovirus h
1186	7	1.6	297	2	Q9SA66	Q9sa66 arabidopsi	1259	7	1.6	320	2	Q68YW0	Q68yw0 maize dwarf
1187	7	1.6	297	2	Q9HY18	Q9hy18 pseudomonas	1260	7	1.6	320	2	Q77DK8	Q7tdk8 halovirus h
1188	7	1.6	298	2	Q61061	Q61061 plasmodium	1261	7	1.6	321	2	Q92MP7	Q92mp7 rhizobium m
1189	7	1.6	298	2	Q85944	Q85944 sphingomona	1262	7	1.6	321	2	Q7NGB4	Q7ngb4 gloeobacter
1190	7	1.6	298	2	Q67P11	Q67p11 symbiobacte	1263	7	1.6	321	2	Q9KDA6	Q9kda6 bacillus ha
1191	7	1.6	299	2	Q9Y4N3	Q9y4n3 homo sapien	1264	7	1.6	322	2	Q8WQK5	Q8wqk5 calliphora
1192	7	1.6	299	2	Q98JQ4	Q98jq4 rhizobium l	1265	7	1.6	322	2	Q69P59	Q69p59 oryza sativ
1193	7	1.6	299	2	Q87RR5	Q87rr5 vibrio para	1266	7	1.6	323	1	KLFE_HUMAN	Q8td94 homo sapien
1194	7	1.6	300	2	Q7PRT4	Q7prt4 anopheles g	1267	7	1.6	323	2	Q6LX22	Q6lx22 methanococc
1195	7	1.6	300	2	Q8RXG4	Q8rxg4 arabidopsi	1268	7	1.6	323	2	Q6CDB8	Q6cdb8 yarrowia li
1196	7	1.6	300	2	Q8J111	Q8j111 brachydanio	1269	7	1.6	323	2	Q6BC34	Q6bc34 patinopecte
1197	7	1.6	301	1	AQPA_HUMAN	Q96ps8 homo sapien	1270	7	1.6	323	2	Q7Q197	Q7q197 anopheles g
1198	7	1.6	301	1	VHED_BPT4	P03695 bacterioph	1271	7	1.6	324	1	HME2_MOUSE	P09066 mus musculu
1199	7	1.6	302	2	Q9VND7	Q9vnd7 drosophila	1272	7	1.6	324	2	Q7SDB1	Q7sdb1 neurospora

1273	7	1.6	324	2	Q873A5	O873a5 neurospora	1346	7	1.6	350	2	Q692Q4	O692q4 citrus tris
1274	7	1.6	324	2	Q7QH82	Q7qh82 anopheles g	1347	7	1.6	351	1	RSH1_MAIZE	Q41853 zea mays (m
1275	7	1.6	325	2	Q7XR2	Q7xr2 oryza sativ	1348	7	1.6	352	2	Q8T089	O41089 drosophila
1276	7	1.6	325	2	Q8MR03	Q8mr03 drosophila	1349	7	1.6	352	2	Q84DD2	Q84dd2 uncultured
1277	7	1.6	325	2	Q7QH81	Q7qh81 anopheles g	1350	7	1.6	352	2	Q7NF17	Q7nf17 gloebacter
1278	7	1.6	326	2	Q7Y1K8	Q7y1k8 oryza sativ	1351	7	1.6	353	1	ROD RAT	Q9j154 rattus norv
1279	7	1.6	328	2	Q757X0	Q757x0 ashbya goss	1352	7	1.6	353	2	Q8MRN0	Q8mrn0 drosophila
1280	7	1.6	328	2	Q89MW9	Q89mw9 bradyrhizob	1353	7	1.6	353	2	Q61KW2	Q61kw2 drosophila
1281	7	1.6	329	2	Q9M2K4	Q9m2k4 arabidopsis	1354	7	1.6	353	2	Q7F0Q2	Q7f0q2 oryza sativ
1282	7	1.6	330	2	Q652X5	Q652x5 oryza sativ	1355	7	1.6	353	2	Q8B4G1	Q8b4g1 hepaticis b
1283	7	1.6	330	2	Q921Q4	Q921q4 rhizobium m	1356	7	1.6	353	2	Q7SKL1	Q7skl1 brachydanio
1284	7	1.6	330	2	Q899Q3	Q899q3 murid herpe	1357	7	1.6	354	2	Q7XUH5	Q7xuh5 oryza sativ
1285	7	1.6	331	2	Q7XFD0	Q7xfdo oryza sativ	1358	7	1.6	354	2	Q9LEN4	Q9len4 cicar ariet
1286	7	1.6	331	2	Q9AUN4	Q9aun4 oryza sativ	1359	7	1.6	354	2	Q9LRY5	Q9lry5 arabidopsis
1287	7	1.6	331	2	Q89W98	Q89w98 bradyrhizob	1360	7	1.6	354	2	Q6P898	Q6p898 xenopus tro
1288	7	1.6	331	2	Q6DGL6	Q6dgl6 brachydanio	1361	7	1.6	356	1	APTX_FUGRU	P61800 fugu rubrip
1289	7	1.6	332	1	HBPB_WHEAT	P23923 triticum ae	1362	7	1.6	356	2	Q6C2J9	Q6c2j9 yarrowia li
1290	7	1.6	332	1	Q7WPH0	Q7wph0 bordetella	1363	7	1.6	356	2	Q8R8B5	Q8rb85 thermoanaer
1291	7	1.6	333	2	Q8S9P2	Q8sp2 oryza sativ	1364	7	1.6	357	2	Q8INJ1	Q8inj1 drosophila
1292	7	1.6	335	2	Q8T3W1	Q8t3w1 drosophila	1365	7	1.6	357	2	Q65034	Q65034 oryza sativ
1293	7	1.6	335	2	Q8W048	Q8w048 oryza sativ	1366	7	1.6	357	2	Q93Z19	Q93zi9 arabidopsis
1294	7	1.6	336	2	Q8PPZ6	Q8ppz6 xanthomonas	1367	7	1.6	357	2	Q6K8S6	Q6k8s6 oryza sativ
1295	7	1.6	336	2	Q745J7	Q745j7 mycobacteri	1368	7	1.6	357	2	Q8BLH9	Q8blh9 mus musculu
1296	7	1.6	337	2	Q62022	Q62022 caenorhabdi	1369	7	1.6	358	2	Q9HFZ2	Q9hfz2 candida alb
1297	7	1.6	337	2	Q6N314	Q6n314 rhodopseudo	1370	7	1.6	358	2	Q8WRT8	Q8wrt8 bicyclus an
1298	7	1.6	337	2	Q91708	Q91708 xenopus lae	1371	7	1.6	358	2	Q69XD4	Q69xd4 oryza sativ
1299	7	1.6	338	2	Q8L6T5	Q8l6t5 arabidopsis	1372	7	1.6	358	2	Q89K27	Q89k27 bradyrhizob
1300	7	1.6	339	1	DJBI_MOUSE	Q9qj73 mus musculu	1373	7	1.6	358	2	Q9CZ48	Q9cz48 mus musculu
1301	7	1.6	339	2	Q6CAL8	Q6cal8 yarrowia li	1374	7	1.6	358	2	Q702R6	Q702r6 xenopus tro
1302	7	1.6	339	2	Q750Z8	Q750z8 ashbya goss	1375	7	1.6	359	2	Q97Y95	Q97y95 sulfobolus
1303	7	1.6	339	2	Q8INR1	Q8inr1 drosophila	1376	7	1.6	359	2	Q96L53	Q96l53 homo sapien
1304	7	1.6	339	2	Q98S17	Q98s17 xenopus lae	1377	7	1.6	359	2	Q7PF57	Q7pf57 anopheles g
1305	7	1.6	340	2	Q94816	Q94816 trichinella	1378	7	1.6	359	2	Q7XZ87	Q7xz87 lycopersico
1306	7	1.6	340	2	Q63G11	Q63g11 bacillus ce	1379	7	1.6	359	2	Q9QX6	Q9qx6 mesocricetu
1307	7	1.6	340	2	Q98P78	Q98p78 rhizobium l	1380	7	1.6	360	2	Q70D55	Q70d55 xenopus lae
1308	7	1.6	340	2	Q86893	Q86893 maize dwarf	1381	7	1.6	361	2	Q9LZQ3	Q9lzk3 arabidopsis
1309	7	1.6	341	2	Q7NGU1	Q7ngu1 gloebacter	1382	7	1.6	361	2	Q73JX2	Q73jx2 treponema d
1310	7	1.6	341	2	Q82C28	Q82c28 streptomyc	1383	7	1.6	361	2	Q82JY4	Q82jy4 streptomyc
1311	7	1.6	341	2	Q88284	Q88284 mus musculu	1384	7	1.6	362	2	Q786D8	Q786d8 neurospora
1312	7	1.6	342	2	Q8SX59	Q8sx59 drosophila	1385	7	1.6	362	2	Q6W492	Q6w492 drosophila
1313	7	1.6	342	2	Q9W2U5	Q9w2u5 drosophila	1386	7	1.6	362	2	Q6W493	Q6w493 drosophila
1314	7	1.6	342	2	Q8RYX7	Q8ryx7 oryza sativ	1387	7	1.6	362	2	Q6W494	Q6w494 drosophila
1315	7	1.6	342	2	Q41240	Q41240 solanum tub	1388	7	1.6	362	2	Q6W495	Q6w495 drosophila
1316	7	1.6	342	2	Q9M3Z4	Q9m3z4 cicar ariet	1389	7	1.6	362	2	Q6W4A6	Q6w4a6 drosophila
1317	7	1.6	342	2	Q6HNZ6	Q6hnz6 bacillus th	1390	7	1.6	362	2	Q6W4B4	Q6w4b4 drosophila
1318	7	1.6	343	2	Q7R748	Q7r748 plasmodium	1391	7	1.6	362	2	Q6H849	Q6h849 oryza sativ
1319	7	1.6	343	2	Q917J4	Q917j4 drosophila	1392	7	1.6	362	2	Q9SXX6	Q9sxx6 oryza sativ
1320	7	1.6	343	2	Q9XXU0	Q9xxu0 caenorhabdi	1393	7	1.6	362	2	Q8JYX2	Q8jyx2 sugarcane m
1321	7	1.6	343	2	Q81761	Q81761 arabidopsis	1394	7	1.6	362	2	Q8UYU4	Q8uyu4 sugarcane m
1322	7	1.6	343	2	Q94CS1	Q94cs1 oryza sativ	1395	7	1.6	362	2	Q8UYU5	Q8uyu5 sugarcane m
1323	7	1.6	343	2	Q7XT06	Q7xt06 oryza sativ	1396	7	1.6	362	2	Q8UYU6	Q8uyu6 sugarcane m
1324	7	1.6	345	2	Q87VX1	Q87vx1 pseudomonas	1397	7	1.6	363	2	Q86DR2	Q86dr2 drosophila
1325	7	1.6	345	2	Q88DM9	Q88dm9 pseudomonas	1398	7	1.6	363	2	Q86DR3	Q86dr3 drosophila
1326	7	1.6	345	2	Q9HX31	Q9hx31 pseudomonas	1399	7	1.6	363	2	Q86DR4	Q86dr4 drosophila
1327	7	1.6	345	2	Q9DM86	Q9dm86 rat cytomeg	1400	7	1.6	363	2	Q86DR5	Q86dr5 drosophila
1328	7	1.6	346	2	Q6VW58	Q6vw58 acanthisatt	1401	7	1.6	363	2	Q86DR6	Q86dr6 drosophila
1329	7	1.6	347	2	Q6KYZ5	Q6kyz5 picophilus	1402	7	1.6	363	2	Q86DR7	Q86dr7 drosophila
1330	7	1.6	348	1	DJB5_MOUSE	Q89114 mus musculu	1403	7	1.6	363	2	Q86DR8	Q86dr8 drosophila
1331	7	1.6	348	2	Q6BQB0	Q6bqb0 debaryomyce	1404	7	1.6	363	2	Q86DR9	Q86dr9 drosophila
1332	7	1.6	348	2	Q75GJ3	Q75gj3 ashbya goss	1405	7	1.6	363	2	Q86DS0	Q86ds0 drosophila
1333	7	1.6	348	2	Q94H66	Q94h66 oryza sativ	1406	7	1.6	363	2	Q86DS1	Q86ds1 drosophila
1334	7	1.6	348	2	Q6MQ17	Q6mq17 bdellovibri	1407	7	1.6	363	2	Q86DS2	Q86ds2 drosophila
1335	7	1.6	348	2	Q74DF1	Q74df1 geobacter s	1408	7	1.6	363	2	Q86DS3	Q86ds3 drosophila
1336	7	1.6	348	2	Q9F220	Q9f220 streptomyc	1409	7	1.6	363	2	Q86DS4	Q86ds4 drosophila
1337	7	1.6	349	2	Q6C605	Q6c605 yarrowia li	1410	7	1.6	363	2	Q86DS5	Q86ds5 drosophila
1338	7	1.6	349	2	Q6W489	Q6w489 drosophila	1411	7	1.6	363	2	Q9ZS11	Q9zsl1 arabidopsis
1339	7	1.6	349	2	Q6W490	Q6w490 drosophila	1412	7	1.6	364	2	Q7S222	Q7s222 neurospora
1340	7	1.6	350	2	Q6H511	Q6h511 oryza sativ	1413	7	1.6	365	2	Q9HL12	Q9hl12 thermoplas
1341	7	1.6	350	2	Q692P7	Q692p7 citrus tris	1414	7	1.6	365	2	Q7KWL1	Q7kwl1 dictyosteli
1342	7	1.6	350	2	Q692P9	Q692p9 citrus tris	1415	7	1.6	366	2	Q961C8	Q961c8 drosophila
1343	7	1.6	350	2	Q692Q1	Q692q1 citrus tris	1416	7	1.6	366	2	Q964C6	Q964c6 musca domes
1344	7	1.6	350	2	Q692Q2	Q692q2 citrus tris	1417	7	1.6	368	2	Q77297	Q77297 echinococcu
1345	7	1.6	350	2	Q692Q3	Q692q3 citrus tris	1418	7	1.6	368	2	Q81BZ2	Q81bz2 plasmodium

1419	7	1.6	368	2	Q94120	Q94120 oryza sativ
1420	7	1.6	368	2	Q7XG36	Q7XG36 oryza sativ
1421	7	1.6	368	2	Q9JLR0	Q9JLR0 mus musculus
1422	7	1.6	368	2	Q6WNT4	Q6WNT4 fugu rubrip
1423	7	1.6	369	2	Q8MSF1	Q8MSF1 drosophila
1424	7	1.6	369	2	Q6K4Q0	Q6K4Q0 oryza sativ
1425	7	1.6	369	2	Q706M0	Q706M0 pseudomonas
1426	7	1.6	369	2	Q8GPF0	Q8GPF0 pseudomonas
1427	7	1.6	369	2	Q8GQ36	Q8GQ36 pseudomonas
1428	7	1.6	369	2	Q8PKD3	Q8PKD3 xanthomonas
1429	7	1.6	369	2	Q9JRV1	Q9JRV1 chlamydia p
1430	7	1.6	369	2	Q9Z6X7	Q9Z6X7 chlamydia p
1431	7	1.6	369	2	Q6AEC0	Q6AEC0 leifsonia x
1432	7	1.6	371	2	Q8TKK8	Q8TKK8 methanobarc
1433	7	1.6	371	2	Q8LDM5	Q8LDM5 arabidopsis
1434	7	1.6	371	2	Q9SUT1	Q9SUT1 arabidopsis
1435	7	1.6	372	2	Q8IG95	Q8IG95 drosophila
1436	7	1.6	372	2	Q8LHG0	Q8LHG0 oryza sativ
1437	7	1.6	372	2	Q8RUF2	Q8RUF2 oryza sativ
1438	7	1.6	372	2	Q67UC6	Q67UC6 oryza sativ
1439	7	1.6	372	2	Q8UDS5	Q8UDS5 agrobacteri
1440	7	1.6	373	1	DWT1_PIG	Q9Tt01 sus scrofa
1441	7	1.6	373	2	Q978T9	Q978T9 thermoplas
1442	7	1.6	373	2	Q6MYN8	Q6MYN8 aspergillus
1443	7	1.6	373	2	Q7CY01	Q7CY01 agrobacteri
1444	7	1.6	373	2	Q7UP35	Q7UP35 rhodospirell
1445	7	1.6	373	2	Q9CVL4	Q9CVL4 mus musculu
1446	7	1.6	374	1	SIA6_MOUSE	P97325 r cmp-n-ace
1447	7	1.6	374	1	SIA6_RAT	Q02734 r cmp-n-ace
1448	7	1.6	374	2	Q8MS61	Q8MS61 drosophila
1449	7	1.6	374	2	Q8TOK2	Q8TOK2 drosophila
1450	7	1.6	374	2	Q7Q3Y8	Q7Q3Y8 anopheles g
1451	7	1.6	374	2	Q6H8M8	Q6H8M8 bos taurus
1452	7	1.6	374	2	Q70D54	Q70D54 sus scrofa
1453	7	1.6	374	2	Q9DBB6	Q9DBB6 mus musculu
1454	7	1.6	374	2	Q922X5	Q922X5 mus musculu
1455	7	1.6	375	1	SIA6_HUMAN	Q11203 h cmp-n-ace
1456	7	1.6	375	1	SIA6_PANTR	P61132 p cmp-n-ace
1457	7	1.6	376	2	Q7R4G8	Q7R4G8 giardia lam
1458	7	1.6	376	2	Q8JQW7	Q8JQW7 wheat strea
1459	7	1.6	376	2	Q8JOY2	Q8JOY2 wheat strea
1460	7	1.6	376	2	Q8JQZ7	Q8JQZ7 wheat strea
1461	7	1.6	377	2	Q8T8P4	Q8T8P4 wheat strea
1462	7	1.6	377	2	Q95VK3	Q95VK3 junonia coe
1463	7	1.6	377	2	Q9W4Q2	Q9W4Q2 drosophila
1464	7	1.6	377	2	Q8JQX3	Q8JQX3 wheat strea
1465	7	1.6	377	2	Q8JQY0	Q8JQY0 wheat strea
1466	7	1.6	377	2	Q8JQY7	Q8JQY7 wheat strea
1467	7	1.6	377	2	Q8JRL3	Q8JRL3 wheat strea
1468	7	1.6	377	2	Q9YHD0	Q9YHD0 petromyzon
1469	7	1.6	378	2	Q6CY49	Q6CY49 kluyveromyc
1470	7	1.6	378	2	Q76736	Q76736 dictyosteli
1471	7	1.6	378	2	Q9VRR9	Q9VRR9 drosophila
1472	7	1.6	379	1	HM1_SOYBN	P46608 glycine max
1473	7	1.6	379	2	Q692G2	Q692G2 nephila cla
1474	7	1.6	379	2	Q8H198	Q8H198 arabidopsis
1475	7	1.6	379	2	Q91UV7	Q91UV7 plasmid pip
1476	7	1.6	379	2	Q9AEW6	Q9AEW6 pseudomonas
1477	7	1.6	380	2	Q8WD61	Q8WD61 carangoides
1478	7	1.6	381	2	Q9GP09	Q9GP09 ixodes ric
1479	7	1.6	381	2	Q73P22	Q73P22 treponema d
1480	7	1.6	382	1	LMXA_HUMAN	Q8TE12 homo sapien
1481	7	1.6	382	1	LMXA_MESAU	Q04650 mesocricetu
1482	7	1.6	382	1	LMXA_MOUSE	Q9JKU8 mus musculu
1483	7	1.6	382	2	P91703	P91703 drosophila
1484	7	1.6	383	2	Q9VTY5	Q9VTY5 drosophila
1485	7	1.6	383	2	Q9LSD7	Q9LSD7 streptococc
1486	7	1.6	384	2	Q810C5	Q810C5 caenorhabdi
1487	7	1.6	384	2	Q9RS74	Q9RS74 deinococcus
1488	7	1.6	385	1	CYB_ASPNG	Q33798 aspergillus
1489	7	1.6	385	1	RO32_XENLA	P51932 xenopus lae
1490	7	1.6	385	2	Q7QVQ7	Q7QVQ7 giardia lam
1491	7	1.6	385	2	Q36831	Q36831 trimorphomy

RESULT 1

Q6UXC7 PRELIMINARY; PRT; 440 AA.

AC Q6UXC7; 385 2 Q6J9U7 06j9u7 cryptococcu

DT 05-JUL-2004 (TReMBLrel. 27, Created) 385 2 Q6J9U9 06j9u9 cryptococcu

DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update) 385 2 Q75GJ0 075g10 oryza sativ

DE KFQG729. 385 2 Q67NW7 067nw7 symbiobacte

GN ORFNames=UNQ729; 386 1 CYB\_TRIRU 06zz40 trichophyto

OS Homo sapiens (Human) 386 2 Q01759 001759 pneumocycati

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; 386 2 Q811B8 0811b8 drosophila

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 386 2 Q8EVB2 08evb2 mycoplasma

OX NCBI\_TaxID=9606; 387 1 CYB\_EMBNI 000161 emericeella

RN [1] SEQUENCE FROM N.A. 387 1 CYB\_EMBNI 000161 emericeella

RP MEDLINE=22887236; PubMed=12975309; DOI=10.1101/gr.1293003; 387 1 CYB\_EMBNI 000161 emericeella

RX Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., 387 1 CYB\_EMBNI 000161 emericeella

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., 387 1 CYB\_EMBNI 000161 emericeella

RA Batton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S., 387 1 CYB\_EMBNI 000161 emericeella

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., 387 1 CYB\_EMBNI 000161 emericeella

RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., 387 1 CYB\_EMBNI 000161 emericeella

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., 387 1 CYB\_EMBNI 000161 emericeella

RA Vandier K., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D., 387 1 CYB\_EMBNI 000161 emericeella

RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., 387 1 CYB\_EMBNI 000161 emericeella

RA Godowski P.; 387 1 CYB\_EMBNI 000161 emericeella

RT "The secreted protein discovery initiative (SPDI), a large-scale 387 1 CYB\_EMBNI 000161 emericeella

RT effort to identify novel human secreted and transmembrane proteins: a 387 1 CYB\_EMBNI 000161 emericeella

RT bioinformatics assessment."; 387 1 CYB\_EMBNI 000161 emericeella

RL Genome Res. 13:2265-2270(2003). 387 1 CYB\_EMBNI 000161 emericeella

DR ENBL; AY358412; AAQ88778.1; -. 387 1 CYB\_EMBNI 000161 emericeella

SQ SEQUENCE 440 AA; 42208 MW; B4COAFDCAAE18B0 CRC64; 387 1 CYB\_EMBNI 000161 emericeella

Query Match 100.0%; Score 440; DB 2; Length 440; 387 1 CYB\_EMBNI 000161 emericeella

Best Local Similarity 100.0%; Pred. No. 0; 387 1 CYB\_EMBNI 000161 emericeella

Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 387 1 CYB\_EMBNI 000161 emericeella

QY 1 MKFQGPLACLLALCLGSGEAGPLQSGEESTGTNIGELHGLDGLSEGKAIKKEAG 60 387 1 CYB\_EMBNI 000161 emericeella

DB 1 MKFQGPLACLLALCLGSGEAGPLQSGEESTGTNIGELHGLDGLSEGKAIKKEAG 60 387 1 CYB\_EMBNI 000161 emericeella

QY 61 GAAGSKVSEALGGTREAAGTGTGVRQVPGFAGADALNRVGEAAHAGTGHETGROAEDV 120 387 1 CYB\_EMBNI 000161 emericeella

DB 61 GAAGSKVSEALGGTREAAGTGTGVRQVPGFAGADALNRVGEAAHAGTGHETGROAEDV 120 387 1 CYB\_EMBNI 000161 emericeella

QY 121 IRHGADAVRSGVQVPGHSGAMETSGHIGFGSGGLGGQGGQGGTGTGTPWHGYPGNS 180 387 1 CYB\_EMBNI 000161 emericeella

DB 121 IRHGADAVRSGVQVPGHSGAMETSGHIGFGSGGLGGQGGQGGTGTGTPWHGYPGNS 180 387 1 CYB\_EMBNI 000161 emericeella

QY 181 AGSFNGNPGQAPWGQGGNGGPPNFGTNTQCAVAQPGYGVSRASQNGEGCTNPPPSGGGG 240 387 1 CYB\_EMBNI 000161 emericeella

DB 181 AGSFNGNPGQAPWGQGGNGGPPNFGTNTQCAVAQPGYGVSRASQNGEGCTNPPPSGGGG 240 387 1 CYB\_EMBNI 000161 emericeella

QY 241 SSSSG 300 387 1 CYB\_EMBNI 000161 emericeella

DB 241 SSSSG 300 387 1 CYB\_EMBNI 000161 emericeella

QY 301 RGDSSSESSWGSTGSSSGNHGSGCGNGHKGKCEKPGNEARCSGSGIQQFRGQGVSSN 360 387 1 CYB\_EMBNI 000161 emericeella

DB 301 RGDSSSESSWGSTGSSSGNHGSGCGNGHKGKCEKPGNEARCSGSGIQQFRGQGVSSN 360 387 1 CYB\_EMBNI 000161 emericeella

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QY 361 MREISKEGNRLGSGCDNYRGSSWGSAGGDAVGGVNTVNTSPTCMENFDTFWKNFKS 420
DB 361 MREISKEGNRLGSGCDNYRGSSWGSAGGDAVGGVNTVNTSPTCMENFDTFWKNFKS 420
QY 421 KLGFINWDINKDQSRIP 440
DB 421 KLGFINWDINKDQSRIP 440

RESULT 2
Q6E0U4 PRELIMINARY; PRT; 476 AA.
AC Q6E0U4; 2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Dermokine-beta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15234001; DOI=10.1016/j.ygeno.2004.03.010;
RA Matsui T., Hayaishi-Kisumi F., Kinoshita Y., Katahira S., Morita K.,
RA Miyachi Y., Ono Y., Inai Y., Tanigawa Y., Komiya T., Tsukita S.;
RT "Identification of novel keratinocyte-secreted peptides dermokine-
RT alpha/-beta and a new stratified epithelium-secreted protein gene
RT complex on human chromosome 19q13.1.";
RL Genomics 84:384-397(2004).
DR EMBL; AY622965; AAT68269.1; -.
SQ SEQUENCE 476 AA; 47010 MW; E2206CC8E64AC4992 CRC64;

Query Match 40.5%; Score 178; DB 2; Length 476;
Best Local Similarity 99.6%; Pred. No. 4.9e-153;
Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFGPLACLLALCLGSGAGPLQSGESTGTNIGALGHGLDALSSEGVAIKKEAG 60
DB 1 MKFGPLACLLALCLGSGAGPLQSGESTGTNIGALGHGLDALSSEGVAIKKEAG 60
QY 61 GAAGSKVSEALGGTTRAVGTGVRQVPGFCAADALGNRVGEAAHALGNTGHEIGRAEDV 120
DB 61 GAAGSKVSEALGGTTRAVGTGVRQVPGFCAADALGNRVGEAAHALGNTGHEIGRAEDV 120
QY 121 IRHGADAVRGSWGVPVGHSGAWETSGGHGIFGSGGLGGQGNPGGLGTPWVHGYPGNS 180
DB 121 IRHGADAVRGSWGVPVGHSGAWETSGGHGIFGSGGLGGQGNPGGLGTPWVHGYPGNS 180
QY 181 AGSFGMNPQAPWQGGNGGPPNFGTNTQGAVAQPGYGSVRASQNEGCTNPPPSGGG 240
DB 181 AGSFGMNPQAPWQGGNGGPPNFGTNTQGAVAQPGYGSVRASQNEGCTNPPPSGGG 240
QY 241 SSNSGGSGSGSGSGSGSGNDNNGSGSGSGSGSGSSG 279
DB 241 SSNSGGSGSGSGSGSGSGNDNNGSGSGSGSGSGSSG 279

RESULT 3
Q96EW8 PRELIMINARY; PRT; 137 AA.
AC Q96EW8; Q9BSY6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ZD52F10 protein.
GN Name=ZD52F10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011886; AAH11886.1; -.
DR EMBL; BC004493; AAH04493.2; -.
SQ SEQUENCE 137 AA; 15484 MW; 5830C737DA329566 CRC64;

Query Match 5.7%; Score 25; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 408 MFNFDTFWKNFKSKLGFINDAINK 432
DB 1 MFNFDTFWKNFKSKLGFINDAINK 25

RESULT 4
Q9CR91 PRELIMINARY; PRT; 182 AA.
AC Q9CR91;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
DE library, clone:4833420N21 product:weakly similar to EPIDERMAL
DE DIFFERENTIATION COMPLEX PROTEIN LIKE PROTEIN (Mus musculus 18-day
DE embryo whole body cDNA, RIKEN full-length enriched library,
DE clone:1110019L16 product:weakly similar to EPIDERMAL DIFFERENTIATION
DE COMPLEX PROTEIN LIKE PROTEIN) (Mus musculus 18-day embryo whole body
DE cDNA, RIKEN full-length enriched library, clone:1110059L13
DE product:weakly similar to EPIDERMAL DIFFERENTIATION COMPLEX PROTEIN
DE LIKE PROTEIN).
GN Name=Sprl10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head, and whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
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OC Alteromonadaceae; Microbulbifer.
OX NCBI_TaxID=48074;
RN [1]
RP SEQUENCE FROM N.A.
RA Howard M.B., Ekborg N.A., Taylor L.B. Jr., Weiner R.M.,
RA Hutchesson S.W.;
RT "Complex polysaccharide metabolic profiles of Microbulbifer sp. and
RT analysis of chitinases and other degradative enzymes of Microbulbifer
RT hydrolyticus.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
DR EMBL; AY646089; AAT81215.1; -.
DR GO; GO:0004553; F:Hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008985; ConA_like lec.gl.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PRO0911; GLHYDLASE11.
DR PROSITE; PS00776; GLYCOSYL HYDROL F11.1; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 417 AA; 43930 MW; 76B5B56035323C91 CRC64;

Query Match 3.4%; Score 15; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 SSGSGSGSGSGSGSG 295
DB 387 SSGSGSGSGSGSGSG 401

RESULT 7
Q7UJ76 PRELIMINARY; PRT; 456 AA.
AC Q7UJ76;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Keratin.
GN OrderedLocusNames=RB12076;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Anann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294154; CAD77382.1; -.
KW Complete proteome.
SQ SEQUENCE 456 AA; 46867 MW; 0F68B67323907F53 CRC64;

Query Match 3.4%; Score 15; DB 2; Length 456;
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 SSGSGSGSGSGSGSG 295
DB 106 SSGSGSGSGSGSGSG 120

RESULT 8
Q8PV5 PRELIMINARY; PRT; 792 AA.
AC Q8PV5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Conserved protein.
GN OrderedLocusNames=MM0384;
OS Methanosarcina maezi (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=1215824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wieser T., Christmann A., Boemecke M., Steckel S.,
RA Bruggemann H., Lienard T., Christmann A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Bhattacharyya A., Lykidis A.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina maezi: evidence for lateral gene
RT transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AE013263; AAM30080.1; -.
DR InterPro; IPR006626; PbH1.
DR InterPro; IPR011050; Pectin_lyas_like.
DR Pfam; PF00801; PKD; 2.
DR SMART; SM00710; PbH1; 6.
DR SMART; SM00089; PKD; 2.
DR PROSITE; PS50093; PKD; 2.
KW Complete proteome.
SQ SEQUENCE 792 AA; 84670 MW; 64EC06653D0CF3BA CRC64;

Query Match 3.2%; Score 14; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 GSSSGSGSGSGSGSG 279
DB 546 GSSSGSGSGSGSGSG 559

RESULT 9
Q6ZUH6 PRELIMINARY; PRT; 120 AA.
AC Q6ZUH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ43707.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Esophageal;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuna M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK125695; BAC86249.1; -.
SQ SEQUENCE 120 AA; 13768 MW; A1CBA83310422C1B CRC64;

Query Match 3.0%; Score 13; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 350 QGFRGGVSSNMR 362  
 Db 104 QGFRGGVSSNMR 116

## RESULT 10

Q94476 ID Q94476 PRELIMINARY; PRT; 199 AA.  
 AC Q94476  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE ORFvigil13 (Fragment).  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AX4;  
 RA Loomis W.F.;  
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U6523; AAB06786.1; -;  
 DR HSP; P11376; 2EQL.  
 DR DictyBase; DB0185118; rcDBB.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR InterPro; IPR001916; Glyco\_hydro\_22.  
 DR SMART; SM00263; LY21; 1.  
 FT NON TER 1  
 SQ SEQUENCE 199 AA; 19335 MW; DBE0D17B1BC81A3A CRC64;

Query Match 3.0%; Score 13; DB 2; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 0.0031;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GSSSGSSGSSSG 283  
 Db 145 GSSSGSSGSSSG 157

## RESULT 11

Q8MML4 ID Q8MML4 PRELIMINARY; PRT; 202 AA.  
 AC Q8MML4; Q8T171;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE HypoPutative Glycosidase (Similar to Dictyostelium discoideum (Slime mold). ORFvigil13).  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AX4;  
 RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,  
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,  
 RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 [2]

Query Match 3.0%; Score 13; DB 2; Length 202;  
 Best Local Similarity 100.0%; Pred. No. 0.0044;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GSSSGSSGSSSG 283  
 Db 98 GSSSGSSGSSSG 110

RESULT 13

Q86HE5 ID Q86HE5 PRELIMINARY; PRT; 297 AA.  
 AC Q86HE5;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Component of the counting factor complex.  
 GN Name=cf45-1;  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]

DR EMBL; AC123513; AAM4373.1; -;  
 DR EMBL; AC117070; AAM09345.2; -;  
 DR HSP; P11376; 2EQL.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR001916; Glyco\_hydro\_22.  
 DR SMART; SM00263; LY21; 1.  
 KW Glycosidase.  
 SQ SEQUENCE 202 AA; 19375 MW; 3905406541395584 CRC64;

Query Match 3.0%; Score 13; DB 2; Length 202;  
 Best Local Similarity 100.0%; Pred. No. 0.0032;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GSSSGSSGSSSG 283  
 Db 148 GSSSGSSGSSSG 160

## RESULT 12

Q8MYJ1 ID Q8MYJ1 PRELIMINARY; PRT; 262 AA.  
 AC Q8MYJ1;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Similar to Haliotis rufescens (California red abalone). LUSTRIN  
 DE A.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AX4;  
 RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,  
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,  
 RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;  
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";  
 RL Nature 418:79-85(2002).  
 RN [2]

Query Match 3.0%; Score 13; DB 2; Length 262;  
 Best Local Similarity 100.0%; Pred. No. 0.004;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GSSSGSSGSSSG 283  
 Db 98 GSSSGSSGSSSG 110

Query Match 3.0%; Score 13; DB 2; Length 262;  
 Best Local Similarity 100.0%; Pred. No. 0.0044;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GSSSGSSGSSSG 283  
 Db 98 GSSSGSSGSSSG 110

## RESULT 13

Q86HE5 ID Q86HE5 PRELIMINARY; PRT; 297 AA.  
 AC Q86HE5;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Component of the counting factor complex.  
 GN Name=cf45-1;  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=22793726; PubMed=12912898; DOI=10.1128/EC.2.4.788-797.2003;
RA Brock D.A., Hutton R.D., Giurgiu D.V., Scott B., Jang W.,
RA Ammann R., Comer R.H.;
RT "CF45-1, a secreted protein which participates in Dictyostelium group
RT size regulation.";
RL Eukaryotic Cell 2:788-797(2003).
DR EMBL; AY212268; AAO52749.1; -.
DR DictyBase; DDB0191161; CF45-1.
DR GO; GO:0003796; F:lysozyme activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002053; Glyco_hydro_25.
DR ProDom; PD04620; Glyco_hydro_25; 1.
DR SEQUENCE 297 AA; 29304 MW; A77398C396A3BCB CRC64;

Query Match 3.0%; Score 13; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GSSSGSGSGSGSSG 283
Db 234 GSSSGSGSGSGSSG 246

RESULT 14
Q8TI63 PRELIMINARY; PRT; 375 AA.
AC Q8TI63
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MA4293.
GN OrderedLocuNames=MA4293.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Graham D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE011143; AAM07637.1; -.
DR InterPro; IPR008962; PapD-like.
KW Complete proteome.
SQ SEQUENCE 375 AA; 40367 MW; DAE26D2B548FD621 CRC64;

Query Match 3.0%; Score 13; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 GSSSGSGSGSGSS 290
Db 134 GSSSGSGSGSGSS 146

RESULT 15
Q9GRU6 PRELIMINARY; PRT; 418 AA.
ID Q9GRU6

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AC Q9GRU6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-1,4-endoglucanase 1 (Fragment).
GN Name=engl;
OS Heterodera schachtii.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
OX NCBI_TaxID=97005;
RN [1]
RP SEQUENCE FROM N.A.
RA De Meutter J., Tytgat T., Gheysen G.D.C., Coomans A., Gheysen G.D.R.;
RT "Biochemical characterisation of pharyngeal secretions from Heterodera
RT schachtii stage 2 juveniles.";
RL Eur. J. Biochem. 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RA De Meutter J.J.;
RL Submitted (JCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ299386; CAC12958.1; -.
DR HSSP; P07103; IEG2.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001919; Bac_cellose-bind.
DR InterPro; IPR008965; Cellul_bind.
DR InterPro; IPR001547; Glyco_hydro_5.
DR Pfam; PF00150; Cellulase; 1.
DR SMART; SM00637; CBD_II; 1.
FT NON TER 1
SQ SEQUENCE 418 AA; 43739 MW; EAA16B402EDCSA9C CRC64;

Query Match 3.0%; Score 13; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GSSSGSGSGSGSSG 283
Db 275 GSSSGSGSGSGSSG 287

Search completed: April 7, 2005, 00:39:56
Job time : 212 secs

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OM protein - protein search, using sw model  
Run on: April 7, 2005, 00:02:45 ; Search time 75 Seconds  
(without alignments)  
2268.994 Million cell updates/sec

Title: US-10-063-561-52  
Perfect score: 2363  
Sequence: 1 MKFGPLACLLALCLGSGE.....KLGFINWDINKDQSSRIP 440  
Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5  
Total number of hits satisfying chosen parameters: 2105692  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqpl980s:\*  
2: Geneseqpl990s:\*  
3: Geneseqpl990s:\*  
4: Geneseqpl990s:\*  
5: Geneseqpl990s:\*  
6: Geneseqpl990s:\*  
7: Geneseqpl990s:\*  
8: Geneseqpl990s:\*  
9: Geneseqpl990s:\*  
10: Geneseqpl990s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AA99354	standard; protein; 440 AA.				
DE	Human PRO1411 (UNQ729) amino acid sequence SEQ ID NO:52.					
PN	WO200012708-A2.					
PD	03-MAR-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 2363;	DB 3;	Length 440;		
Best Local Similarity	100.0%;	Pred. No. 2.4e-137;				
RESULT 2						
ID	AA866103	standard; protein; 440 AA.				
DE	Protein of the invention #15.					
PN	WO200078961-A1.					
PD	28-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 2363;	DB 3;	Length 440;		
Best Local Similarity	100.0%;	Pred. No. 2.4e-137;				
RESULT 3						
ID	AA331205	standard; protein; 440 AA.				
DE	Amino acid sequence of human polypeptide PRO1411.					
PN	WO200077037-A2.					
PD	21-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 2363;	DB 4;	Length 440;		
Best Local Similarity	100.0%;	Pred. No. 2.4e-137;				
RESULT 4						
ID	AAU29124	standard; protein; 440 AA.				
DE	Human PRO polypeptide sequence #101.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 2363;	DB 4;	Length 440;		
Best Local Similarity	100.0%;	Pred. No. 2.4e-137;				
RESULT 5						
ID	AA87551	standard; protein; 440 AA.				
DE	Human PRO1411.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 2363;	DB 4;	Length 440;		
Best Local Similarity	100.0%;	Pred. No. 2.4e-137;				
RESULT 6						
ID	AAU83669	standard; protein; 440 AA.				

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DE Human PRO protein, Seq ID No 156.  
PN WO200208288-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 5; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 7  
ID ABB95876 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 5; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 8  
ID ABB84891 standard; protein; 440 AA.  
DE Human PRO1411 protein sequence SEQ ID NO:150.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 5; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 9  
ID ABB95497 standard; protein; 440 AA.  
DE Human angiogenesis related protein PRO1411 SEQ ID NO: 150.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODO/) GODDARD A.  
PA (GODD/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J P.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 2363; DB 5; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 10  
ID ABUS8500 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 11  
ID ABUS8048 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 12  
ID ABUS4363 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 13  
ID ABR66237 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 14  
ID ABR65627 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 15  
ID ABU99567 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 16  
ID ABR2806 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 17  
ID ABR9927 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 18  
ID ABR68176 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 19  
ID ASU96229 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 20  
ID ASU92660 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 21  
ID ABU08016 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003036635-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 22  
ID ABO08737 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 23  
ID ABO02789 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 24  
ID ABR74943 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 25  
ID ABR94705 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 26  
ID ABO5176 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO141.  
PN US2003040014-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 27  
ID ABO33782 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 28  
ID ABU85678 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 29  
ID ABU98838 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 30  
ID ABU98053 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 31  
ID ABU91759 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 32  
ID ABU89452 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 33  
ID ABU86293 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 34

ID ABU67506 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 35  
ID ABU80534 standard; protein; 440 AA.  
DE Human PRO protein #101.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 36  
ID ABU90901 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 37  
ID ABO33960 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO411.  
PN US200309013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 38  
ID ABR99452 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 39  
ID ABR98842 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 40  
ID ABO16365 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 41  
ID ABR92265 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 42  
ID ABO18906 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 43  
ID ABR78327 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 44  
ID ABU71977 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 45  
ID ABU85063 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 46  
ID ABO00202 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 47  
ID ABO11534 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 48  
ID ABO02179 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 49  
ID ABU8753 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 50  
ID ABU67294 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032063-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 51  
ID ABU83448 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 52  
ID ABO06249 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 53  
ID ABR59285 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

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RESULT 54
ID ABO09347 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 55
ID ABO19211 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 56
ID ABO11229 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 57
ID ABR66847 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 58
ID ABO16060 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 59
ID ABO13766 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 60
ID ABU71531 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 61
ID ABU65669 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, SEQ ID 202.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 62
ID ABO07517 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 63
ID ABO03704 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 64
ID ABR67152 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027286-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 65
ID ABO15755 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 66
ID ABU56036 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO1411.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 67
ID ABU72312 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 68
ID ABU65364 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032182-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 69
ID ABU95309 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 70
ID ABU71212 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 71
ID ABO07822 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 72
ID ABR70063 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 73
ID ABR69396 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 74
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ID ABO01537 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 75  
ID ABU81339 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 76  
ID ABR60136 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 77  
ID ASU90985 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 78  
ID ABR6781 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 79  
ID ABR65259 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 80  
ID ABR69481 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 81  
ID ABR71893 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 82  
ID ABU85373 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 83  
ID ABU89063 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 84  
ID ABO01537 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 85  
ID ABU94999 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 86  
ID ABU90547 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 87  
ID ABU84058 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 88  
ID ABU93709 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 89  
ID ABR64954 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 90  
ID ABR68786 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 91  
ID ABO06602 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 92  
ID ABR99147 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 93  
ID ABUS7031 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 94  
ID ABU72062 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.

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PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 95
ID ABUS85983 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 96
ID ABUS82270 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 97
ID ABUS87281 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 98
ID ABUS7163 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 99
ID ABUS753 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 100
ID ABO08127 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 101
ID ABUS2501 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 102
ID ABUS1838 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 103
ID ABUS66002 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 104
ID ABUS1171 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411.
PN US2002027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 105
ID ABR59831 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 106
ID ABUS4019 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 107
ID ABUS9872 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 108
ID ABUS2125 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 109
ID ABR6542 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 110
ID ABR90960 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 111
ID ABO53286 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 112
ID ABUS4387 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 113
ID ABUS79269 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 114
ID ABUS6598 standard; protein; 440 AA.
```

DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 115  
ID ABU86903 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 116  
ID ABU94692 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 117  
ID ABO04619 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 118  
ID ABR70368 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 119  
ID ABU98533 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 120  
ID ABR65932 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 121  
ID ABR64649 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 122  
ID ABU79574 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 123  
ID ABU92965 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 124  
ID ABU95924 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003036145-A1.

PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 125  
ID ABU91144 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 126  
ID ABU90237 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 127  
ID ABO09652 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 128  
ID ABO10924 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 129  
ID ABR70978 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 130  
ID ABU98288 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 131  
ID ABU87586 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 132  
ID ABU91454 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 133  
ID ABU89293 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 134  
ID ABU84668 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032116-A1.  
PD 13-FEB-2003.

Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 135  
ID ABR69758 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 136  
ID ABU80135 standard; protein; 440 AA.  
DE Human PRO protein #101.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 137  
ID ABU82500 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 138  
ID ABU93404 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 139  
ID ABO09957 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 140  
ID ABO09042 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 141  
ID ABU96464 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003027993-A1.  
PD 08-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 142  
ID ABU10610 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein #101.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 143  
ID ABU72134 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 144  
ID ABU95619 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032115-A1.

PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 145  
ID ABU79805 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003032057-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 146  
ID ABU96828 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 147  
ID ABR70673 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 148  
ID ABO05024 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 149  
ID ABO08432 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 150  
ID ABO05639 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 151  
ID ABR74028 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 152  
ID ABR95620 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 153  
ID ABR80917 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 154  
ID ABR81222 standard; protein; 440 AA.



DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 155  
ID ABO00918 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 156  
ID ABR88520 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 157  
ID ABR77341 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 158  
ID ABO28825 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 159  
ID ABO31570 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 160  
ID ABR07987 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 161  
ID ABO40467 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 162  
ID ABO35892 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 163  
ID ABO44031 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.

PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 164  
ID ADA77954 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 165  
ID ABM24826 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 166  
ID ABO03094 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 167  
ID ABR90350 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 168  
ID ABM17264 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 169  
ID ABR95010 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 170  
ID ABR95315 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 171  
ID ABJ72305 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 172  
ID ADB17109 standard; protein; 440 AA.  
DE Human transmembrane PRO polypeptide (SeqID 52).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 173  
ID ABO21553 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 174  
ID ABR97817 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 175  
ID ABR87605 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003088705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 176  
ID ABR77646 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 177  
ID ABR27876 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 178  
ID ABR06157 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 179  
ID ABR03663 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 180  
ID ABR35114 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 181  
ID ABR26351 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 182  
ID ABO48133 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 183  
ID ABR92875 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 184  
ID ABO24636 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 185  
ID ABR11647 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 186  
ID ABR02748 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 187  
ID ABR16044 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 188  
ID ABO27605 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 189  
ID ABR29096 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 190  
ID ABR07072 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 191  
ID ABR21166 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 192  
ID ABO09512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 193  
ID ABO41382 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 194  
ID ABO36197 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 195  
ID ABO43726 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 196  
ID ABM76426 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 197  
ID ABM76122 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 198  
ID ABM25741 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 199  
ID ABM26046 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 200  
ID ABO03399 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 201  
ID ABO02484 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 202  
ID ABO44264 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO 1411.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 203  
ID ABR90655 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 204  
ID ABR73723 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 205  
ID ABO16975 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 206  
ID ABR94400 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 207  
ID ABR75907 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 208  
ID ABR71283 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 209  
ID ABR93180 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 210  
ID ABR93485 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054478-A1.  
PD 20-MAR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 211
ID ABR87910 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 212
ID ABO33596 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 213
ID ABO27910 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 214
ID ABO30045 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 215
ID ABO33254 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 216
ID ABO4942 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 217
ID ABO8902 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 218
ID ABO36502 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 219
ID ABO35587 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 220
ID ABO39552 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 221
ID ABO10427 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 222
ID ABO11952 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 223
ID ABO52098 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 224
ID ABO52403 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 225
ID ADA19914 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 226
ID ABO23721 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 227
ID ADB17297 standard; protein; 440 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 228
ID ABR97207 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
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RESULT 229  
ID ABR86995 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 230  
ID ABR11037 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 231  
ID ABR28181 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 232  
ID ABO32180 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 233  
ID ABR15307 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 234  
ID ABR08462 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 235  
ID ABR04273 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 236  
ID ABR22386 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 237  
ID ABR07682 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 238  
ID ABR97512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.

ID ABO40772 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 239  
ID ABR35419 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 240  
ID ABR33182 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 241  
ID ABO52708 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 242  
ID ABO50268 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 243  
ID ABR99262 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 244  
ID ABO04314 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 245  
ID ABO05944 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 246  
ID ABR18484 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 247  
ID ABR97512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 248  
ID ABR80612 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 249  
ID ABR01223 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 250  
ID ABR8825 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073169-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 251  
ID ABR13477 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 252  
ID ABR20861 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 253  
ID ABO41992 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 254  
ID ABO42602 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 255  
ID ABR010122 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 256  
ID ABO38637 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 257  
ID ABR32877 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 258  
ID ABR22691 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 259  
ID ABR74902 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 260  
ID ADA79746 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 261  
ID ABR96292 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 262  
ID ABR02443 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 263  
ID ABR86385 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 264  
ID ABR86690 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 265  
ID ABR16654 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003084448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 266  
ID ABR29706 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064456-A1.  
PD 03-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 267  
ID ABO29130 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 268  
ID AM23911 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 269  
ID ABM23301 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 270  
ID ADA47278 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO1411.  
PN US2003044844-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 271  
ID ABM22081 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 272  
ID ABO37722 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 273  
ID ABM28486 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 274  
ID ABM28791 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 275  
ID ABM66435 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 276  
ID ABM75817 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 277  
ID ABM34097 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 278  
ID ABM34402 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 279  
ID ABO20333 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 280  
ID ABO21248 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 281  
ID ABO22163 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 282  
ID ADA20086 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 283  
ID ABR96597 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 284  
ID ABR85775 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 285  
ID ABR99757 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

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PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 285
ID ABO16670 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 296
ID ABO18296 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 297
ID ABO22723 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 298
ID ABO23028 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 299
ID ABR92570 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 300
ID ABR81527 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 301
ID ABM77951 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 302
ID ABR89740 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 303
ID ABM26656 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 304
ID ABM13782 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064458-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 286
ID ABO00613 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 287
ID ABO00308 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 288
ID ABO29740 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 289
ID ABM23606 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 290
ID ABM29401 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 291
ID ABO38332 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 292
ID ABO45632 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 293
ID ABM20556 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 294
ID ADA81473 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
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PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 305  
ID ABO47828 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 306  
ID ABO30350 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 307  
ID ABO07377 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 308  
ID ABO03968 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 309  
ID ABO37112 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 310  
ID ABO41687 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 311  
ID ABO35282 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 312  
ID ABO25131 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 313  
ID ABO47523 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 314  
ID ABO47828 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 315  
ID ABO48438 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 316  
ID ABO51488 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 317  
ID ABO51793 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 318  
ID ABO50573 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 319  
ID ABR79697 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 320  
ID ABM16959 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 321  
ID ABO17991 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 322  
ID ABO20943 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 323  
ID ABR96902 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US200304462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 324  
ID ABM12257 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 325  
ID ABM16349 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 326  
ID ABM24216 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 327  
ID ABM14697 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 328  
ID ABM04578 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 329  
ID ABM05767 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 330  
ID ABM09207 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 331  
ID ABO39247 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 332  
ID ABM75512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 333  
ID ABM25436 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 334  
ID ABM19946 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 335  
ID ABO46852 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 336  
ID ABO47157 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 337  
ID ADA83271 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 338  
ID ABR71588 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 339  
ID ABR72198 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 340  
ID ABR98537 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 341  
ID ABO06907 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 342  
ID ABR84860 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 343  
ID ABR73418 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 344  
ID ABR76512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 345  
ID ABR73113 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 346  
ID ABR72433 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 347  
ID ARM18179 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 348  
ID ABO20638 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 349  
ID ABO25381 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 350  
ID ABO25686 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 351  
ID ABR94095 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 352  
ID ABR80002 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 353  
ID ABM11342 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 354  
ID ABO32949 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 355  
ID ABO30655 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 356  
ID ABO30960 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 357  
ID ABM27266 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 358  
ID ABM30011 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 359  
ID ABM05547 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 360  
ID ABM15612 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 361  
ID ABM08597 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 362  
ID ABO42297 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 363  
ID ABO38027 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 364  
ID ABO45937 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 365  
ID ABO66740 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 366  
ID ADB20314 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 367  
ID AEM19641 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 368  
ID ABO49353 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 369  
ID ABO49658 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 370  
ID ADA78566 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003073181-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 371  
ID ABO34328 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO 1411.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 372  
ID ABR8215 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003086720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 373  
ID ADA00383 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO 411.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 374  
ID ABM26961 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 375  
ID ABM03358 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003086763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 376  
ID ABO39857 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 377  
ID ABO49963 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 7; Length 440;  
RESULT 378  
ID ABO50878 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 7; Length 440;  
RESULT 379  
ID ABO5334 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036126-A1.  
PD 20-FEB-2003.

Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 380  
ID ABR74638 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 381  
ID ABO44449 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 382  
ID ABR77117 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 383  
ID ABM17874 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 384  
ID ABR5925 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 385  
ID ABO21858 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 386  
ID ABO20028 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 387  
ID ABO24331 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 388  
ID ABR86080 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 389  
ID ABM10732 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064455-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 390  
ID ABM76731 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 391  
ID ABR89435 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 392  
ID ABM12562 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 393  
ID ABM05852 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 394  
ID ABO34977 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 395  
ID ABM03053 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 396  
ID ABM19031 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 397  
ID ABM19336 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 398  
ID ABO46547 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 399  
ID ABO49048 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 400  
ID ABR69091 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 401  
ID ABR89130 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 402  
ID ABR7503 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 403  
ID ABR74333 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 404  
ID ABR018601 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 405  
ID ABR80307 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 406  
ID ABR01528 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 407  
ID ABR02138 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 408  
ID ABR87300 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 409  
ID ABM12867 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 410  
ID ABM30621 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 411  
ID ABM24521 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 412  
ID ABO29435 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 413  
ID ABO31265 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 414  
ID ABM14392 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 415  
ID ABM09817 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 416  
ID ABO38942 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 417  
ID ABM34707 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104538-A1.

PD 05-JUN-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 418  
ID ABO51183 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 419  
ID ABO04009 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 420  
ID ABO10479 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 421  
ID ABR77722 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 422  
ID ABR78932 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 423  
ID ABO24026 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 424  
ID ABR93790 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 425  
ID ABO1833 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 426  
ID ABR78256 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 427  
ID ABO33473 standard; protein; 440 AA.

DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073129-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 428  
ID ABR90045 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 429  
ID ABM27571 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 430  
ID ABM13172 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 431  
ID ABO31875 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 432  
ID ABM14087 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068683-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 433  
ID ABM08292 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 434  
ID ABO40162 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068681-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 435  
ID ABM74597 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 436  
ID ABM33792 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096358-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 437  
ID ABM20251 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 438  
ID ABO48743 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 439  
ID ABR72808 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 440  
ID ABO15450 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 441  
ID ABR8165 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 442  
ID ABO15145 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 443  
ID ABO17280 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 444  
ID ABO19663 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 445  
ID ABM17569 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 446  
ID ABJ72135 standard; protein; 440 AA.  
DE Human membrane bound receptor/protein PRO1411 amino acid sequence.

PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 447  
ID ABR85470 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 448  
ID ABM77036 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 449  
ID ABO28215 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 450  
ID ABM22996 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 451  
ID ABM30316 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 452  
ID ABM21776 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 453  
ID ABM21471 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 454  
ID ABM15002 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 455  
ID ABO41077 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068694-A1.



PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 456  
ID ABO36807 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 457  
ID ABO37417 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 458  
ID ABO75207 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 459  
ID ABO33487 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 460  
ID ABO46242 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 461  
ID ADA82637 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 462  
ID ADB85625 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 463  
ID ADB83646 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 464  
ID ADB80752 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088068-A1.  
PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 465  
ID ADB73293 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 466  
ID ABO31841 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 467  
ID ADB78375 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 468  
ID ABO31231 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 469  
ID ADB85023 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 470  
ID ADB78129 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 471  
ID ADB85945 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 472  
ID ABO32146 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 473  
ID ABO32451 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 474  
ID ABO32451 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;

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Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 474
ID ADB87195 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 475
ID ADB84777 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 476
ID ADB68304 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 477
ID ADB68111 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 478
ID ADB31536 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 479
ID ADB30926 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 480
ID ADB83892 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 481
ID ADB73047 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 482
ID ADB90928 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 483
ID ADC07008 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 484
ID ADC17921 standard; protein; 440 AA.
DE Human PRO polypeptide #15.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 485
ID ADC17187 standard; protein; 440 AA.
DE Mammalian PRO polypeptide (SeqID 52).
PN US2003055143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 486
ID ADC14895 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 487
ID ADC36885 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 488
ID ADC52380 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 489
ID ADC21875 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 490
ID ADC49906 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 491
ID ADC49105 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 492
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ID ADC49622 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 493  
ID ADC47483 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 494  
ID ADC47228 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 495  
ID ADC78103 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 496  
ID ADD06338 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 497  
ID ADD05675 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 498  
ID ADD10439 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 499  
ID ADC77857 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 500  
ID ADD11399 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 501  
ID ADD50820 standard; protein; 440 AA.

DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 502  
ID ADD51066 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 503  
ID ADD70567 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 504  
ID ADD39644 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 505  
ID ADD70090 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 506  
ID ADD37192 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 507  
ID ADD36056 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 508  
ID ADD38211 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 509  
ID ADD39167 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 510  
ID ADD50547 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.

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PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 511
ID ADD50301 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 512
ID ADD38690 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 513
ID ADD40121 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 514
ID ADD51312 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 515
ID ADE50342 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 516
ID ADE19954 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 517
ID ADE49865 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 518
ID ADE21423 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 519
ID ADF29848 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003204053-A1.

PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 520
ID ADF5741 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 521
ID ADG01057 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 522
ID ADG08610 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 523
ID ADG02670 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 524
ID ADG01377 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 525
ID ADF95552 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 526
ID ADF95231 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 527
ID ADG12367 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 528
ID ADH24084 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 529  
ID ADH34110 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 530  
ID ADH29943 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 531  
ID ADH23914 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 532  
ID ADH09027 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 533  
ID ADG8318 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 534  
ID ADH24594 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 535  
ID ADH37450 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO411.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 536  
ID ADH02039 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 537  
ID ADH37620 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO411.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;

Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 538  
ID ADG85658 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 539  
ID ADH24254 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 540  
ID ADH38548 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 541  
ID ADG63787 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO1411.  
PN US2003170721-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 542  
ID ADG83669 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 543  
ID ADH29477 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 544  
ID ADH27593 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 545  
ID ADH37790 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO1411.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 546  
ID ADH37967 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO411.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

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RESULT 547
ID ADH57387 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 548
ID ADH53529 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 549
ID ADH53699 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 550
ID ADH52035 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 551
ID ADH49890 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 552
ID ADI25400 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 553
ID ADH90193 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 554
ID ADI25570 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 555
ID ADH97744 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 556
ID ADH98084 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 557
ID ADH99245 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003085142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 558
ID ADI11949 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 559
ID ADH90023 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 560
ID ADH98424 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 561
ID ADI11099 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 562
ID ADI11609 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 563
ID ADH98254 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 564
ID ADH98594 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 565
ID ADH98084 standard; protein; 440 AA.
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DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 566  
ID ADI05072 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 567  
ID ADI03422 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO411.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 568  
ID ADI04817 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 569  
ID ADH78271 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181658-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 570  
ID ADI19615 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 571  
ID ADH90363 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 572  
ID ADI03082 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 573  
ID ADH77931 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 574  
ID ADH97914 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.

PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 575  
ID ADI01299 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 576  
ID ADI01994 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 577  
ID ADI03252 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 578  
ID ADI11439 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 579  
ID ADI02341 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 580  
ID ADI11779 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 581  
ID ADI05416 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 582  
ID ADH79488 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 583  
ID ADI19445 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181675-A1.

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PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 584
ID ADI05246 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 585
ID ADH79658 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 586
ID ADI01484 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 587
ID ADI01654 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 588
ID ADI01824 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 589
ID ADH79828 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 590
ID ADI04646 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 591
ID ADI02782 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 592
ID ADH78101 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 593
ID ADI25740 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 594
ID ADI25910 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 595
ID ADK65422 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 596
ID ADH98764 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 597
ID ADH80005 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 598
ID ADM30342 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 599
ID ADL93736 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 600
ID ADC48859 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 601
ID ADC52190 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 602  
ID ADE21030 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 603  
ID ADE05874 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 604  
ID ADD75103 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 605  
ID ADD75849 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 606  
ID ADD85081 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 607  
ID ADD86907 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 608  
ID ADE20784 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 609  
ID ADE39081 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 610  
ID ADE05628 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;

Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 611  
ID ADD73613 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 612  
ID ADD78453 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 613  
ID ADE41400 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 614  
ID ADE74339 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 615  
ID ADE21276 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100736-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 616  
ID ADD77391 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100732-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 617  
ID ADE20538 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100733-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 618  
ID ADD75603 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100064-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 619  
ID ADD74119 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100708-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 620  
ID ADD75603 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100708-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

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ID ADD74365 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 621
ID ADD76095 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 622
ID ADD85587 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 623
ID ADE05136 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 624
ID ADD75349 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 625
ID ADD76893 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 626
ID ADD86661 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 627
ID ADE41201 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 628
ID ADD78129 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 629
ID ADE74951 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100724-A1.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 630
ID ADD77637 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 631
ID ADD77893 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 632
ID ADD85341 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 633
ID ADD73873 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 634
ID ADD74611 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 635
ID ADD77139 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 636
ID ADD85833 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 637
ID ADE05382 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 638
ID ADD74857 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100724-A1.
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PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 639  
ID ADE96425 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 640  
ID ADF25736 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 641  
ID ADF24635 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 642  
ID ADF29371 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 643  
ID ADE96902 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 644  
ID ADG05669 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 645  
ID ADG27223 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 646  
ID ADF96164 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 647  
ID ADG11286 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 648  
ID ADG04435 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 649  
ID ADG12065 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 650  
ID ADG00595 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 651  
ID ADF94622 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 652  
ID ADG06718 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 653  
ID ADH06622 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 654  
ID ADH06452 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 655  
ID ADG68873 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 656  
ID ADH27763 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;  
RESULT 657  
ID ADH27763 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

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Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 657
ID ADH25104 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 658
ID ADH33736 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 659
ID ADG82851 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 660
ID ADH02940 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 661
ID ADH02379 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 662
ID ADH07986 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 663
ID ADG69383 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 664
ID ADH39204 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 665
ID ADH03894 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 666
ID ADH03417 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 667
ID ADH26132 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 668
ID ADG83944 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 669
ID ADH39062 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 670
ID ADG85488 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 671
ID ADG63636 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 672
ID ADH06282 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 673
ID ADH30112 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 674
ID ADH24424 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 675
ID ADH03894 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
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ID ADH33101 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 676  
ID ADG69553 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 677  
ID ADH07816 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 678  
ID ADG85928 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 679  
ID ADH39374 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 680  
ID ADH33566 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 681  
ID ADH33906 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 682  
ID ADH01116 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 683  
ID ADG69723 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 684  
ID ADH02209 standard; protein; 440 AA.

DE Human PRO polypeptide #26.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 685  
ID ADG69213 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 686  
ID ADG85998 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 687  
ID ADH24934 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 688  
ID ADH39551 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 689  
ID ADH02549 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 690  
ID ADG69043 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 691  
ID ADH07646 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 692  
ID ADG86168 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 693  
ID ADH24764 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.

PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 694  
ID ADH25812 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 695  
ID ADH38378 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 696  
ID ADH57217 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 697  
ID ADH43583 standard; protein; 440 AA.  
DE Human PRO polypeptide #75.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 698  
ID ADH52323 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 699  
ID ADG34152 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 700  
ID ADH04371 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2004005626-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 701  
ID ADH49571 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 702  
ID ADH90533 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181700-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 703  
ID ADI11269 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 704  
ID ADH98934 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 705  
ID ADI33622 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 706  
ID ADI02164 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 707  
ID ADH69716 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2004019183-A1.  
PD 29-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 708  
ID ADH61372 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 709  
ID ADH90703 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 710  
ID ADI29877 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 711  
ID ADJ54840 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2004023321-A1.  
PD 05-FEB-2004.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 712  
ID ADJ98578 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 713  
ID ADJ98748 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 714  
ID ADH78907 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 715  
ID ADJ99141 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 716  
ID ADJ99111 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 717  
ID ADJ98929 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 718  
ID ADH79077 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 719  
ID ADK00937 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 720  
ID ADK14458 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 721  
ID ADM27274 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 722  
ID ADK82928 standard; protein; 440 AA.  
DE Human PRO polypeptide #75.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 723  
ID ADJ64611 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 724  
ID ADK66632 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 725  
ID ADM31507 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 726  
ID ADM36554 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 727  
ID ADM40359 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 728  
ID ADM80907 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 729  
ID ADL94571 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;

Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 730  
ID AON37967 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 731  
ID ADL32808 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 99.7%; Score 2357; DB 7; Length 440;  
Best Local Similarity 99.8%; Pred. No. 5.5e-137;  
RESULT 732  
ID AAB38324 standard; protein; 387 AA.  
DE Human secreted protein encoded by gene 4 clone HKAJK47.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 85.9%; Score 2030; DB 3; Length 387;  
Best Local Similarity 87.5%; Pred. No. 6e-117;  
RESULT 733  
ID AAY50941 standard; protein; 479 AA.  
DE Human adult skin cDNA clone vd4\_1 derived protein.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 95.1%; Score 2010.5; DB 3; Length 479;  
Best Local Similarity 87.6%; Pred. No. 1.2e-115;  
RESULT 734  
ID ABO27306 standard; protein; 372 AA.  
DE Human secreted/transmembrane polypeptide PRO411.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 83.1%; Score 1963; DB 6; Length 372;  
Best Local Similarity 84.5%; Pred. No. 7.5e-113;  
RESULT 735  
ID ABO34192 standard; protein; 372 AA.  
DE Human secreted/transmembrane polypeptide PRO 1411.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 83.1%; Score 1963; DB 6; Length 372;  
Best Local Similarity 84.5%; Pred. No. 7.5e-113;  
RESULT 736  
ID AAY50940 standard; protein; 369 AA.  
DE Human adult skin cDNA clone vd3\_1 derived protein #2.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 81.5%; Score 1925.5; DB 3; Length 369;  
Best Local Similarity 83.4%; Pred. No. 1.5e-110;  
RESULT 737  
ID AAY50939 standard; protein; 358 AA.  
DE Human adult skin cDNA clone vd3\_1 derived protein #1.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 71.6%; Score 1692; DB 3; Length 358;  
Best Local Similarity 95.8%; Pred. No. 3.2e-96;  
RESULT 738  
ID ADP07783 standard; protein; 186 AA.  
DE Human secreted protein, seq id 266.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 37.1%; Score 875.5; DB 8; Length 186;  
Best Local Similarity 92.3%; Pred. No. 2.5e-46;

RESULT 739  
ID AAY60056 standard; protein; 230 AA.  
DE Human endometrium tumour EST encoded protein 116.  
PN DE19817948-A1.  
PD 21-OCT-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 28.3%; Score 669; DB 2; Length 230;  
Best Local Similarity 98.4%; Pred. No. 1.5e-33;  
RESULT 740  
ID ABO23519 standard; protein; 1079 AA.  
DE Mycobacterium tuberculosis outlier protein #3.  
PN US2003039963-A1.  
PD 27-FEB-2003.  
PA (BRAH/) BRAHMACHARI S K.  
PA (RAMA/) RAMACHANDRAN S.  
PA (NAND/) NANDI T.  
PA (BHIM/) BHIMARAO C.  
Query Match 19.1%; Score 450.5; DB 7; Length 1079;  
Best Local Similarity 30.5%; Pred. No. 1.7e-19;  
RESULT 741  
ID ABU36481 standard; protein; 1306 AA.  
DE Protein encoded by Prokaryotic essential gene #22008.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 18.6%; Score 439.5; DB 6; Length 1306;  
Best Local Similarity 30.9%; Pred. No. 9.6e-19;  
RESULT 742  
ID AAO16495 standard; protein; 400 AA.  
DE Kukulcania hibernalis spider silk protein #2.  
PN WO200299082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 18.4%; Score 434; DB 6; Length 400;  
Best Local Similarity 33.4%; Pred. No. 6.8e-19;  
RESULT 743  
ID ABU36971 standard; protein; 1381 AA.  
DE Protein encoded by Prokaryotic essential gene #22498.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 17.6%; Score 415.5; DB 6; Length 1381;  
Best Local Similarity 29.9%; Pred. No. 3e-17;  
RESULT 744  
ID ABM15873 standard; protein; 484 AA.  
DE Mycobacterium tuberculosis mycobacterial antigen protein SEQ ID NO:111.  
PN WO2003033530-A2.  
PD 24-APR-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Query Match 17.5%; Score 412.5; DB 6; Length 484;  
Best Local Similarity 33.6%; Pred. No. 1.7e-17;  
RESULT 745  
ID ABU36943 standard; protein; 484 AA.  
DE Protein encoded by Prokaryotic essential gene #22470.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 17.5%; Score 412.5; DB 6; Length 484;  
Best Local Similarity 33.6%; Pred. No. 1.7e-17;  
RESULT 746  
ID ABO23518 standard; protein; 484 AA.  
DE Mycobacterium tuberculosis outlier protein #2..  
PN US2003039963-A1.  
PD 27-FEB-2003.  
PA (BRAH/) BRAHMACHARI S K.  
PA (RAMA/) RAMACHANDRAN S.  
PA (NAND/) NANDI T.  
PA (BHIM/) BHIMARAO C.  
Query Match 17.5%; Score 412.5; DB 7; Length 484;  
Best Local Similarity 33.6%; Pred. No. 1.7e-17;  
RESULT 747  
ID AAM16105 standard; protein; 357 AA.  
DE Peptide #2539 encoded by probe for measuring cervical gene expression.



PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 748  
ID ABB35090 standard; peptide; 357 AA.  
DE Peptide #2596 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 749  
ID AAM28596 standard; protein; 357 AA.  
DE Peptide #2633 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 750  
ID ABB29912 standard; peptide; 357 AA.  
DE Peptide #2563 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 751  
ID ABB20509 standard; protein; 357 AA.  
DE Protein #2508 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 752  
ID AAM68282 standard; protein; 357 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28588.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 753  
ID AAM55912 standard; protein; 357 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28017.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 754  
ID ABB49940 standard; peptide; 357 AA.  
DE Human liver peptide, SEQ ID NO 28588.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 755  
ID AAM03832 standard; protein; 357 AA.  
DE Peptide #2514 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 756  
ID ABB37823 standard; peptide; 357 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 27488.  
PN WO200186003-A2.

PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 5; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 757  
ID ABB36734 standard; protein; 532 AA.  
DE Protein encoded by Prokaryotic essential gene #22261.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 17.1%; Score 404.5; DB 6; Length 532;  
Best Local Similarity 32.2%; Pred. No. 5.8e-17;  
RESULT 758  
ID AAB80940 standard; protein; 1177 AA.  
DE SLPIII protein comprising the gagags of silk fibroin.  
PN WO8803533-A.  
PD 19-MAY-1988.  
PA (SYTR) SYNTRO CORP.  
Query Match 17.0%; Score 402.5; DB 1; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 759  
ID AAR05307 standard; protein; 1177 AA.  
DE SLP III (Silk-fibroin like protein).  
PN WO9005177-A.  
PD 17-MAY-1990.  
PA (SYTR) SYNTRO CORP.  
Query Match 17.0%; Score 402.5; DB 2; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 760  
ID AAR95105 standard; protein; 1177 AA.  
DE Silk like protein (SLP)III.  
PN US5514581-A.  
PD 07-MAY-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 2; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 761  
ID AAW26342 standard; protein; 1177 AA.  
DE Silk-like protein slpIII.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 2; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 762  
ID AAY78277 standard; peptide; 1177 AA.  
DE SLPIII amino acid sequence SEQ ID NO:64.  
PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 3; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 763  
ID AAB63995 standard; protein; 1177 AA.  
DE SLPIII protein sequence SEQ ID 31.  
PN US6140072-A.  
PD 31-OCT-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 4; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 764  
ID AAB72725 standard; protein; 1177 AA.  
DE Repetitive protein polymer protein sequence #25.  
PN US6184348-B1.  
PD 06-FEB-2001.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 4; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 765  
ID ABB69267 standard; protein; 1177 AA.  
DE Silk-like protein SLPIII.  
PN US6355776-B1.  
PD 12-MAR-2002.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 5; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 766  
ID ADE44959 standard; protein; 1177 AA.  
DE Silk fibroin protein repeating peptide related protein seq id 64.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 7; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 767  
ID AAR41007 standard; protein; 1178 AA.  
DE Silk-like protein Slp-III multimer.  
PN US5243038-A.  
PD 07-SEP-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 2; Length 1178;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 768  
ID AAW53518 standard; protein; 1178 AA.  
DE Amino acid sequence of the synthetic SlpIII protein.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 2; Length 1178;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 769  
ID AAP82962 standard; protein; 1059 AA.  
DE SLP4 protein comprising gagags of silk fibroin.  
PN WO8803533-A.  
PD 19-MAY-1988.  
PA (SYTR) SYNTRO CORP.  
Query Match 17.0%; Score 401; DB 1; Length 1059;  
Best Local Similarity 30.4%; Pred. No. 1.8e-16;  
RESULT 770  
ID AAW53524 standard; protein; 1023 AA.  
DE Amino acid sequence of the SLP4 protein.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 16.9%; Score 399; DB 2; Length 1023;  
Best Local Similarity 30.4%; Pred. No. 2.3e-16;  
RESULT 771  
ID AAR41013 standard; protein; 1059 AA.  
DE SLP4 multimeric protein.  
PN US5243038-A.  
PD 07-SEP-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 16.9%; Score 399; DB 2; Length 1059;  
Best Local Similarity 30.4%; Pred. No. 2.4e-16;  
RESULT 772  
ID AAW26348 standard; protein; 1059 AA.  
DE SLP4 synthetic protein.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 16.9%; Score 399; DB 2; Length 1059;  
Best Local Similarity 30.4%; Pred. No. 2.4e-16;  
RESULT 773  
ID AAW78283 standard; protein; 1101 AA.  
DE SLP4 amino acid sequence SEQ ID NO:83.  
PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 16.9%; Score 399; DB 3; Length 1101;  
Best Local Similarity 30.4%; Pred. No. 2.5e-16;  
RESULT 774  
ID AAG69273 standard; protein; 1101 AA.  
DE Silk/Elastin-like protein SLP4.  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 16.9%; Score 399; DB 5; Length 1101;  
Best Local Similarity 30.4%; Pred. No. 2.5e-16;  
RESULT 775  
ID ADE44978 standard; protein; 1101 AA.  
DE Recombinant structural protein SLP4 protein seq id 83.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 16.9%; Score 399; DB 7; Length 1101;  
Best Local Similarity 30.4%; Pred. No. 2.5e-16;  
RESULT 776  
ID ABU36550 standard; protein; 923 AA.  
DE Protein encoded by Prokaryotic essential gene #22077.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 16.6%; Score 392.5; DB 6; Length 923;  
Best Local Similarity 27.7%; Pred. No. 5.3e-16;  
RESULT 777  
ID ABP53453 standard; protein; 1062 AA.  
DE Pre-gelled protein Polymer SLP3 related amino acid sequence #2.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPF/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 16.4%; Score 386.5; DB 5; Length 1062;  
Best Local Similarity 31.5%; Pred. No. 1.4e-15;  
RESULT 778  
ID ABU36827 standard; protein; 778 AA.  
DE Protein encoded by Prokaryotic essential gene #22354.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 16.3%; Score 386; DB 6; Length 778;  
Best Local Similarity 31.2%; Pred. No. 1.1e-15;  
RESULT 779  
ID AAY28843 standard; protein; 641 AA.  
DE Epstein Barr Virus Nuclear Antigen 1 (EBNA 1).  
PN WO9947647-A1.  
PD 23-SEP-1999.  
PA (PHAR-) PHARMACOEPIA INC.  
Query Match 16.2%; Score 383; DB 2; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
RESULT 780  
ID AAY95856 standard; protein; 641 AA.  
DE Epstein Barr virus nuclear antigen 1 protein (EBNA1).  
PN WO200047778-A1.  
PD 17-AUG-2000.  
PA (PHAR-) PHARMACOEPIA INC.  
Query Match 16.2%; Score 383; DB 3; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
RESULT 781  
ID AAB62332 standard; protein; 641 AA.  
DE EBV tethering protein EBNA1.  
PN WO200125484-A2.  
PD 12-APR-2001.  
PA (UNMI) UNIV MICHIGAN.  
Query Match 16.2%; Score 383; DB 4; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
RESULT 782  
ID ABP72663 standard; protein; 641 AA.  
DE Epstein-Barr virus nuclear antigen 1.  
PN WO2003018754-A2.  
PD 06-MAR-2003.  
PA (NEUR-) NEURONZ LTD.  
PA (NEUR-) NEURONZ BIOSCIENCES INC.  
Query Match 16.2%; Score 383; DB 6; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
RESULT 783  
ID AAE34812 standard; protein; 641 AA.  
DE Epstein-barr virus nuclear antigen 1 (EBNA1).  
PN WO200290558-A1.  
PD 14-NOV-2002.

PA (FITB-) FIT BIOTECH OYJ PLC.  
 Query Match 16.2%; Score 383; DB 6; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 784  
 ID ADK65581 standard; protein; 641 AA.  
 DE Human herpesvirus 4 nuclear antigen-1 protein.  
 PN DE10207135-A1.  
 PD 11-SEP-2003.  
 PA (EURO-) EUROIMMUN GMBH.  
 Query Match 16.2%; Score 383; DB 7; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 785  
 ID ADJ57052 standard; protein; 641 AA.  
 DE Epstein-Barr virus nuclear antigen 1.  
 PN WO2004007536-A2.  
 PD 22-JAN-2004.  
 PA (AFFI-) AFFINIUM PHARM INC.  
 Query Match 16.2%; Score 383; DB 8; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 786  
 ID ADP12515 standard; protein; 641 AA.  
 DE Protein encoded by mRNA of the invention #125.  
 PN WO2004042346-A2.  
 PD 21-MAY-2004.  
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
 Query Match 16.2%; Score 383; DB 8; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 787  
 ID AQ94586 standard; protein; 641 AA.  
 DE Epstein-Barr virus EBNA1 protein.  
 PN US2004141995-A1.  
 PD 22-JUL-2004.  
 PA (WANG/) WANG R.  
 PA (VOOK/) VOOK K.  
 Query Match 16.2%; Score 383; DB 8; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 788  
 ID ABU36438 standard; protein; 837 AA.  
 DE Protein encoded by Prokaryotic essential gene #21965.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 16.1%; Score 380.5; DB 6; Length 837;  
 Best Local Similarity 30.5%; Pred. No. 2.7e-15;  
 RESULT 789  
 ID AP53456 standard; protein; 996 AA.  
 DE Pre-gelated protein polymer SLP4 related amino acid sequence #2.  
 PN US2002045567-A1.  
 PD 18-APR-2002.  
 PA (CAPP/) CAPPELLO J.  
 PA (STED/) STEDRONSKY E R.  
 Query Match 16.0%; Score 379; DB 5; Length 996;  
 Best Local Similarity 31.8%; Pred. No. 3.9e-15;  
 RESULT 790  
 ID AAE18319 standard; protein; 1002 AA.  
 DE Silk-like protein, SLP4.  
 PN WO200200016-A1.  
 PD 03-JAN-2002.  
 PA (LUMI-) LUMINIS PTY LTD.  
 PA (SAUR-) SOUTH AUSTRALIAN RES & DEV INST.  
 Query Match 16.0%; Score 379; DB 5; Length 1002;  
 Best Local Similarity 31.8%; Pred. No. 3.9e-15;  
 RESULT 791  
 ID ABU36945 standard; protein; 588 AA.  
 DE Protein encoded by Prokaryotic essential gene #22472.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 16.0%; Score 378; DB 6; Length 588;  
 Best Local Similarity 30.1%; Pred. No. 2.7e-15;  
 RESULT 792  
 ID ADM40790 standard; protein; 588 AA.  
 DE Mycobacterial disease detection method related RV3367 protein.

PN WO2003073101-A2.  
 PD 04-SEP-2003.  
 PA (UVNY ) UNIV NEW YORK STATE.  
 Query Match 16.0%; Score 378; DB 7; Length 588;  
 Best Local Similarity 30.1%; Pred. No. 2.7e-15;  
 RESULT 793  
 ID AAW27178 standard; protein; 646 AA.  
 DE Nephila clavipes spider silk protein.  
 PN WO9708315-A1.  
 PD 06-MAR-1997.  
 PA (BASE/) BASEL R M.  
 PA (ELIO/) ELION G R.  
 Query Match 16.0%; Score 378; DB 2; Length 646;  
 Best Local Similarity 29.0%; Pred. No. 3e-15;  
 RESULT 794  
 ID ADB61321 standard; protein; 646 AA.  
 DE Spider silk related MasPi protein.  
 PN WO2003060099-A2.  
 PD 24-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 PA (ALWA/) ALWATTARI A.  
 Query Match 16.0%; Score 378; DB 7; Length 646;  
 Best Local Similarity 31.5%; Pred. No. 3e-15;  
 RESULT 795  
 ID ADC35240 standard; protein; 646 AA.  
 DE MasPi silk protein, SEQ ID 1.  
 PN WO2003057727-A1.  
 PD 17-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 Query Match 16.0%; Score 378; DB 7; Length 646;  
 Best Local Similarity 31.5%; Pred. No. 3e-15;  
 RESULT 796  
 ID ADM46149 standard; protein; 646 AA.  
 DE Nephila clavipes spidroin 1 (MasPi) protein.  
 PN WO2003057720-A2.  
 PD 17-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 Query Match 16.0%; Score 378; DB 7; Length 646;  
 Best Local Similarity 31.5%; Pred. No. 3e-15;  
 RESULT 797  
 ID AAR95107 standard; protein; 1038 AA.  
 DE Fibronectin cell binding seq. contg. silk like protein (SLP)III.  
 PN US5514581-A.  
 PD 07-MAY-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.9%; Score 376.5; DB 2; Length 1038;  
 Best Local Similarity 28.5%; Pred. No. 5.7e-15;  
 RESULT 798  
 ID AAB63997 standard; protein; 1038 AA.  
 DE FCB-SLP protein from pSY1521 SEQ ID 36.  
 PN US6140072-A.  
 PD 31-OCT-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.9%; Score 376.5; DB 4; Length 1038;  
 Best Local Similarity 28.5%; Pred. No. 5.7e-15;  
 RESULT 799  
 ID AAB72727 standard; protein; 1038 AA.  
 DE Repetitive protein polymer protein sequence #27.  
 PN US6184348-B1.  
 PD 06-FEB-2001.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.9%; Score 376.5; DB 4; Length 1038;  
 Best Local Similarity 28.5%; Pred. No. 5.7e-15;  
 RESULT 800  
 ID ADO08760 standard; protein; 452 AA.  
 DE Novel surgical dressing-related protein SeqID47.  
 PN JE2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN ) SANYO CHEM IND LTD.  
 PA (ALCA-) ALCARE KK.  
 Query Match 15.9%; Score 375.5; DB 8; Length 452;  
 Best Local Similarity 29.9%; Pred. No. 3e-15;  
 RESULT 801

ID ABU36682 standard; protein; 914 AA.  
DE Protein encoded by Prokaryotic essential gene #22209.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.9%; Score 375; DB 6; Length 914;  
Best Local Similarity 33.0%; Pred. No. 6.3e-15;  
RESULT 802  
ID AAM50037 standard; protein; 1255 AA.  
DE N. clavipes spidroin synthetic homologue SO1S01 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 15.8%; Score 374; DB 5; Length 1255;  
Best Local Similarity 30.5%; Pred. No. 9.8e-15;  
RESULT 803  
ID AAM50039 standard; protein; 1880 AA.  
DE N. clavipes spidroin synthetic homologue SO1S01S01 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 15.8%; Score 374; DB 5; Length 1880;  
Best Local Similarity 30.5%; Pred. No. 1.4e-14;  
RESULT 804  
ID RAO16497 standard; protein; 520 AA.  
DE Argiope trifasciata spider silk protein #1.  
PN WO200299082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.8%; Score 373.5; DB 6; Length 520;  
Best Local Similarity 30.0%; Pred. No. 4.5e-15;  
RESULT 805  
ID ABU36979 standard; protein; 584 AA.  
DE Protein encoded by Prokaryotic essential gene #22506.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.8%; Score 373.5; DB 6; Length 584;  
Best Local Similarity 32.3%; Pred. No. 5.1e-15;  
RESULT 806  
ID ABU36570 standard; protein; 667 AA.  
DE Protein encoded by Prokaryotic essential gene #22097.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.8%; Score 373.5; DB 6; Length 667;  
Best Local Similarity 28.5%; Pred. No. 5.7e-15;  
RESULT 807  
ID ADE28209 standard; protein; 203 AA.  
DE Human MDTT protein - SEQ ID 59.  
PN WO2003046152-A2.  
PD 05-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 15.8%; Score 373; DB 7; Length 203;  
Best Local Similarity 58.9%; Pred. No. 2e-15;  
RESULT 808  
ID ABU36802 standard; protein; 694 AA.  
DE Protein encoded by Prokaryotic essential gene #22329.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.7%; Score 372; DB 6; Length 694;  
Best Local Similarity 30.3%; Pred. No. 7.4e-15;  
RESULT 809  
ID ABU36862 standard; protein; 615 AA.  
DE Protein encoded by Prokaryotic essential gene #22389.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.7%; Score 371; DB 6; Length 615;  
Best Local Similarity 31.0%; Pred. No. 7.6e-15;  
RESULT 810  
ID AAY40097 standard; protein; 651 AA.  
DE Spider silk protein spidroine major 1.  
PN FR274588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 15.7%; Score 371; DB 2; Length 651;  
Best Local Similarity 30.1%; Pred. No. 8e-15;  
RESULT 811  
ID AAU11781 standard; protein; 651 AA.  
DE Spider natural silk protein Spidroin 1.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.7%; Score 371; DB 5; Length 651;  
Best Local Similarity 30.1%; Pred. No. 8e-15;  
RESULT 812  
ID AAR14308 standard; protein; 718 AA.  
DE N. clavipes dragline silk protein-1.  
PN EP452925-A.  
PD 23-OCT-1991.  
PA (UYWY-) UNIV OF WYOMING.  
Query Match 15.7%; Score 371; DB 2; Length 718;  
Best Local Similarity 30.1%; Pred. No. 8.8e-15;  
RESULT 813  
ID AAM53346 standard; protein; 718 AA.  
DE Nephila clavipes spider silk protein.  
PN US5728810-A.  
PD 17-MAR-1998.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.7%; Score 371; DB 2; Length 718;  
Best Local Similarity 30.1%; Pred. No. 8.8e-15;  
RESULT 814  
ID AAY59070 standard; protein; 718 AA.  
DE N. clavipes spider silk protein 1.  
PN US5989894-A.  
PD 23-NOV-1999.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.7%; Score 371; DB 3; Length 718;  
Best Local Similarity 30.1%; Pred. No. 8.8e-15;  
RESULT 815  
ID ABU36634 standard; protein; 491 AA.  
DE Protein encoded by Prokaryotic essential gene #22161.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.7%; Score 370.5; DB 6; Length 491;  
Best Local Similarity 28.3%; Pred. No. 6.6e-15;  
RESULT 816  
ID AAR81318 standard; protein; 980 AA.  
DE Adhesion protein.  
PN WO9519791-A1.  
PD 27-JUL-1995.  
PA (USNA) US SEC OF NAVY.  
PA (CELL-) CELLCO INC.  
Query Match 15.7%; Score 370.5; DB 2; Length 980;  
Best Local Similarity 29.6%; Pred. No. 1.3e-14;  
RESULT 817  
ID AAR05312 standard; protein; 1066 AA.  
DE Sequence encoding SLP-LI monomer (similar to silk fibroin).  
PN WO9005177-A.  
PD 17-MAY-1990.  
PA (SYTR) SYNTRO CORP.  
Query Match 15.7%; Score 370; DB 2; Length 1066;  
Best Local Similarity 27.9%; Pred. No. 1.5e-14;  
RESULT 818  
ID AAM50038 standard; protein; 989 AA.  
DE N. clavipes spidroin synthetic homologue SO1SM12 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 15.6%; Score 369.5; DB 5; Length 989;  
Best Local Similarity 30.8%; Pred. No. 1.5e-14;  
RESULT 819  
ID AAR41010 standard; protein; 2025 AA.

DE SLP1 multimeric protein.  
 PN US5243038-A.  
 PD 07-SEP-1993.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.6%; Score 369; DB 2; Length 2025;  
 Best Local Similarity 27.4%; Pred. No. 3.1e-14;  
 RESULT 820  
 ID AAP82959 standard; protein; 2107 AA.  
 DE SEPL1 protein comprising gagags of silk fibroin and gvgvp of elastin.  
 PN WO803533-A.  
 PD 19-MAY-1988.  
 PA (SYTR ) SYNTHRO CORP.  
 Query Match 15.6%; Score 369; DB 1; Length 2107;  
 Best Local Similarity 27.4%; Pred. No. 3.3e-14;  
 RESULT 821  
 ID AAY78287 standard; protein; 1011 AA.  
 DE SELPF amino acid sequence SEQ ID NO:94.  
 PN US6018030-A.  
 PD 23-JAN-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 367; DB 3; Length 1011;  
 Best Local Similarity 27.8%; Pred. No. 2.1e-14;  
 RESULT 822  
 ID AAG69277 standard; protein; 1011 AA.  
 DE Silk/Elastin-like protein SELPF.  
 PN US6355776-B1.  
 PD 12-MAR-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 367; DB 5; Length 1011;  
 Best Local Similarity 27.8%; Pred. No. 2.1e-14;  
 RESULT 823  
 ID ADE44989 standard; protein; 1011 AA.  
 DE Recombinant structural protein SELPF protein seq id 94.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 367; DB 7; Length 1011;  
 Best Local Similarity 27.8%; Pred. No. 2.1e-14;  
 RESULT 824  
 ID AAW26351 standard; protein; 1170 AA.  
 DE SELPF synthetic protein.  
 PN US5641648-A.  
 PD 24-JUN-1997.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 367; DB 2; Length 1170;  
 Best Local Similarity 27.8%; Pred. No. 2.5e-14;  
 RESULT 825  
 ID ABB67896 standard; protein; 610 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 30480.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 15.5%; Score 366; DB 4; Length 610;  
 Best Local Similarity 32.5%; Pred. No. 1.5e-14;  
 RESULT 826  
 ID AAE36887 standard; protein; 691 AA.  
 DE Dolomedes tenebrosus fibroin 2 protein.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UTWY-) UNIV WYOMING.  
 Query Match 15.5%; Score 366; DB 6; Length 691;  
 Best Local Similarity 27.0%; Pred. No. 1.7e-14;  
 RESULT 827  
 ID AAW53526 standard; protein; 695 AA.  
 DE Amino acid sequence of FCB-SLP1II protein.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 2; Length 695;  
 Best Local Similarity 27.3%; Pred. No. 1.7e-14;  
 RESULT 828  
 ID AAW26349 standard; protein; 766 AA.  
 DE FCB-SLP1II (57 kDa) synthetic protein.

PN US5641648-A.  
 PD 24-JUN-1997.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 2; Length 766;  
 Best Local Similarity 27.3%; Pred. No. 1.9e-14;  
 RESULT 829  
 ID AAY78285 standard; peptide; 766 AA.  
 DE FCB-SLP1II amino acid sequence SEQ ID NO:88.  
 PN US6018030-A.  
 PD 25-JAN-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 3; Length 766;  
 Best Local Similarity 27.3%; Pred. No. 1.9e-14;  
 RESULT 830  
 ID AAG69275 standard; protein; 766 AA.  
 DE Fibronectin FCB portion/silk-like protein, FCB-SLP1II #1.  
 PN US6355776-B1.  
 PD 12-MAR-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 5; Length 766;  
 Best Local Similarity 27.3%; Pred. No. 1.9e-14;  
 RESULT 831  
 ID ADE44983 standard; protein; 766 AA.  
 DE Recombinant structural protein FCB-SLP1II protein seq id 88.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 7; Length 766;  
 Best Local Similarity 27.3%; Pred. No. 1.9e-14;  
 RESULT 832  
 ID AAY78286 standard; protein; 979 AA.  
 DE FCB-SLP1II amino acid sequence SEQ ID NO:89.  
 PN US6018030-A.  
 PD 25-JAN-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 3; Length 979;  
 Best Local Similarity 27.3%; Pred. No. 2.4e-14;  
 RESULT 833  
 ID AAG69276 standard; protein; 979 AA.  
 DE Fibronectin FCB portion/silk-like protein, FCB-SLP1II #2.  
 PN US6355776-B1.  
 PD 12-MAR-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 5; Length 979;  
 Best Local Similarity 27.3%; Pred. No. 2.4e-14;  
 RESULT 834  
 ID ADE44984 standard; protein; 979 AA.  
 DE Recombinant structural protein FCB-SLP1II protein seq id 89.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 7; Length 979;  
 Best Local Similarity 27.3%; Pred. No. 2.4e-14;  
 RESULT 835  
 ID AAW26350 standard; protein; 1050 AA.  
 DE FCB-SLP1II (72 kDa) synthetic protein.  
 PN US5641648-A.  
 PD 24-JUN-1997.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 2; Length 1050;  
 Best Local Similarity 27.3%; Pred. No. 2.6e-14;  
 RESULT 836  
 ID AAW53527 standard; protein; 1170 AA.  
 DE Amino acid sequence of SELPF protein.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 2; Length 1170;  
 Best Local Similarity 27.8%; Pred. No. 2.8e-14;  
 RESULT 837  
 ID AAW50042 standard; protein; 630 AA.  
 DE N. Clavipes spidroin synthetic homologue SO1 protein.  
 PN DE10113781-A1.

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PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENTIK & KULTURPFLANZE.
Query Match 15.4%; Score 365.5; DB 5; Length 630;
Best Local Similarity 29.6%; Pred. No. 1.7e-14;
RESULT 838
ID AAM50047 standard; protein; 676 AA.
DE N. clavipes epidroin synthetic homologue SO1 protein #2.
PD D810113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENTIK & KULTURPFLANZE.
Query Match 15.5%; Score 365.5; DB 5; Length 676;
Best Local Similarity 29.6%; Pred. No. 1.8e-14;
RESULT 839
ID ABU36623 standard; protein; 576 AA.
DE Protein encoded by Prokaryotic essential gene #22150.
PD WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.4%; Score 365; DB 6; Length 576;
Best Local Similarity 30.2%; Pred. No. 1.7e-14;
RESULT 840
ID ABU36439 standard; protein; 591 AA.
DE Protein encoded by Prokaryotic essential gene #21966.
PD WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.4%; Score 365; DB 6; Length 591;
Best Local Similarity 29.4%; Pred. No. 1.7e-14;
RESULT 841
ID ABG69270 standard; protein; 2018 AA.
DE Silk/Elastin-like protein SELP1.
PD US6355776-B1.
PD 12-MAR-2002.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364.5; DB 5; Length 2018;
Best Local Similarity 27.4%; Pred. No. 5.9e-14;
RESULT 842
ID ADE44975 standard; protein; 2018 AA.
DE Recombinant structural protein SELPI protein seq id 80.
PD US2003083464-A1.
PD 01-MAY-2003.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364.5; DB 7; Length 2018;
Best Local Similarity 27.4%; Pred. No. 5.9e-14;
RESULT 843
ID AAY78280 standard; peptide; 2100 AA.
DE SELPI amino acid sequence SEQ ID NO:80.
PD US6018030-A.
PD 25-JAN-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364.5; DB 3; Length 2100;
Best Local Similarity 27.4%; Pred. No. 6.1e-14;
RESULT 844
ID ABU36540 standard; protein; 606 AA.
DE Protein encoded by Prokaryotic essential gene #22067.
PD WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.4%; Score 364; DB 6; Length 606;
Best Local Similarity 29.8%; Pred. No. 2e-14;
RESULT 845
ID AAR95112 standard; protein; 649 AA.
DE Silk like protein (SLP)-L2.
PD US5514581-A.
PD 07-MAY-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 2; Length 649;
Best Local Similarity 27.7%; Pred. No. 2.1e-14;
RESULT 846
ID AAB64002 standard; protein; 649 AA.
DE SLP-L1 protein SEQ ID 49.
PD US6140072-A.
PD 31-OCT-2000.
PA (ELIT-) ELITRA PHARM INC.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 4; Length 649;
Best Local Similarity 27.7%; Pred. No. 2.1e-14;
RESULT 847
ID AAB72732 standard; protein; 649 AA.
DE Repetitive protein polymer protein sequence #32.
PD US6184348-B1.
PD 06-FEB-2001.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 4; Length 649;
Best Local Similarity 27.7%; Pred. No. 2.1e-14;
RESULT 848
ID AAR95111 standard; protein; 784 AA.
DE Silk like protein (SLP)-L1.
PD US5514581-A.
PD 07-MAY-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 2; Length 784;
Best Local Similarity 31.3%; Pred. No. 2.6e-14;
RESULT 849
ID AAB64001 standard; protein; 784 AA.
DE SLP-L1 protein SEQ ID 48.
PD US6140072-A.
PD 31-OCT-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 4; Length 784;
Best Local Similarity 31.3%; Pred. No. 2.6e-14;
RESULT 850
ID AAB72731 standard; protein; 784 AA.
DE Repetitive protein polymer protein sequence #31.
PD US6184348-B1.
PD 06-FEB-2001.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 4; Length 784;
Best Local Similarity 31.3%; Pred. No. 2.6e-14;
RESULT 851
ID AAR05309 standard; protein; 946 AA.
DE SLP-L2 polymer (similar to silk fibroin).
PD WO9005177-A.
PD 17-MAY-1990.
PA (SYTR ) SYNTRO CORP.
Query Match 15.4%; Score 364; DB 2; Length 946;
Best Local Similarity 27.7%; Pred. No. 3.1e-14;
RESULT 852
ID AAW01496 standard; protein; 1018 AA.
DE Silk-like protein SLP-L3.0 polymer.
PD WO9501998-A2.
PD 19-JAN-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES.
Query Match 15.4%; Score 364; DB 2; Length 1018;
Best Local Similarity 30.5%; Pred. No. 3.3e-14;
RESULT 853
ID AAW26345 standard; protein; 2107 AA.
DE SELPI synthetic elastomeric protein.
PD US5641648-A.
PD 24-JUN-1997.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 2; Length 2107;
Best Local Similarity 27.4%; Pred. No. 6.6e-14;
RESULT 854
ID AAW53521 standard; protein; 2107 AA.
DE Amino acid sequence of the SELPI protein.
PD WO9810063-A1.
PD 12-MAR-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 2; Length 2107;
Best Local Similarity 27.4%; Pred. No. 6.6e-14;
RESULT 855
ID ABU36685 standard; protein; 639 AA.
DE Protein encoded by Prokaryotic essential gene #22212.
PD WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
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Query Match 15.4%; Score 363; DB 6; Length 639;  
Best Local Similarity 30.5%; Pred. No. 2.4e-14;  
RESULT 856  
ID AAR99057 standard; protein; 604 AA.  
DE Spider dragline variant, DP-1B.16 polymer.  
PN W09429450-A2.  
PD 22-DEC-1994.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.3%; Score 362; DB 2; Length 604;  
Best Local Similarity 29.7%; Pred. No. 2.7e-14;  
RESULT 857  
ID AAR95109 standard; protein; 1332 AA.  
DE Silk like protein (SLP)-C.  
PN US5514581-A.  
PD 07-MAY-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.3%; Score 362; DB 2; Length 1332;  
Best Local Similarity 28.3%; Pred. No. 5.7e-14;  
RESULT 858  
ID AAB63999 standard; protein; 1332 AA.  
DE SLP-C protein sequence SEQ ID 41.  
PN US6140072-A.  
PD 31-OCT-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.3%; Score 362; DB 4; Length 1332;  
Best Local Similarity 28.3%; Pred. No. 5.7e-14;  
RESULT 859  
ID AAB72729 standard; protein; 1332 AA.  
DE Repetitive protein polymer protein sequence #29.  
PN US6184348-B1.  
PD 06-FEB-2001.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.3%; Score 362; DB 4; Length 1332;  
Best Local Similarity 28.3%; Pred. No. 5.7e-14;  
RESULT 860  
ID AAR2960 standard; protein; 2055 AA.  
DE SELP2 protein comprising gagags of silk fibroin and gvgvp of elastin.  
PN W08803533-A.  
PD 19-MAY-1988.  
PA (SVTR) SYNTRO CORP.  
Query Match 15.3%; Score 360.5; DB 1; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.1e-13;  
RESULT 861  
ID ABU36590 standard; protein; 562 AA.  
DE Protein encoded by Prokaryotic essential gene #22117.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.2%; Score 360; DB 6; Length 562;  
Best Local Similarity 28.9%; Pred. No. 3.3e-14;  
RESULT 862  
ID ABB76672 standard; protein; 655 AA.  
DE Protein related to Bombyx mori silk fibroin.  
PN W0200240528-A1.  
PD 23-MAY-2002.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match 15.2%; Score 360; DB 5; Length 655;  
Best Local Similarity 28.7%; Pred. No. 3.8e-14;  
RESULT 863  
ID ABU36665 standard; protein; 1011 AA.  
DE Protein encoded by Prokaryotic essential gene #22192.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.2%; Score 359.5; DB 6; Length 1011;  
Best Local Similarity 31.2%; Pred. No. 6.2e-14;  
RESULT 864  
ID AAE36926 standard; protein; 490 AA.  
DE Nephila clavipes minor ampullate spidroin 1 consensus protein #1.  
PN W02003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.2%; Score 359; DB 6; Length 490;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;  
Best Local Similarity 27.9%; Pred. No. 3.3e-14;  
RESULT 865  
ID AAO16492 standard; protein; 525 AA.  
DE Phidippus audax fibronin 1 protein.  
PN W0200299082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.2%; Score 359; DB 6; Length 525;  
Best Local Similarity 28.9%; Pred. No. 3.6e-14;  
RESULT 866  
ID AAE36893 standard; protein; 525 AA.  
DE Phidippus audax fibroin 1 protein.  
PN W02003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.2%; Score 359; DB 6; Length 525;  
Best Local Similarity 28.9%; Pred. No. 3.6e-14;  
RESULT 867  
ID AAE36886 standard; protein; 854 AA.  
DE Delomedes tenebrosus fibroin 1 protein.  
PN W02003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.2%; Score 359; DB 6; Length 854;  
Best Local Similarity 26.2%; Pred. No. 5.7e-14;  
RESULT 868  
ID AAY40099 standard; protein; 615 AA.  
DE Spider silk protein spidroine minor 1.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 15.2%; Score 358.5; DB 2; Length 615;  
Best Local Similarity 28.7%; Pred. No. 4.4e-14;  
RESULT 869  
ID AAR41011 standard; protein; 2055 AA.  
DE SELP2 multimeric protein.  
PN US5243038-A.  
PD 07-SEP-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 2; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;  
RESULT 870  
ID AAW26346 standard; protein; 2055 AA.  
DE SELP2 synthetic elastomeric protein.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 2; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;  
RESULT 871  
ID AAW53522 standard; protein; 2055 AA.  
DE Amino acid sequence of the SELP2 protein.  
PN W09810083-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 2; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;  
RESULT 872  
ID AAY78281 standard; peptide; 2055 AA.  
DE SELP2 amino acid sequence SEQ ID NO:81.  
PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 3; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;  
RESULT 873  
ID ADE44976 standard; protein; 2055 AA.  
DE Recombinant structural protein SELP2 protein seq id 81.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 7; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;

RESULT 874  
ID AAR99053 standard; protein; 606 AA.  
DE Spider dragline variant, DP-1A.9 polymer.  
PN WO9429450-A2.  
PD 22-DEC-1994.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 29.2%; Pred. No. 4.7e-14;  
RESULT 875  
ID AAR99055 standard; protein; 606 AA.  
DE Spider dragline variant, DP-1B.9 polymer.  
PN WO9429450-A2.  
PD 22-DEC-1994.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 30.3%; Pred. No. 4.7e-14;  
RESULT 876  
ID AAY40101 standard; protein; 606 AA.  
DE Polymer of an analogue of spider silk protein spidroine major 1.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA ) L'OREAL SA.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 30.3%; Pred. No. 4.7e-14;  
RESULT 877  
ID AAY40102 standard; protein; 606 AA.  
DE Polymer of an analogue of spider silk protein spidroine major 1.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA ) L'OREAL SA.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 30.3%; Pred. No. 4.7e-14;  
RESULT 878  
ID AAY40100 standard; protein; 606 AA.  
DE Polymer of an analogue of spider silk protein spidroine major 1.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA ) L'OREAL SA.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 29.2%; Pred. No. 4.7e-14;  
RESULT 879  
ID AAU11793 standard; protein; 809 AA.  
DE Dragline protein 1 analogue DP-1B 8mer.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 5; Length 809;  
Best Local Similarity 30.3%; Pred. No. 6.2e-13;  
RESULT 880  
ID AAU11797 standard; protein; 818 AA.  
DE Dragline protein 1 analogue DP-1B/his tag 8mer.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 5; Length 818;  
Best Local Similarity 30.3%; Pred. No. 6.3e-14;  
RESULT 881  
ID AAU11794 standard; protein; 1617 AA.  
DE Dragline protein 1 analogue DP-1B 16mer.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 5; Length 1617;  
Best Local Similarity 30.3%; Pred. No. 1.2e-13;  
RESULT 882  
ID AAU11798 standard; protein; 1626 AA.  
DE Dragline protein 1 analogue DP-1B/his tag 16mer.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 5; Length 1626;  
Best Local Similarity 30.3%; Pred. No. 1.2e-13;  
RESULT 883

ID AAO16494 standard; protein; 761 AA.  
DE Kukulcania hibernalis spider silk protein #1.  
PN WO20029082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.1%; Score 357; DB 6; Length 761;  
Best Local Similarity 28.1%; Pred. No. 6.7e-14;  
RESULT 884  
ID ABG69271 standard; protein; 2055 AA.  
DE Silk/Elastin-like protein SELP2.  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.0%; Score 354.5; DB 5; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 2.5e-13;  
RESULT 885  
ID AAW01494 standard; protein; 945 AA.  
DE Silk-like protein SLP-F9 polymer.  
PN WO9501998-A2.  
PD 19-JAN-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES.  
Query Match 15.0%; Score 354; DB 2; Length 945;  
Best Local Similarity 25.6%; Pred. No. 1.3e-13;  
RESULT 886  
ID ABU34417 standard; protein; 505 AA.  
DE Protein encoded by Prokaryotic essential gene #19944.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.9%; Score 353; DB 6; Length 505;  
Best Local Similarity 32.4%; Pred. No. 8e-14;  
RESULT 887  
ID AAP82961 standard; protein; 2257 AA.  
DE SELP3 protein comprising gagags of silk fibroin and gvgvp of elastin.  
PN WO8803533-A.  
PD 19-MAY-1988.  
PA (SYTR ) SYNTRO CORP.  
Query Match 14.9%; Score 352.5; DB 1; Length 2257;  
Best Local Similarity 29.6%; Pred. No. 3.6e-13;  
RESULT 888  
ID ABU36613 standard; protein; 603 AA.  
DE Protein encoded by Prokaryotic essential gene #22140.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.9%; Score 352; DB 6; Length 603;  
Best Local Similarity 30.0%; Pred. No. 1.1e-13;  
RESULT 889  
ID AAR80254 standard; peptide; 1056 AA.  
DE Polymer SELP3.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 14.9%; Score 351.5; DB 2; Length 1056;  
Best Local Similarity 26.5%; Pred. No. 2e-13;  
RESULT 890  
ID ABP53475 standard; protein; 1056 AA.  
DE Protein polymer SELP3 polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPF/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 14.9%; Score 351.5; DB 5; Length 1056;  
Best Local Similarity 26.5%; Pred. No. 2e-13;  
RESULT 891  
ID ABU36437 standard; protein; 957 AA.  
DE Protein encoded by Prokaryotic essential gene #21964.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.9%; Score 351; DB 6; Length 957;  
Best Local Similarity 28.0%; Pred. No. 2e-13;  
RESULT 892



ID ABU36926 standard; protein; 461 AA.  
 DE Protein encoded by Prokaryotic essential gene #22353.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 14.8%; Score 350.5; DB 6; Length 461;  
 Best Local Similarity 31.3%; Pred. No. 1e-13;  
 RESULT 893  
 ID AAR41012 standard; protein; 2257 AA.  
 DE SELP3 multimeric protein.  
 PN US5243038-A.  
 PD 07-SEP-1993.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 14.8%; Score 350.5; DB 2; Length 2257;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;  
 RESULT 894  
 ID AAW26347 standard; protein; 2257 AA.  
 DE SELP3 synthetic elastomeric protein.  
 PN US5641648-A.  
 PD 24-JUN-1997.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 14.8%; Score 350.5; DB 2; Length 2257;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;  
 RESULT 895  
 ID AAW53523 standard; protein; 2257 AA.  
 DE Amino acid sequence of the SELP3 protein.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 14.8%; Score 350.5; DB 2; Length 2257;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;  
 RESULT 896  
 ID AAY78282 standard; peptide; 2257 AA.  
 DE SELP3 amino acid sequence SEQ ID NO:82.  
 PN US6018030-A.  
 PD 25-JAN-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 14.8%; Score 350.5; DB 3; Length 2257;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;  
 RESULT 897  
 ID ABG69272 standard; protein; 2257 AA.  
 DE Silk/Elastin-like protein SELP3.  
 PN US6355776-B1.  
 PD 12-MAR-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 14.8%; Score 350.5; DB 5; Length 2257;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;  
 RESULT 898  
 ID ADE44977 standard; protein; 2257 AA.  
 DE Recombinant structural protein SELP3 protein seq id 82.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 14.8%; Score 350.5; DB 7; Length 2257;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;  
 RESULT 899  
 ID ADQ19957 standard; protein; 316 AA.  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2777.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 14.8%; Score 350; DB 8; Length 316;  
 Best Local Similarity 35.3%; Pred. No. 7.8e-14;  
 RESULT 900  
 ID ABU36684 standard; protein; 618 AA.  
 DE Protein encoded by Prokaryotic essential gene #22211.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 14.8%; Score 349; DB 6; Length 618;  
 Best Local Similarity 29.9%; Pred. No. 1.7e-13;  
 RESULT 901  
 ID AAB82611 standard; protein; 528 AA.

DE Spider recombinant silk protein pETNCD5.  
 PN WO200153333-A1.  
 PD 26-JUL-2001.  
 PA (MELL/) MELLO C M.  
 PA (ARCI/) ARCIDIACONO S.  
 PA (BUTL/) BUTLER M M.  
 PA (USSA) US SEC OF ARMY.  
 Query Match 14.7%; Score 348.5; DB 4; Length 528;  
 Best Local Similarity 29.0%; Pred. No. 1.6e-13;  
 RESULT 902  
 ID AAR80168 standard; protein; 831 AA.  
 DE PMISSI MISP spider silk protein insert product.  
 PN WO9525165-A1.  
 PD 21-SEP-1995.  
 PA (UWVY-) UNIV WYOMING.  
 Query Match 14.7%; Score 348.5; DB 2; Length 831;  
 Best Local Similarity 28.1%; Pred. No. 2.4e-13;  
 RESULT 903  
 ID AAE36869 standard; protein; 648 AA.  
 DE Argiope trifasciata major ampullate spidroin 1 (MasPl) protein.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UWVY-) UNIV WYOMING.  
 Query Match 14.6%; Score 346; DB 6; Length 648;  
 Best Local Similarity 27.3%; Pred. No. 2.7e-13;  
 RESULT 904  
 ID ADO8772 standard; protein; 441 AA.  
 DE Novel surgical dressing-related protein SeqID59.  
 PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN) SANYO CHEM IND LTD.  
 PA (ALCA-) ALCARE KK.  
 Query Match 14.6%; Score 345.5; DB 8; Length 441;  
 Best Local Similarity 27.2%; Pred. No. 2e-13;  
 RESULT 905  
 ID AAW31853 standard; protein; 898 AA.  
 DE Mycobacterium tuberculosis 77 kDa protein.  
 PN WO9741252-A2.  
 PD 06-NOV-1997.  
 PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.  
 Query Match 14.6%; Score 344.5; DB 2; Length 898;  
 Best Local Similarity 26.8%; Pred. No. 4.6e-13;  
 RESULT 906  
 ID AAM17023 standard; protein; 283 AA.  
 DE Peptide #3457 encoded by probe for measuring cervical gene expression.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 4; Length 283;  
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 907  
 ID ABB36017 standard; peptide; 283 AA.  
 DE Peptide #3523 encoded by human foetal liver single exon probe.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 4; Length 283;  
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 908  
 ID AAW29514 standard; protein; 283 AA.  
 DE Peptide #3551 encoded by probe for measuring placental gene expression.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 4; Length 283;  
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 909  
 ID ABB30839 standard; peptide; 283 AA.  
 DE Peptide #3490 encoded by breast cell single exon nucleic acid probe.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 4; Length 283;

Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
RESULT 910  
ID ABB21422 standard; protein; 283 AA.  
DE Protein #3421 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
RESULT 911  
ID AAM69190 standard; protein; 283 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29456.  
PN WO200157276-A2.  
PD 03-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
RESULT 912  
ID AAM56810 standard; protein; 283 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28915.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
RESULT 913  
ID ABG50867 standard; peptide; 283 AA.  
DE Human liver peptide, SEQ ID No 29515.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
RESULT 914  
ID AAM04731 standard; protein; 283 AA.  
DE Peptide #3413 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
RESULT 915  
ID ABG38794 standard; peptide; 283 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 28459.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 5; Length 283;  
Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
RESULT 916  
ID AAE36839 standard; protein; 525 AA.  
DE Protein encoded by Prokaryotic essential gene #22366.  
PN WO200207183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.6%; Score 344; DB 6; Length 525;  
Best Local Similarity 30.4%; Pred. No. 3e-13;  
RESULT 917  
ID AAE36884 standard; protein; 651 AA.  
DE Argiope trifasciata flagelliform silk protein (Flag).  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UTWY-) UNIV WYOMING.  
Query Match 14.6%; Score 344; DB 6; Length 651;  
Best Local Similarity 28.4%; Pred. No. 3.6e-13;  
RESULT 918  
ID AAB82609 standard; protein; 681 AA.  
DE Spider recombinant silk protein PQE((SP1)4/(SP2)1)4.  
PN WO200153333-A1.  
PD 26-JUL-2001.  
PA (MELL/) MELLO C M.  
PA (ARCI/) ARCIDIACONO S.  
PA (BUTL/) BUTLER M M.

PA (USSA) US SEC OF ARMY.  
Query Match 14.5%; Score 343; DB 4; Length 681;  
Best Local Similarity 28.3%; Pred. No. 4.4e-13;  
RESULT 919  
ID AAB82610 standard; protein; 691 AA.  
DE Spider recombinant silk protein pET((SP1)4/(SP2)1)4.  
PN WO200153333-A1.  
PD 26-JUL-2001.  
PA (MELL/) MELLO C M.  
PA (ARCI/) ARCIDIACONO S.  
PA (BUTL/) BUTLER M M.  
PA (USSA) US SEC OF ARMY.  
Query Match 14.5%; Score 343; DB 4; Length 691;  
Best Local Similarity 28.3%; Pred. No. 4.4e-13;  
RESULT 920  
ID ADB61323 standard; protein; 629 AA.  
DE Spider silk related ADP-3 protein.  
PN WO2003060099-A2.  
PD 24-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
PA (ALWA/) ALWATTARI A.  
Query Match 14.5%; Score 342.5; DB 7; Length 629;  
Best Local Similarity 29.5%; Pred. No. 4.4e-13;  
RESULT 921  
ID ADC35242 standard; protein; 629 AA.  
DE ADP-3 silk protein, SEQ ID 3.  
PN WO2003057727-A1.  
PD 17-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 14.5%; Score 342.5; DB 7; Length 629;  
Best Local Similarity 29.5%; Pred. No. 4.4e-13;  
RESULT 922  
ID ADM46151 standard; protein; 629 AA.  
DE Nephila clavipes ADP-3 protein.  
PN WO2003057720-A2.  
PD 17-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 14.5%; Score 342.5; DB 7; Length 629;  
Best Local Similarity 29.5%; Pred. No. 4.4e-13;  
RESULT 923  
ID AAM50045 standard; protein; 773 AA.  
DE N. clavipes spidroin homologue SMI2-70xELP for plant expression.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 14.5%; Score 342.5; DB 5; Length 773;  
Best Local Similarity 29.4%; Pred. No. 5.3e-13;  
RESULT 924  
ID AAM50046 standard; protein; 777 AA.  
DE N. clavipes spidroin homologue SMI2-70xELP for E. coli expression.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 14.5%; Score 342.5; DB 5; Length 777;  
Best Local Similarity 29.4%; Pred. No. 5.3e-13;  
RESULT 925  
ID ADO08787 standard; protein; 482 AA.  
DE Novel surgical dressing-related protein SeqID74.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANVO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 14.5%; Score 342; DB 8; Length 482;  
Best Local Similarity 27.1%; Pred. No. 3.6e-13;  
RESULT 926  
ID ABU36689 standard; protein; 515 AA.  
DE Protein encoded by Prokaryotic essential gene #22216.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.5%; Score 342; DB 6; Length 515;  
Best Local Similarity 29.3%; Pred. No. 3.9e-13;  
RESULT 927

ID ABU36423 standard; protein; 487 AA.  
DE Protein encoded by Prokaryotic essential gene #21950.  
PN WO200277183-A2.  
PA (BLIT-) ELITRA PHARM INC.  
Query Match 14.4%; Score 339.5; DB 6; Length 487;  
Best Local Similarity 29.9%; Pred. No. 5.2e-13;  
RESULT 928  
ID AAE36885 standard; protein; 1002 AA.  
DE Argiope trifasciata flag protein fragment.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 14.3%; Score 337; DB 6; Length 1002;  
Best Local Similarity 29.9%; Pred. No. 1.5e-12;  
RESULT 929  
ID AAE18320 standard; protein; 968 AA.  
DE Silk elastin combination protein, SELP3.  
PN WO200200016-A1.  
PD 03-JAN-2002.  
PA (LUMI-) LUMINIS PTY LTD.  
PA (SAUR-) SOUTH AUSTRALIAN RES & DEV INST.  
Query Match 14.2%; Score 336.5; DB 5; Length 968;  
Best Local Similarity 29.6%; Pred. No. 1.5e-12;  
RESULT 930  
ID ABP53479 standard; protein; 1169 AA.  
DE Protein polymer SELPPF polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 14.2%; Score 336; DB 5; Length 1169;  
Best Local Similarity 30.5%; Pred. No. 2e-12;  
RESULT 931  
ID ADQ08775 standard; protein; 482 AA.  
DE Novel surgical dressing-related protein SeqID62.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 14.2%; Score 335; DB 8; Length 482;  
Best Local Similarity 30.6%; Pred. No. 9.8e-13;  
RESULT 932  
ID ADP31119 standard; protein; 8973 AA.  
DE Human secreted protein SEQ ID #1886.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 14.2%; Score 335; DB 8; Length 8973;  
Best Local Similarity 29.9%; Pred. No. 1.6e-11;  
RESULT 933  
ID AAW79137 standard; protein; 261 AA.  
DE FLGA Gly-ala insert present in chimeric IkappaB construct.  
PN WO9822577-A1.  
PD 28-MAY-1998.  
PA (MASU/) MASUCCI M G.  
Query Match 14.2%; Score 334.5; DB 2; Length 261;  
Best Local Similarity 29.1%; Pred. No. 5.8e-13;  
RESULT 934  
ID AAE36927 standard; protein; 440 AA.  
DE Nephila clavipes minor ampullate spidroin 1 consensus protein #2.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 14.1%; Score 334; DB 6; Length 440;  
Best Local Similarity 27.9%; Pred. No. 1e-12;  
RESULT 935  
ID ABP72662 standard; protein; 498 AA.  
DE Rv181c gene product of Mycobacterium tuberculosis.  
PN WO2003018754-A2.  
PD 06-MAR-2003.  
PA (NEUR-) NEURONZ LTD.  
PA (NEUR-) NEURONZ BIOSCIENCES INC.  
Query Match 14.1%; Score 334; DB 6; Length 498;  
Best Local Similarity 29.3%; Pred. No. 1.2e-12;  
RESULT 936  
ID ABU36686 standard; protein; 498 AA.  
DE Protein encoded by Prokaryotic essential gene #22213.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.1%; Score 334; DB 6; Length 498;  
Best Local Similarity 29.3%; Pred. No. 1.2e-12;  
RESULT 937  
ID ABB68951 standard; protein; 342 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 33645.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 14.1%; Score 332.5; DB 4; Length 342;  
Best Local Similarity 29.5%; Pred. No. 1e-12;  
RESULT 938  
ID AAM50043 standard; protein; 364 AA.  
DE N. clavipes spidroin synthetic homologue SM12 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 14.0%; Score 331.5; DB 5; Length 364;  
Best Local Similarity 29.3%; Pred. No. 1.2e-12;  
RESULT 939  
ID AAE36868 standard; protein; 447 AA.  
DE Argiope aurantia major ampullate spidroin 1 (Maspl) protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 14.0%; Score 330; DB 6; Length 447;  
Best Local Similarity 29.5%; Pred. No. 1.8e-12;  
RESULT 940  
ID ADK51951 standard; protein; 780 AA.  
DE Repeat protein polymer repeat sequence, SEQ ID 19.  
PN WO2003099465-A1.  
PD 04-DEC-2003.  
PA (DOWO) DOW CORNING CORP.  
PA (GEVY) GENECOR INT INC.  
Query Match 13.9%; Score 329; DB 8; Length 780;  
Best Local Similarity 26.9%; Pred. No. 3.6e-12;  
RESULT 941  
ID ADR70468 standard; protein; 780 AA.  
DE Silk-elastin polymer SELP47K.  
PN US2004180027-A1.  
PD 16-SEP-2004.  
PA (KUMA/) KUMAR M.  
PA (CUEV/) CUEVAS W A.  
Query Match 13.9%; Score 329; DB 8; Length 780;  
Best Local Similarity 26.9%; Pred. No. 3.6e-12;  
RESULT 942  
ID ADO08759 standard; protein; 302 AA.  
DE Novel surgical dressing-related protein SeqID46.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 13.8%; Score 326.5; DB 8; Length 302;  
Best Local Similarity 29.6%; Pred. No. 2.1e-12;  
RESULT 943  
ID ABB81230 standard; protein; 334 AA.  
DE Mycobacterium bovis BCG strain Pasteur PE-PCRS protein sequence.  
PN WO954487-A2.  
PD 28-OCT-1999.  
PA (INSP) INST PASTEUR.  
Query Match 13.8%; Score 326.5; DB 3; Length 334;  
Best Local Similarity 30.0%; Pred. No. 2.3e-12;  
RESULT 944  
ID ABU36981 standard; protein; 439 AA.  
DE Protein encoded by Prokaryotic essential gene #22508.  
PN WO200277183-A2.

PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.8%; Score 325.5; DB 6; Length 439;  
Best Local Similarity 29.0%; Pred. No. 3.4e-12;  
RESULT 945  
ID ADO08784 standard; protein; 471 AA.  
DE Novel surgical dressing-related protein SeqID71.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 13.7%; Score 324.5; DB 8; Length 471;  
Best Local Similarity 28.1%; Pred. No. 4.2e-12;  
RESULT 946  
ID ADO08764 standard; protein; 482 AA.  
DE Novel surgical dressing-related protein SeqID51.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 13.7%; Score 324; DB 8; Length 482;  
Best Local Similarity 29.3%; Pred. No. 4.6e-12;  
RESULT 947  
ID ADR70478 standard; protein; 1038 AA.  
DE Silk-elastin polymer SEMP 67K.  
PN US2004180027-A1.  
PD 16-SEP-2004.  
PA (KUMA/) KUMAR M.  
PA (CUEV/) CUEVAS W A.  
Query Match 13.7%; Score 324; DB 8; Length 1038;  
Best Local Similarity 25.0%; Pred. No. 9.6e-12;  
RESULT 948  
ID AAR80255 standard; peptide; 972 AA.  
DE Polymer SEMP4.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 13.6%; Score 322.5; DB 2; Length 972;  
Best Local Similarity 24.8%; Pred. No. 1.1e-11;  
RESULT 949  
ID ABP53476 standard; protein; 972 AA.  
DE Protein polymer SEMP4 polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 13.6%; Score 322.5; DB 5; Length 972;  
Best Local Similarity 24.8%; Pred. No. 1.1e-11;  
RESULT 950  
ID AAB70185 standard; peptide; 504 AA.  
DE Peptide dendrimer carrier #10.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 13.6%; Score 321.5; DB 4; Length 504;  
Best Local Similarity 29.1%; Pred. No. 6.9e-12;  
RESULT 951  
ID AAB70186 standard; peptide; 1016 AA.  
DE Peptide dendrimer carrier #11.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 13.6%; Score 321.5; DB 4; Length 1016;  
Best Local Similarity 29.1%; Pred. No. 1.3e-11;  
RESULT 952  
ID AAB70187 standard; peptide; 2040 AA.  
DE Peptide dendrimer carrier #12.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 13.6%; Score 321.5; DB 4; Length 2040;  
Best Local Similarity 29.1%; Pred. No. 2.6e-11;  
RESULT 953

ID ABU36473 standard; protein; 594 AA.  
DE Protein encoded by Prokaryotic essential gene #22000.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.5%; Score 320; DB 6; Length 594;  
Best Local Similarity 31.4%; Pred. No. 1e-11;  
RESULT 954  
ID ABB70834 standard; protein; 620 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39294.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 13.5%; Score 320; DB 4; Length 620;  
Best Local Similarity 26.7%; Pred. No. 1e-11;  
RESULT 955  
ID AAE36881 standard; protein; 1953 AA.  
DE Nephila madagascariensis major ampullate spidroin 2 (Masp2)-like protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 13.5%; Score 320; DB 6; Length 1953;  
Best Local Similarity 26.9%; Pred. No. 3.1e-11;  
RESULT 956  
ID ADP31118 standard; protein; 5820 AA.  
DE Human secreted protein SEQ ID #1885.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 13.5%; Score 318.5; DB 8; Length 5820;  
Best Local Similarity 29.2%; Pred. No. 1.1e-10;  
RESULT 957  
ID ABB81229 standard; protein; 318 AA.  
DE Mycobacterium tuberculosis strain H37Rv PE-PGRS protein sequence.  
PN WO9954487-A2.  
PD 28-OCT-1999.  
PA (INSP) INST PASTEUR.  
Query Match 13.5%; Score 318; DB 3; Length 318;  
Best Local Similarity 32.2%; Pred. No. 7.3e-12;  
RESULT 958  
ID ADR70473 standard; protein; 884 AA.  
DE Silk-elastin polymer SEMP 47-E13.  
PN US2004180027-A1.  
PD 16-SEP-2004.  
PA (KUMA/) KUMAR M.  
PA (CUEV/) CUEVAS W A.  
Query Match 13.5%; Score 318; DB 8; Length 884;  
Best Local Similarity 26.6%; Pred. No. 1.9e-11;  
RESULT 959  
ID AAR80253 standard; peptide; 988 AA.  
DE Polymer SEMP7.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 13.4%; Score 317.5; DB 2; Length 988;  
Best Local Similarity 28.6%; Pred. No. 2.3e-11;  
RESULT 960  
ID ABP53474 standard; protein; 988 AA.  
DE Protein polymer SEMP7 polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 13.4%; Score 317.5; DB 5; Length 988;  
Best Local Similarity 28.6%; Pred. No. 2.3e-11;  
RESULT 961  
ID ADO59401 standard; protein; 2655 AA.  
DE Antheraea yamamai fibroin.  
PN KR2002094304-A.  
PD 18-DEC-2002.  
PA (RURA-) RURAL DEV ADMINISTRATION.  
Query Match 13.4%; Score 317; DB 7; Length 2655;  
Best Local Similarity 25.6%; Pred. No. 6.4e-11;

RESULT 962  
ID ADO08778 standard; protein; 506 AA.  
DE Novel surgical dressing-related protein SeqID65.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 13.4%; Score 316; DB 8; Length 506;  
Best Local Similarity 28.3%; Pred. No. 1.5e-11;  
RESULT 963  
ID ADR70479 standard; protein; 965 AA.  
DE Silk-elastin polymer SELLP 58.  
PN US2004180027-A1.  
PD 16-SEP-2004.  
PA (KUMA/) KUMAR M.  
PA (CUEV/) CUEVAS W A.  
Query Match 13.4%; Score 315.5; DB 8; Length 965;  
Best Local Similarity 26.4%; Pred. No. 3e-11;  
RESULT 964  
ID AAM94219 standard; protein; 116 AA.  
DE Human reproductive system related antigen SEQ ID NO: 2877.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.3%; Score 314; DB 4; Length 116;  
Best Local Similarity 98.2%; Pred. No. 4.9e-12;  
RESULT 965  
ID AAB70180 standard; peptide; 1488 AA.  
DE Peptide dendrimer carrier #5.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 13.2%; Score 312; DB 4; Length 1488;  
Best Local Similarity 28.9%; Pred. No. 7.4e-11;  
RESULT 966  
ID ADG88556 standard; protein; 200 AA.  
DE Poly Gly flexible linker.  
PN US2003176333-A1.  
PD 18-SEP-2003.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 13.1%; Score 309.5; DB 7; Length 200;  
Best Local Similarity 32.3%; Pred. No. 1.6e-11;  
RESULT 967  
ID ADJ84541 standard; protein; 200 AA.  
DE T2R G-protein coupled receptor related linker seq id 94.  
PN US2004038312-A1.  
PD 26-FEB-2004.  
PA (ZUKE/) ZUKER C S.  
PA (ADLE/) ADLER J E.  
PA (HOON/) HOON M.  
PA (RYBA/) RYBA N.  
PA (MUEL/) MUELLER K.  
Query Match 13.1%; Score 309.5; DB 8; Length 200;  
Best Local Similarity 32.3%; Pred. No. 1.6e-11;  
RESULT 968  
ID ADM96215 standard; protein; 200 AA.  
DE Poly Gly flexible linker.  
PN US2004071708-A1.  
PD 15-APR-2004.  
PA (IMMU-) IMMUSOL INC.  
Query Match 13.1%; Score 309.5; DB 8; Length 200;  
Best Local Similarity 32.3%; Pred. No. 1.6e-11;  
RESULT 969  
ID ADO08771 standard; protein; 296 AA.  
DE Novel surgical dressing-related protein SeqID58.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 13.1%; Score 309.5; DB 8; Length 296;  
Best Local Similarity 27.5%; Pred. No. 2.3e-11;  
RESULT 970  
ID ABG71303 standard; protein; 201 AA.  
DE PINPOINT poly-Gly linker protein.  
PN US6444421-B1.  
PD 03-SEP-2002.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 13.1%; Score 309; DB 5; Length 201;  
Best Local Similarity 31.9%; Pred. No. 1.7e-11;  
RESULT 971  
ID AAW05704 standard; peptide; 235 AA.  
DE Glycine-rich repeat sequence of EBV nuclear antigen.  
PN WO9632483-A1.  
PD 17-OCT-1996.  
PA (MASU/) MASUCCI M.  
Query Match 13.0%; Score 308; DB 2; Length 235;  
Best Local Similarity 29.6%; Pred. No. 2.2e-11;  
RESULT 972  
ID AAW79126 standard; protein; 235 AA.  
DE Epstein Barr Virus EBNA1 protein gly-ala repeat region.  
PN WO9822577-A1.  
PD 28-MAY-1998.  
PA (MASU/) MASUCCI M G.  
Query Match 13.0%; Score 308; DB 2; Length 235;  
Best Local Similarity 29.6%; Pred. No. 2.2e-11;  
RESULT 973  
ID AAB70188 standard; peptide; 465 AA.  
DE Peptide dendrimer carrier #13.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 12.9%; Score 305.5; DB 4; Length 465;  
Best Local Similarity 27.9%; Pred. No. 6.1e-11;  
RESULT 974  
ID ABB61734 standard; protein; 1039 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 11994.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 12.9%; Score 305.5; DB 4; Length 1039;  
Best Local Similarity 27.5%; Pred. No. 1.3e-10;  
RESULT 975  
ID ADP31138 standard; protein; 1350 AA.  
DE Human secreted protein SEQ ID #1905.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.9%; Score 304.5; DB 8; Length 1350;  
Best Local Similarity 26.0%; Pred. No. 2e-10;  
RESULT 976  
ID ADP31137 standard; protein; 1719 AA.  
DE Human secreted protein SEQ ID #1904.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.9%; Score 304.5; DB 8; Length 1719;  
Best Local Similarity 26.0%; Pred. No. 2.5e-10;  
RESULT 977  
ID ADO08774 standard; protein; 322 AA.  
DE Novel surgical dressing-related protein SeqID61.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 12.8%; Score 303.5; DB 8; Length 322;  
Best Local Similarity 31.6%; Pred. No. 5.7e-11;  
RESULT 978  
ID ADS28501 standard; protein; 592 AA.  
DE Bacterial polypeptide #17534.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.

Query Match 12.8%; Score 302; DB 8; Length 592;  
Best Local Similarity 27.7%; Pred. No. 1.3e-10;  
RESULT 979  
ID AAR99059 standard; protein; 714 AA.  
DE Spider dragline variant, DP-2A polymer.  
PN WO9429450-A2.  
PD 22-DEC-1994.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 12.8%; Score 302; DB 2; Length 714;  
Best Local Similarity 28.4%; Pred. No. 1.5e-10;  
RESULT 980  
ID RAY40103 standard; protein; 714 AA.  
DE Polymer of an analogue of spider silk protein spidroine major 2.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 12.8%; Score 302; DB 2; Length 714;  
Best Local Similarity 28.4%; Pred. No. 1.5e-10;  
RESULT 981  
ID ADO08790 standard; protein; 506 AA.  
DE Novel surgical dressing-related protein SeqID77.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA) ALCARE KK.  
Query Match 12.7%; Score 301; DB 8; Length 506;  
Best Local Similarity 26.6%; Pred. No. 1.3e-10;  
RESULT 982  
ID ADS88365 standard; protein; 622 AA.  
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 220.  
PN WO2004035783-A2.  
PD 29-APR-2004.  
PA (CELL-) CELLZOME AG.  
Query Match 12.7%; Score 300.5; DB 8; Length 622;  
Best Local Similarity 26.2%; Pred. No. 1.6e-10;  
RESULT 983  
ID ABP53481 standard; protein; 768 AA.  
DE Protein polymer SELP8K polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 12.7%; Score 300.5; DB 5; Length 768;  
Best Local Similarity 26.8%; Pred. No. 2e-10;  
RESULT 984  
ID AAR80341 standard; protein; 884 AA.  
DE Protein polymer adhesive substrate SELP8K.  
PN WO9523611-A1.  
PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 2; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 985  
ID RAO09213 standard; protein; 884 AA.  
DE SELP8K polymer.  
PN WO9634618-A1.  
PD 07-NOV-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 2; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 986  
ID AAW53541 standard; protein; 884 AA.  
DE Expected amino acid sequence of pPT0345 encoding SELP8K polymer.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 2; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 987  
ID AAW49728 standard; protein; 884 AA.  
DE SELP8K polymer.  
PN US5773577-A.  
PD 30-JUN-1998.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 2; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 988  
ID AAY51882 standard; protein; 884 AA.  
DE Plasmid pPT0345 protein fragment containing SELP8K polymer units.  
PN US6033654-A.  
PD 07-MAR-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 3; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 989  
ID ABG31412 standard; protein; 884 AA.  
DE SELP8K polymer encoded by plasmid pPT0345.  
PN US6423333-B1.  
PD 23-JUL-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 5; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 990  
ID ABW01628 standard; protein; 884 AA.  
DE Plasmid pPT0345 SELP8K polymer protein.  
PN US2003104589-A1.  
PD 05-JUN-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 7; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 991  
ID AAW56163 standard; protein; 738 AA.  
DE New DNA sequence isolated from Pinctada fucata.  
PN JP10080285-A.  
PD 31-MAR-1998.  
PA (MIKI-) MIKIMOTO SEIYAKU KK.  
Query Match 12.7%; Score 300; DB 2; Length 738;  
Best Local Similarity 24.4%; Pred. No. 2.1e-10;  
RESULT 992  
ID AAE36879 standard; protein; 373 AA.  
DE Latrodectus geometricus major ampullate spidroin 2 (MaSp2) protein #1.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 12.7%; Score 299; DB 6; Length 373;  
Best Local Similarity 28.0%; Pred. No. 1.2e-10;  
RESULT 993  
ID AAR80256 standard; peptide; 1024 AA.  
DE Polymer SELP5.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.5%; Score 296.5; DB 2; Length 1024;  
Best Local Similarity 21.8%; Pred. No. 4.7e-10;  
RESULT 994  
ID ABP53477 standard; protein; 1024 AA.  
DE Protein polymer SELP5 polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 12.5%; Score 296.5; DB 5; Length 1024;  
Best Local Similarity 21.8%; Pred. No. 4.7e-10;  
RESULT 995  
ID AAY40098 standard; protein; 531 AA.  
DE Spider silk protein spidroine major 2.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 12.5%; Score 296; DB 2; Length 531;  
Best Local Similarity 27.7%; Pred. No. 2.7e-10;  
RESULT 996  
ID AAR14309 standard; protein; 595 AA.  
DE N.clavipes dragline silk protein-2.  
PN EP452925-A.  
PD 23-OCT-1991.

PA (UYWY-) UNIV OF WYOMING.  
 Query Match 12.5%; Score 296; DB 2; Length 595;  
 Best Local Similarity 27.7%; Pred. No. 3e-10;  
 RESULT 997  
 ID AAW53347 standard; protein; 595 AA.  
 DE Nephila clavipes spider silk protein.  
 PN US5728810-A.  
 PD 17-MAR-1998.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 12.5%; Score 296; DB 2; Length 595;  
 Best Local Similarity 27.7%; Pred. No. 3e-10;  
 RESULT 998  
 ID AAY59071 standard; protein; 595 AA.  
 DE N. clavipes spider silk protein 2.  
 PN US5989894-A.  
 PD 23-NOV-1999.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 12.5%; Score 296; DB 3; Length 595;  
 Best Local Similarity 27.7%; Pred. No. 3e-10;  
 RESULT 999  
 ID AAO16488 standard; protein; 624 AA.  
 DE Nephila clavipes dragline silk fibronin protein.  
 PN WO200299082-A2.  
 PD 12-DEC-2002.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 12.5%; Score 296; DB 6; Length 624;  
 Best Local Similarity 27.7%; Pred. No. 3.1e-10;  
 RESULT 1000  
 ID AOC35241 standard; protein; 627 AA.  
 DE Maspil silk protein, SEQ ID 2.  
 PN WO2003057727-A1.  
 PD 17-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 Query Match 12.5%; Score 296; DB 7; Length 627;  
 Best Local Similarity 27.7%; Pred. No. 3.1e-10;  
 RESULT 1001  
 ID AAR80252 standard; peptide; 832 AA.  
 DE Polymer SELP8.  
 PN WO9524478-A1.  
 PD 14-SRP-1995.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 12.5%; Score 294.5; DB 2; Length 832;  
 Best Local Similarity 27.1%; Pred. No. 5.1e-10;  
 RESULT 1002  
 ID ABP53473 standard; protein; 832 AA.  
 DE Protein polymer SELP8 polymer block amino acid sequence.  
 PN US2002045567-A1.  
 PD 18-APR-2002.  
 PA (CAPF/) CAPPELLO J.  
 PA (STED/) STEDRONSKY E R.  
 Query Match 12.5%; Score 294.5; DB 5; Length 832;  
 Best Local Similarity 27.1%; Pred. No. 5.1e-10;  
 RESULT 1003  
 ID AAB23358 standard; protein; 674 AA.  
 DE Human trophinin protein from residue 69 to 749.  
 PN US6111089-A.  
 PD 29-AUG-2000.  
 PA (BURN-) BURNHAM INST.  
 Query Match 12.4%; Score 294; DB 3; Length 674;  
 Best Local Similarity 28.7%; Pred. No. 4.4e-10;  
 RESULT 1004  
 ID ADC86917 standard; protein; 821 AA.  
 DE Human GPCR protein SEQ ID NO:1370.  
 PN EP1270724-A2.  
 PD 02-JAN-2003.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
 Query Match 12.4%; Score 294; DB 7; Length 821;  
 Best Local Similarity 31.1%; Pred. No. 5.4e-10;  
 RESULT 1005  
 ID ABB67074 standard; protein; 586 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 28014.  
 PN WO200171042-A2.

PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 12.4%; Score 293.5; DB 4; Length 586;  
 Best Local Similarity 26.6%; Pred. No. 4.2e-10;  
 RESULT 1006  
 ID ABB62822 standard; protein; 586 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 15258.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 12.4%; Score 293.5; DB 4; Length 586;  
 Best Local Similarity 26.6%; Pred. No. 4.2e-10;  
 RESULT 1007  
 ID ADS96696 standard; protein; 586 AA.  
 DE Drosophila melanogaster protein, SEQ ID 317.  
 PN WO2004039999-A2.  
 PD 13-MAY-2004.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 12.4%; Score 293.5; DB 8; Length 586;  
 Best Local Similarity 26.6%; Pred. No. 4.2e-10;  
 RESULT 1008  
 ID ADA07852 standard; protein; 611 AA.  
 DE Pinctada margaritifera nacrein.  
 PN US2003027258-A1.  
 PD 06-FEB-2003.  
 PA (CHAN/) CHANG F F.  
 PA (LIHH/) LI H.  
 PA (HSIE/) HSIEH-LI H M.  
 Query Match 12.4%; Score 293.5; DB 6; Length 611;  
 Best Local Similarity 26.5%; Pred. No. 4.3e-10;  
 RESULT 1009  
 ID ABO23517 standard; protein; 256 AA.  
 DE Mycobacterium tuberculosis outlier protein #1.  
 PN US2003039963-A1.  
 PD 27-FEB-2003.  
 PA (BRAH/) BRAHMACHARI S K.  
 PA (RAMA/) RAMACHANDRAN S.  
 PA (NAND/) NANDI T.  
 PA (BHIM/) BHIMARAO C.  
 Query Match 12.4%; Score 293; DB 7; Length 256;  
 Best Local Similarity 31.1%; Pred. No. 2e-10;  
 RESULT 1010  
 ID ADO08786 standard; protein; 322 AA.  
 DE Novel surgical dressing-related protein SeqID73.  
 PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN ) SANYO CHEM IND LTD.  
 PA (ALCA-) ALCARE KK.  
 Query Match 12.4%; Score 292.5; DB 8; Length 322;  
 Best Local Similarity 28.8%; Pred. No. 2.7e-10;  
 RESULT 1011  
 ID AAE36889 standard; protein; 912 AA.  
 DE Plectreureys cristatis fibroin 1 protein.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 12.4%; Score 292; DB 6; Length 912;  
 Best Local Similarity 23.4%; Pred. No. 7.9e-10;  
 RESULT 1012  
 ID AAR94895 standard; protein; 749 AA.  
 DE Human trophinin.  
 PN WO9610414-A1.  
 PD 11-APR-1996.  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 Query Match 12.3%; Score 290.5; DB 2; Length 749;  
 Best Local Similarity 27.8%; Pred. No. 8.1e-10;  
 RESULT 1013  
 ID AAB23357 standard; protein; 749 AA.  
 DE Human trophinin protein.  
 PN US6111089-A.  
 PD 29-AUG-2000.  
 PA (BURN-) BURNHAM INST.  
 Query Match 12.3%; Score 290.5; DB 3; Length 749;

Best Local Similarity 27.6%; Pred. No. 8.1e-10;  
RESULT 1014  
ID ABO60408 standard; protein; 805 AA.  
DE Human genome derived single exon protein #6642.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (PENN/) PENN S G.  
PA (HANZ/) HANZEL D K.  
PA (HANZ/) HANZEL D K.  
Query Match 12.3%; Score 290.5; DB 8; Length 805;  
Best Local Similarity 27.6%; Pred. No. 8.6e-10;  
RESULT 1015  
ID AAB94744 standard; protein; 814 AA.  
DE Human protein sequence SEQ ID NO:15790.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 12.3%; Score 290.5; DB 4; Length 814;  
Best Local Similarity 27.6%; Pred. No. 8.7e-10;  
RESULT 1016  
ID AAM94034 standard; protein; 814 AA.  
DE Human stomach cancer expressed polypeptide SEQ ID NO 139.  
PN WO200109317-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 12.3%; Score 290.5; DB 4; Length 814;  
Best Local Similarity 27.6%; Pred. No. 8.7e-10;  
RESULT 1017  
ID AAU32728 standard; protein; 1406 AA.  
DE Novel human secreted protein #3219.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.3%; Score 290.5; DB 4; Length 1406;  
Best Local Similarity 27.6%; Pred. No. 1.5e-09;  
RESULT 1018  
ID AAY04999 standard; protein; 388 AA.  
DE Mycobacterium species protein sequence 50C.  
PN WO9909186-A2.  
PD 25-FEB-1999.  
PA (INSP ) INST PASTEUR.  
Query Match 12.2%; Score 289; DB 2; Length 388;  
Best Local Similarity 30.4%; Pred. No. 5.3e-10;  
RESULT 1019  
ID ADB61322 standard; protein; 627 AA.  
DE Spider silk related MaspiI protein.  
PN WO2003060099-A2.  
PD 24-JUL-2003.  
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
PA (ALMA/) ALMATTARI A.  
Query Match 12.2%; Score 289; DB 7; Length 627;  
Best Local Similarity 28.2%; Pred. No. 8.4e-10;  
RESULT 1020  
ID ADM46150 standard; protein; 627 AA.  
DE Nephila clavipes spidroin 2 (MaspiI) protein.  
PN WO2003057720-A2.  
PD 17-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 12.2%; Score 289; DB 7; Length 627;  
Best Local Similarity 28.2%; Pred. No. 8.4e-10;  
RESULT 1021  
ID ABP53466 standard; protein; 768 AA.  
DE SELP8 related amino acid sequence #2.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 12.2%; Score 288.5; DB 5; Length 768;  
Best Local Similarity 26.6%; Pred. No. 1.1e-09;  
RESULT 1022  
ID AAR80335 standard; protein; 877 AA.  
DE Protein polymeric adhesion substrate 1-G.  
PN WO9523611-A1.

PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.2%; Score 288.5; DB 2; Length 877;  
Best Local Similarity 26.6%; Pred. No. 1.2e-09;  
RESULT 1023  
ID AAM49724 standard; protein; 877 AA.  
DE Protein polymer adhesive substrate PPAS1-G.  
PN US577377-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.2%; Score 288.5; DB 2; Length 877;  
Best Local Similarity 26.6%; Pred. No. 1.2e-09;  
RESULT 1024  
ID ADO8763 standard; protein; 322 AA.  
DE Novel surgical dressing-related protein SeqID50.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN ) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 12.1%; Score 286; DB 8; Length 322;  
Best Local Similarity 29.8%; Pred. No. 6.8e-10;  
RESULT 1025  
ID AAE36882 standard; protein; 563 AA.  
DE Nephila madagascariensis major ampullate spidroin 2 (Masp2) protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 12.1%; Score 286; DB 6; Length 563;  
Best Local Similarity 26.3%; Pred. No. 1.2e-09;  
RESULT 1026  
ID ABB60403 standard; protein; 2112 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.1%; Score 286; DB 4; Length 2112;  
Best Local Similarity 24.3%; Pred. No. 4.1e-09;  
RESULT 1027  
ID AAM78356 standard; protein; 536 AA.  
DE Human protein SEQ ID NO 1018.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.1%; Score 285; DB 4; Length 536;  
Best Local Similarity 29.6%; Pred. No. 1.3e-09;  
RESULT 1028  
ID AAM50044 standard; protein; 271 AA.  
DE N. clavipes spidroin synthetic homologue SF1 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 12.0%; Score 283.5; DB 5; Length 271;  
Best Local Similarity 29.7%; Pred. No. 8.2e-10;  
RESULT 1029  
ID AAB06023 standard; protein; 401 AA.  
DE Polar gelatin P tetramer, P4.  
PN EP1014176-A2.  
PD 28-JUN-2000.  
PA (FUJF ) FUJI PHOTO FILM BV.  
Query Match 12.0%; Score 283.5; DB 3; Length 401;  
Best Local Similarity 33.9%; Pred. No. 1.2e-09;  
RESULT 1030  
ID AAY72375 standard; protein; 599 AA.  
DE Amphiphilic recombinant collagen-like polymer, NIN2P4.  
PN EP1063565-A1.  
PD 27-DEC-2000.  
PA (FUJF ) FUJI PHOTO FILM BV.  
Query Match 12.0%; Score 283.5; DB 4; Length 599;  
Best Local Similarity 33.9%; Pred. No. 1.8e-09;  
RESULT 1031  
ID AAY72374 standard; protein; 599 AA.  
DE Amphiphilic recombinant collagen-like polymer, NIN1P4.  
PN EP1063565-A1.



PD 27-DEC-2000.  
 PA (FOUJ ) FUJI PHOTO FILM BV.  
 Query Match 12.0%; Score 283.5; DB 4; Length 599;  
 Best Local Similarity 33.9%; Pred. No. 1.8e-09;  
 RESULT 1032  
 ID AAB23367 standard; protein; 1160 AA.  
 DE Mouse troponin protein.  
 PN US6111089-A.  
 PD 29-AUG-2000.  
 PA (BURN-) BURNHAM INST.  
 Query Match 12.0%; Score 283; DB 3; Length 1160;  
 Best Local Similarity 29.6%; Pred. No. 3.5e-09;  
 RESULT 1033  
 ID ADO08783 standard; protein; 316 AA.  
 DE Novel surgical dressing-related protein SeqID70.  
 PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN ) SANYO CHEM IND LTD.  
 PA (ALCA-) ALCARE KK.  
 Query Match 12.0%; Score 282.5; DB 8; Length 316;  
 Best Local Similarity 27.6%; Pred. No. 1.1e-09;  
 RESULT 1034  
 ID ADH58964 standard; protein; 258 AA.  
 DE Silk protein related protein #SEQ ID 33.  
 PN WO2003100065-A1.  
 PD 04-DEC-2003.  
 PA (UYNI-) UNIV JAPAN TOKYO AGR.  
 Query Match 11.9%; Score 280.5; DB 8; Length 258;  
 Best Local Similarity 29.4%; Pred. No. 1.2e-09;  
 RESULT 1035  
 ID AAB36876 standard; protein; 444 AA.  
 DE Argiope trifasciata major ampullate spidroin 2 (MasP2) protein.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 11.8%; Score 280; DB 6; Length 444;  
 Best Local Similarity 27.1%; Pred. No. 2.2e-09;  
 RESULT 1036  
 ID ADN35278 standard; protein; 1028 AA.  
 DE Helical domain of type III collagen #2.  
 PN WO2004028404-A2.  
 PD 08-APR-2004.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.8%; Score 280; DB 8; Length 1028;  
 Best Local Similarity 27.4%; Pred. No. 4.8e-09;  
 RESULT 1037  
 ID ADN35277 standard; protein; 1313 AA.  
 DE Helical domain of type III collagen.  
 PN WO2004028404-A2.  
 PD 08-APR-2004.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.8%; Score 280; DB 8; Length 1313;  
 Best Local Similarity 27.4%; Pred. No. 6.1e-09;  
 RESULT 1038  
 ID ADE61480 standard; protein; 1380 AA.  
 DE Rat Protein AAC05725, SEQ ID NO 7400.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 Query Match 11.8%; Score 280; DB 7; Length 1380;  
 Best Local Similarity 31.7%; Pred. No. 6.4e-09;  
 RESULT 1039  
 ID ABB50291 standard; protein; 1466 AA.  
 DE Collagen type III alpha-1 ovarian tumour marker protein, SEQ ID NO:72.  
 PN WO200175177-A2.  
 PD 11-OCT-2001.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 11.8%; Score 280; DB 4; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
 RESULT 1040  
 ID ABB90747 standard; protein; 1466 AA.  
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 226.

PN WO200210217-A2.  
 PD 07-FEB-2002.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 Query Match 11.8%; Score 280; DB 5; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
 RESULT 1041  
 ID ABUS4454 standard; protein; 1466 AA.  
 DE Human tumour endothelial marker TEM 15.  
 PN WO200283874-A2.  
 PD 24-OCT-2002.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 Query Match 11.8%; Score 280; DB 6; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
 RESULT 1042  
 ID ABR47418 standard; protein; 1466 AA.  
 DE Breast cancer associated protein sequence SEQ ID NO:68.  
 PN WO2003004989-A2.  
 PD 16-JAN-2003.  
 PA (MILL-) MILLENIUM PHARM INC.  
 Query Match 11.8%; Score 280; DB 6; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
 RESULT 1043  
 ID ADP65248 standard; protein; 1466 AA.  
 DE Human alpha 1 type III collagen preproprotein.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 11.8%; Score 280; DB 7; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
 RESULT 1044  
 ID ADP65210 standard; protein; 1466 AA.  
 DE Human alpha 1 type III collagen preproprotein.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 11.8%; Score 280; DB 7; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
 RESULT 1045  
 ID ADQ26091 standard; protein; 1466 AA.  
 DE Type III, alpha 1 collagen.  
 PN WO2004056386-A2.  
 PD 08-JUL-2004.  
 PA (UYLE-) RIJKSUNIV LEIDEN.  
 Query Match 11.8%; Score 280; DB 8; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
 RESULT 1046  
 ID ADQ29677 standard; protein; 1466 AA.  
 DE Human colorectal cancer-associated protein #32.  
 PN EPI439393-A2.  
 PD 21-JUL-2004.  
 PA (FARB ) BAYER HEALTHCARE LLC.  
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
 Query Match 11.8%; Score 280; DB 8; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
 RESULT 1047  
 ID ADR16802 standard; protein; 1466 AA.  
 DE Human collagen III alpha2 (III) fragment protein.  
 PN US2004151731-A1.  
 PD 05-AUG-2004.  
 PA (JICH//) JICHA D L.  
 Query Match 11.8%; Score 280; DB 8; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
 RESULT 1048  
 ID ADR16427 standard; protein; 1466 AA.  
 DE Human collagen I alpha2 (III) fragment protein.  
 PN US2004151732-A1.  
 PD 05-AUG-2004.  
 PA (JICH//) JICHA D L.  
 PA (PELU//) PELUSE S.  
 Query Match 11.8%; Score 280; DB 8; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
 RESULT 1049  
 ID ABM80366 standard; protein; 1466 AA.

DE Tumour-associated antigenic target (TAT) polypeptide PRO2665, SEQ:922.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 11.8%; Score 280; DB 8; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1050  
ID ADR67267 standard; protein; 1466 AA.  
DE Human bladder cancer associated amino acid sequence.  
PN WO2004076613-A2.  
PD 10-SEP-2004.  
PA (HERR/) HERR A.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (STAU/) STAUB E.  
PA (PILA/) PILARSKY C.  
PA (SPEC/) SPECHT T.  
Query Match 11.8%; Score 280; DB 8; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1051  
ID ABG15191 standard; protein; 1469 AA.  
DE Novel human diagnostic protein #15182.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.8%; Score 280; DB 4; Length 1469;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1052  
ID ADE09399 standard; protein; 1470 AA.  
DE Novel protein-related contig polypeptide sequence #465.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.8%; Score 280; DB 7; Length 1470;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1053  
ID ABR42661 standard; protein; 1726 AA.  
DE Decorin-modified pro-alpha chain.  
PN WO2003035692-A2.  
PD 01-MAY-2003.  
PA (UYMA-) UNIV VICTORIA MANCHESTER.  
Query Match 11.8%; Score 280; DB 6; Length 1726;  
Best Local Similarity 27.4%; Pred. No. 7.9e-09;  
RESULT 1054  
ID ADO08777 standard; protein; 338 AA.  
DE Novel surgical dressing-related protein SeqID64.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN ) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 11.8%; Score 279; DB 8; Length 338;  
Best Local Similarity 29.2%; Pred. No. 1.9e-09;  
RESULT 1055  
ID ADP99004 standard; protein; 1096 AA.  
DE C. albicans specific gene, CayMR047C, protein sequence.  
PN WO2004056965-A2.  
PD 08-JUL-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 11.8%; Score 279; DB 8; Length 1096;  
Best Local Similarity 27.4%; Pred. No. 5.9e-09;  
RESULT 1056  
ID AAW78355 standard; protein; 526 AA.  
DE Human protein SEQ ID NO 1017.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.8%; Score 278.5; DB 4; Length 526;  
Best Local Similarity 27.7%; Pred. No. 3.1e-09;  
RESULT 1057  
ID ABG95081 standard; protein; 526 AA.  
DE Human translocation (12; 16)(q13; p11) protein #2.  
PN WO200269900-A2.

PD 12-SEP-2002.  
PA (CONF-) CONFORMA THERAPEUTICS CORP.  
Query Match 11.8%; Score 278.5; DB 5; Length 526;  
Best Local Similarity 27.7%; Pred. No. 3.1e-09;  
RESULT 1058  
ID ADI26117 standard; protein; 526 AA.  
DE Human protein that promotes STAT6 activation #41.  
PN WO2003104277-A2.  
PD 18-DEC-2003.  
PA (ASAH ) ASAH KASEI KK.  
Query Match 11.8%; Score 278.5; DB 8; Length 526;  
Best Local Similarity 27.7%; Pred. No. 3.1e-09;  
RESULT 1059  
ID ABM81732 standard; protein; 526 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO82568, SEQ:4466.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 11.8%; Score 278.5; DB 8; Length 526;  
Best Local Similarity 27.7%; Pred. No. 3.1e-09;  
RESULT 1060  
ID ADS88302 standard; protein; 526 AA.  
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 157.  
PN WO2004035783-A2.  
PD 29-APR-2004.  
PA (CELL-) CELLZOME AG.  
Query Match 11.8%; Score 278.5; DB 8; Length 526;  
Best Local Similarity 27.7%; Pred. No. 3.1e-09;  
RESULT 1061  
ID ABB61650 standard; protein; 2280 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 11742.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 11.8%; Score 278.5; DB 4; Length 2280;  
Best Local Similarity 26.3%; Pred. No. 1.3e-08;  
RESULT 1062  
ID RAR71704 standard; protein; 1078 AA.  
DE Collagen alpha 1 (III) chain precursor.  
PN WO9508115-A1.  
PD 23-MAR-1995.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.8%; Score 278; DB 2; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 6.7e-09;  
RESULT 1063  
ID ABU40120 standard; protein; 237 AA.  
DE Protein encoded by Prokaryotic essential gene #25647.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 11.7%; Score 277; DB 6; Length 237;  
Best Local Similarity 30.7%; Pred. No. 1.8e-09;  
RESULT 1064  
ID ABP53461 standard; protein; 768 AA.  
DE SELP5 related amino acid sequence #3.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 11.7%; Score 276.5; DB 5; Length 768;  
Best Local Similarity 23.1%; Pred. No. 6e-09;  
RESULT 1065  
ID ADE59683 standard; protein; 1372 AA.  
DE Rat Protein P02466, SEQ ID NO 5579.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1e-08;  
RESULT 1066  
ID ADD45148 standard; protein; 1372 AA.  
DE Rat Protein P02466, SEQ ID NO 10581.

PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1e-08;  
RESULT 1067  
ID ADD45604 standard; protein; 1372 AA.  
DE Rat Protein P02466, SEQ ID NO 11270.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1e-08;  
RESULT 1068  
ID ADE59687 standard; protein; 1372 AA.  
DE Rat Protein P02466, SEQ ID NO 5593.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1e-08;  
RESULT 1069  
ID ADD47529 standard; protein; 1372 AA.  
DE Rat Protein AAD41775, SEQ ID NO 13225.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1e-08;  
RESULT 1070  
ID AAY84548 standard; protein; 1040 AA.  
DE A human collagen 1 (alpha2) protein helical region.  
PN EP92586-A2.  
PD 12-APR-2000.  
PA (USSU ) US SURGICAL CORP.  
Query Match 11.7%; Score 276; DB 3; Length 1040;  
Best Local Similarity 29.8%; Pred. No. 8.6e-09;  
RESULT 1071  
ID AAY84547 standard; protein; 1040 AA.  
DE A human collagen 1 (alpha2) protein helical region.  
PN EP92586-A2.  
PD 12-APR-2000.  
PA (USSU ) US SURGICAL CORP.  
Query Match 11.7%; Score 276; DB 3; Length 1040;  
Best Local Similarity 29.8%; Pred. No. 8.6e-09;  
RESULT 1072  
ID AAY96125 standard; peptide; 1078 AA.  
DE Collagen type III alpha-1.  
PN US6110689-A.  
PD 29-AUG-2000.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.7%; Score 276; DB 3; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 8.9e-09;  
RESULT 1073  
ID AAE16478 standard; protein; 1078 AA.  
DE Human collagen alpha1 (III) protein.  
PN US6323314-B1.  
PD 27-NOV-2001.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.7%; Score 276; DB 5; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 8.9e-09;  
RESULT 1074  
ID ABB80736 standard; protein; 1078 AA.  
DE Collagen type III-alpha1 protein.  
PN US6355442-B1.  
PD 12-MAR-2002.  
PA (OSTE-) OSTEOMETER BIOTECH AS.  
Query Match 11.7%; Score 276; DB 5; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 8.9e-09;

RESULT 1075  
ID ABB09628 standard; peptide; 1078 AA.  
DE Amino acid sequence of human collagen type III alpha1.  
PN US6342361-B1.  
PD 29-JAN-2002.  
PA (OSTE-) OSTEOMETER BIOTECH AS.  
Query Match 11.7%; Score 276; DB 5; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 8.9e-09;  
RESULT 1076  
ID ADF13078 standard; protein; 1078 AA.  
DE Human collagen alpha1(III) chain precursor.  
PN US2003119058-A1.  
PD 26-JUN-2003.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.7%; Score 276; DB 7; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 8.9e-09;  
RESULT 1077  
ID AAY56801 standard; protein; 1366 AA.  
DE Human preproalpha 2 (I) collagen.  
PN EP967226-A2.  
PD 29-DEC-1999.  
PA (COHE-) COHESION TECHNOLOGIES INC.  
Query Match 11.7%; Score 276; DB 3; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1078  
ID ABB90751 standard; protein; 1366 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 234.  
PN W0200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.7%; Score 276; DB 5; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1079  
ID ABB90766 standard; protein; 1366 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 265.  
PN W0200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.7%; Score 276; DB 5; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1080  
ID ABB90741 standard; protein; 1366 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 214.  
PN W0200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.7%; Score 276; DB 5; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1081  
ID ABU54448 standard; protein; 1366 AA.  
DE Human tumour endothelial marker TEM 10.  
PN W0200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.7%; Score 276; DB 6; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1082  
ID ABU54473 standard; protein; 1366 AA.  
DE Human tumour endothelial marker TEM 40.  
PN W0200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.7%; Score 276; DB 6; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1083  
ID ABU54458 standard; protein; 1366 AA.  
DE Human tumour endothelial marker TEM 20.  
PN W0200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.7%; Score 276; DB 6; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1084

ID ABR92065 standard; protein; 1366 AA.  
DE Human cervical cancer cell marker protein SEQ ID NO:38.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.7%; Score 276; DB 6; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1085  
ID ADK70437 standard; protein; 1366 AA.  
DE Respiratory disease differentially expressed protein #3.  
PN WO2003101283-A2.  
PD 11-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 11.7%; Score 276; DB 8; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1086  
ID ADQ29669 standard; protein; 1366 AA.  
DE Human colorectal cancer-associated protein #24.  
PN EP1439393-A2.  
PD 21-JUL-2004.  
PA (FARB) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 11.7%; Score 276; DB 8; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1087  
ID ABO59421 standard; protein; 208 AA.  
DE Human genome derived single exon protein #5655.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 11.6%; Score 275; DB 8; Length 208;  
Best Local Similarity 32.1%; Pred. No. 2.1e-09;  
RESULT 1088  
ID ABG95084 standard; protein; 525 AA.  
DE Human translocation (12; 16)(q13; p11) protein #5.  
PN WO200269900-A2.  
PD 12-SEP-2002.  
PA (CONF-) CONFORMA THERAPEUTICS CORP.  
Query Match 11.6%; Score 275; DB 5; Length 525;  
Best Local Similarity 27.5%; Pred. No. 5.1e-09;  
RESULT 1089  
ID ADR14649 standard; protein; 525 AA.  
DE Human NP-kappaB pathway-associated protein SeqID650.  
PN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 11.6%; Score 275; DB 8; Length 525;  
Best Local Similarity 27.5%; Pred. No. 5.1e-09;  
RESULT 1090  
ID ABB61800 standard; protein; 944 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 12192.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEXE) PE CORP NY.  
Query Match 11.6%; Score 275; DB 4; Length 944;  
Best Local Similarity 24.4%; Pred. No. 9e-09;  
RESULT 1091  
ID ADH13201 standard; protein; 593 AA.  
DE Human malignant neoplasia-related protein SeqID50.  
PN EP135034-A2.  
PD 26-NOV-2003.  
PA (FARB) BAYER AG.  
Query Match 11.6%; Score 274; DB 8; Length 593;  
Best Local Similarity 36.9%; Pred. No. 6.7e-09;  
RESULT 1092  
ID ADF5631 standard; protein; 600 AA.  
DE Protein (SEQ ID I) related to oyster pearl keratin protein.  
PN JP2003012696-A.  
PD 15-JAN-2003.  
PA (MATS/) MATSUSHIRO A.  
Query Match 11.6%; Score 274; DB 7; Length 600;

Best Local Similarity 24.5%; Pred. No. 6.7e-09;  
RESULT 1093  
ID AAG29582 standard; protein; 730 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35222.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 11.6%; Score 274; DB 3; Length 730;  
Best Local Similarity 28.9%; Pred. No. 8.1e-09;  
RESULT 1094  
ID AAG29581 standard; protein; 752 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35221.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 11.6%; Score 274; DB 3; Length 752;  
Best Local Similarity 28.9%; Pred. No. 8.3e-09;  
RESULT 1095  
ID ADN35279 standard; protein; 1313 AA.  
DE Synthetic collagen used as sealant tissue protein.  
PN WO2004028404-A2.  
PD 08-APR-2004.  
PA (FIER-) FIBROGEN INC.  
Query Match 11.6%; Score 274; DB 8; Length 1313;  
Best Local Similarity 27.2%; Pred. No. 1.4e-08;  
RESULT 1096  
ID AAU31850 standard; protein; 2367 AA.  
DE Novel human secreted protein #2341.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.6%; Score 273; DB 4; Length 2367;  
Best Local Similarity 27.0%; Pred. No. 2.9e-08;  
RESULT 1097  
ID AAW49739 standard; protein; 479 AA.  
DE Protein polymer adhesive substrate PPAS2-F.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 272.5; DB 2; Length 479;  
Best Local Similarity 26.2%; Pred. No. 6.7e-09;  
RESULT 1098  
ID ABO77606 standard; protein; 619 AA.  
DE Pseudomonas aeruginosa polypeptide #9781.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 11.5%; Score 272.5; DB 7; Length 619;  
Best Local Similarity 25.2%; Pred. No. 8.6e-09;  
RESULT 1099  
ID ADK51953 standard; protein; 696 AA.  
DE Repeat protein polymer repeat sequence, SEQ ID 21.  
PN WO2003099465-A1.  
PD 04-DEC-2003.  
PA (DOWO) DOW CORNING CORP.  
PA (GEMV) GENECOR INT INC.  
Query Match 11.5%; Score 272.5; DB 8; Length 696;  
Best Local Similarity 28.6%; Pred. No. 9.6e-09;  
RESULT 1100  
ID AAW09214 standard; protein; 1065 AA.  
DE CLP6 polymer.  
PN WO9634618-A1.  
PD 07-NOV-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 272.5; DB 2; Length 1065;  
Best Local Similarity 27.7%; Pred. No. 1.4e-08;  
RESULT 1101  
ID ABB57364 standard; protein; 1373 AA.  
DE Mouse ischaemic condition related protein sequence SEQ ID NO:1029.  
PN WO200186188-A2.  
PD 22-NOV-2001.  
PA (UNYI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Query Match 11.5%; Score 272.5; DB 5; Length 1373;  
Best Local Similarity 30.3%; Pred. No. 1.8e-08;  
RESULT 1102

ID AAB82608 standard; protein; 291 AA.  
 DE Spider recombinant silk protein POE(ep1)7.  
 PN WO200153333-A1.  
 PD 26-JUL-2001.  
 PA (MELL/) MELLO C M.  
 PA (ARCI/) ARCIACONNO S.  
 PA (BUTL/) BUTLER M M.  
 PA (USSA) US SEC OF ARMY.  
 Query Match  
 Best Local Similarity 11.5%; Score 272; DB 4; Length 291;  
 RESULT 1103  
 ID AAB20586 standard; protein; 671 AA.  
 DE Novel human diagnostic protein #20577.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 11.5%; Score 272; DB 4; Length 671;  
 RESULT 1104  
 ID AAB3470 standard; peptide; 696 AA.  
 DE SLP9K related amino acid sequence #1.  
 PN US2002045567-A1.  
 PD 18-APR-2002.  
 PA (CAPP/) CAPPELLO J.  
 PA (STED/) STEDRONSKY E R.  
 Query Match  
 Best Local Similarity 11.5%; Score 272; DB 5; Length 696;  
 RESULT 1105  
 ID AAB53482 standard; protein; 696 AA.  
 DE Protein polymer SLP9K polymer block amino acid sequence.  
 PN US2002045567-A1.  
 PD 18-APR-2002.  
 PA (CAPP/) CAPPELLO J.  
 PA (STED/) STEDRONSKY E R.  
 Query Match  
 Best Local Similarity 11.5%; Score 272; DB 5; Length 696;  
 RESULT 1106  
 ID ADK51955 standard; protein; 696 AA.  
 DE Repeat protein polymer repeat sequence, SEQ ID 23.  
 PN WO2003099465-A1.  
 PD 04-DEC-2003.  
 PA (DOMO) DOW CORNING CORP.  
 PA (GENM) GENENCOR INT INC.  
 Query Match  
 Best Local Similarity 11.5%; Score 272; DB 8; Length 696;  
 RESULT 1107  
 ID ABU36642 standard; protein; 370 AA.  
 DE Protein encoded by Prokaryotic essential gene #22169.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (BLIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 11.5%; Score 271.5; DB 6; Length 370;  
 RESULT 1108  
 ID AAM79339 standard; protein; 569 AA.  
 DE Human protein SEQ ID NO 2985.  
 PN WO200157190-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 11.5%; Score 271.5; DB 4; Length 569;  
 RESULT 1109  
 ID AAM79340 standard; protein; 569 AA.  
 DE Human protein SEQ ID NO 2986.  
 PN WO200157190-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 11.5%; Score 271.5; DB 4; Length 569;  
 RESULT 1110  
 ID AAR80324 standard; protein; 762 AA.  
 DE Protein polymeric adhesion substrate 1-A.  
 PN WO9523611-A1.

PD 08-SEP-1995.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match  
 Best Local Similarity 11.5%; Score 271; DB 2; Length 762;  
 RESULT 1111  
 ID AAW57666 standard; peptide; 762 AA.  
 DE Collagen-like polymer.  
 PN US5773249-A.  
 PD 30-JUN-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match  
 Best Local Similarity 11.5%; Score 271; DB 2; Length 762;  
 RESULT 1112  
 ID AAW53535 standard; protein; 762 AA.  
 DE Amino acid sequence of the plasmid encoding fibrin gamma PPAS1-A.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match  
 Best Local Similarity 11.5%; Score 271; DB 2; Length 762;  
 RESULT 1113  
 ID AAW49713 standard; protein; 762 AA.  
 DE Protein polymer adhesive substrate PPAS1-A.  
 PN US5773577-A.  
 PD 30-JUN-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match  
 Best Local Similarity 11.5%; Score 271; DB 2; Length 762;  
 RESULT 1114  
 ID ABO58348 standard; protein; 2338 AA.  
 DE Human genome derived single exon protein #4582.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 Query Match  
 Best Local Similarity 11.5%; Score 271; DB 8; Length 2338;  
 RESULT 1115  
 ID ADR16801 standard; protein; 1366 AA.  
 DE Human collagen I alpha2 (I) chain protein.  
 PN US2004151731-A1.  
 PD 05-AUG-2004.  
 PA (JICH/) JICHA D L.  
 Query Match  
 Best Local Similarity 11.4%; Score 270.5; DB 8; Length 1366;  
 RESULT 1116  
 ID ADR16426 standard; protein; 1366 AA.  
 DE Human collagen I alpha2 (I) chain protein.  
 PN US2004151732-A1.  
 PD 05-AUG-2004.  
 PA (JICH/) JICHA D L.  
 PA (PELU/) PELUSE S.  
 Query Match  
 Best Local Similarity 11.4%; Score 270.5; DB 8; Length 1366;  
 RESULT 1117  
 ID ADR99147 standard; protein; 1366 AA.  
 DE Collagen, type 1, alpha 2, COL1A2, SEQ ID 153.  
 PN WO2004078035-A2.  
 PD 16-SEP-2004.  
 PA (FARB) BAYER PHARM CORP.  
 Query Match  
 Best Local Similarity 11.4%; Score 270.5; DB 8; Length 1366;  
 RESULT 1118  
 ID ADC87061 standard; protein; 920 AA.  
 DE Human GPCR protein SEQ ID NO:1514.  
 PN EP1270724-A2.  
 PD 02-JAN-2003.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
 Query Match  
 Best Local Similarity 11.4%; Score 270; DB 7; Length 920;  
 RESULT 1119

ID AAR28916 standard; protein; 1196 AA.  
DE Type III procollagen (prior art).  
PN WO9219754-A1.  
PD 12-NOV-1992.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
Query Match 11.4%; Score 270; DB 2; Length 1196;  
Best Local Similarity 29.0%; Pred. No. 2.3e-08;  
RESULT 1120  
ID AAE02537 standard; protein; 1466 AA.  
DE Porcine alaphal(III) collagen.  
PN WO200134647-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 11.4%; Score 270; DB 4; Length 1466;  
Best Local Similarity 29.0%; Pred. No. 2.8e-08;  
RESULT 1121  
ID AAE36870 standard; protein; 360 AA.  
DE Latrodectus geometricus major ampullate spidroin 1 (MaSp1) protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 11.4%; Score 269.5; DB 6; Length 360;  
Best Local Similarity 25.1%; Pred. No. 7.8e-09;  
RESULT 1122  
ID ADP31413 standard; protein; 951 AA.  
DE Human secreted protein SEQ ID #2180.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 11.4%; Score 269.5; DB 8; Length 951;  
Best Local Similarity 25.8%; Pred. No. 2e-08;  
RESULT 1123  
ID AEG31413 standard; protein; 1065 AA.  
DE CLP6 polymer encoded by plasmid pPT0246.  
PN US6423333-B1.  
PD 23-JUL-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.4%; Score 269.5; DB 5; Length 1065;  
Best Local Similarity 26.7%; Pred. No. 2.2e-08;  
RESULT 1124  
ID ABB70198 standard; protein; 272 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 37386.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 11.4%; Score 269; DB 4; Length 272;  
Best Local Similarity 29.9%; Pred. No. 6.4e-09;  
RESULT 1125  
ID ADC35284 standard; protein; 410 AA.  
DE ADP-4 silk protein.  
PN WO2003057727-A1.  
PD 17-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 11.4%; Score 269; DB 7; Length 410;  
Best Local Similarity 27.1%; Pred. No. 9.5e-09;  
RESULT 1126  
ID ADP31157 standard; protein; 474 AA.  
DE Human secreted protein SEQ ID #1924.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 11.4%; Score 269; DB 8; Length 474;  
Best Local Similarity 28.9%; Pred. No. 1.1e-08;  
RESULT 1127  
ID AAB70184 standard; peptide; 248 AA.  
DE Peptide dendrimer carrier #9.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 11.4%; Score 268.5; DB 4; Length 248;  
Best Local Similarity 31.2%; Pred. No. 6.3e-09;  
RESULT 1128  
ID ADL92144 standard; protein; 1027 AA.

DE Collagen protein sequence.  
PN WO200309862-A1.  
PD 04-DEC-2003.  
PA (NANO-) APPLIED NANOSYSTEMS BV.  
Query Match 11.4%; Score 268.5; DB 8; Length 1027;  
Best Local Similarity 27.7%; Pred. No. 2.4e-08;  
RESULT 1129  
ID AAR80327 standard; protein; 762 AA.  
DE Protein polymeric adhesion substrate 1-B.  
PN WO9523611-A1.  
PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.3%; Score 268; DB 2; Length 762;  
Best Local Similarity 27.9%; Pred. No. 2e-08;  
RESULT 1130  
ID AAW57668 standard; peptide; 762 AA.  
DE Collagen-like polymer.  
PN US5773249-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.3%; Score 268; DB 2; Length 762;  
Best Local Similarity 27.9%; Pred. No. 2e-08;  
RESULT 1131  
ID AAW49715 standard; protein; 762 AA.  
DE Protein polymer adhesive substrate PPAS1-B.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.3%; Score 268; DB 2; Length 762;  
Best Local Similarity 27.9%; Pred. No. 2e-08;  
RESULT 1132  
ID AAR71702 standard; protein; 1366 AA.  
DE Collagen alpha 2 (I) chain precursor.  
PN WO9508115-A1.  
PD 23-MAR-1995.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.3%; Score 267.5; DB 2; Length 1366;  
Best Local Similarity 30.3%; Pred. No. 3.7e-08;  
RESULT 1133  
ID AAY96123 standard; peptide; 1366 AA.  
DE Collagen type I alpha-2.  
PN US6110689-A.  
PD 29-AUG-2000.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.3%; Score 267.5; DB 3; Length 1366;  
Best Local Similarity 30.3%; Pred. No. 3.7e-08;  
RESULT 1134  
ID ABB50293 standard; protein; 1366 AA.  
DE Collagen type I alpha-2 ovarian tumour marker protein, SEQ ID NO:76.  
PN WO200175177-A2.  
PD 11-OCT-2001.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 11.3%; Score 267.5; DB 4; Length 1366;  
Best Local Similarity 30.3%; Pred. No. 3.7e-08;  
RESULT 1135  
ID AAE16476 standard; protein; 1366 AA.  
DE Human collagen alpha 2-type I protein.  
PN US6323314-B1.  
PD 27-NOV-2001.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.3%; Score 267.5; DB 5; Length 1366;  
Best Local Similarity 30.3%; Pred. No. 3.7e-08;  
RESULT 1136  
ID ABB80734 standard; protein; 1366 AA.  
DE Protein sequence related to human collagen.  
PN US6355442-B1.  
PD 12-MAR-2002.  
PA (OSTE-) OSTEOMETER BIOTECH AS.  
Query Match 11.3%; Score 267.5; DB 5; Length 1366;  
Best Local Similarity 30.3%; Pred. No. 3.7e-08;  
RESULT 1137  
ID ABB09626 standard; peptide; 1366 AA.  
DE Amino acid sequence of human collagen type I alpha2.

ID ADK51954 standard; protein; 1008 AA.  
 DE Repeat protein polymer repeat sequence, SEQ ID 22.  
 FN WO200309465-A1.  
 PD 04-DEC-2003.  
 PA (DOW) DOW CORNING CORP.  
 PA (GENV) GENENCOR INT INC.  
 Query Match 11.2%; Score 264.5; DB 8; Length 1008;  
 Best Local Similarity 27.5%; Pred. No. 4.2e-08;  
 RESULT 1147  
 ID ADR70477 standard; protein; 1063 AA.  
 DE Collagen-like protein.  
 FN US2004180027-A1.  
 PD 16-SEP-2004.  
 PA (KUMA/) KUMAR M.  
 PA (CUEV/) CUEVAS W A.  
 Query Match 11.2%; Score 264.5; DB 8; Length 1063;  
 Best Local Similarity 27.5%; Pred. No. 4.5e-08;  
 RESULT 1148  
 ID AAR37748 standard; protein; 1065 AA.  
 DE Collagen-like polymer DCP6 encoded by clone pPT 0246.  
 FN WO9310154-A1.  
 PD 27-MAY-1993.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 2; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 4.5e-08;  
 RESULT 1149  
 ID AAR93259 standard; protein; 1065 AA.  
 DE Collagen-like polymer sequence D gene 6 polymer protein (pPT0246).  
 FN US5496712-A.  
 PD 05-MAR-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 2; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 4.5e-08;  
 RESULT 1150  
 ID AAN57656 standard; peptide; 1065 AA.  
 DE Collagen-like polymer.  
 FN US5773249-A.  
 PD 30-JUN-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 2; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 4.5e-08;  
 RESULT 1151  
 ID AAY51893 standard; protein; 1065 AA.  
 DE Plasmid pPT0246 protein fragment containing CLP6 polymer units.  
 FN US6033654-A.  
 PD 07-MAR-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 3; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 4.5e-08;  
 RESULT 1152  
 ID ABW01629 standard; protein; 1065 AA.  
 DE Plasmid pPT0246 CLP6 polymer protein.  
 FN US2003104589-A1.  
 PD 05-JUN-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 7; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 4.5e-08;  
 RESULT 1153  
 ID AAE02534 standard; protein; 1466 AA.  
 DE Bovine alpha(III) collagen #2.  
 FN WO200134647-A2.  
 PD 17-MAY-2001.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.1%; Score 262.5; DB 4; Length 1466;  
 Best Local Similarity 26.3%; Pred. No. 8e-08;  
 RESULT 1154  
 ID AAE02533 standard; protein; 1466 AA.  
 DE Bovine alpha(III) collagen #1.  
 FN WO200134647-A2.  
 PD 17-MAY-2001.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.1%; Score 262.5; DB 4; Length 1466;  
 Best Local Similarity 26.3%; Pred. No. 8e-08;

## RESULT 1155

ID ADF63307 standard; protein; 553 AA.  
DE Human lung specific protein sequence SEQ ID NO:64.  
PN WO2003102137-A2.  
PD 11-DEC-2003.  
PA (DIAD-) DIADEXUS INC.

Query Match 11.1%; Score 262; DB 8; Length 553;  
Best Local Similarity 26.1%; Pred. No. 3.4e-08;

## RESULT 1156

ID ABB58985 standard; protein; 1937 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 3747.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.

Query Match 11.1%; Score 261.5; DB 4; Length 1937;  
Best Local Similarity 24.9%; Pred. No. 1.2e-07;

## RESULT 1157

ID ADR86371 standard; protein; 1049 AA.  
DE Aspergillus fumigatus essential gene protein #421.  
PN WO2004067709-A2.  
PD 12-AUG-2004.  
PA (ELIT-) ELITRA PHARM INC.

Query Match 11.0%; Score 261; DB 8; Length 1049;  
Best Local Similarity 23.7%; Pred. No. 7.2e-08;

## RESULT 1158

ID ABB63141 standard; protein; 828 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 16215.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.

Query Match 11.0%; Score 260.5; DB 4; Length 828;  
Best Local Similarity 26.5%; Pred. No. 6.2e-08;

## RESULT 1159

ID ADQ08606 standard; protein; 1104 AA.  
DE Ciona intestinalis nervous system associated protein SeqID8.  
PN JP2004057127-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JTGYODAN.

Query Match 11.0%; Score 260.5; DB 8; Length 1104;  
Best Local Similarity 28.6%; Pred. No. 8.1e-08;

## RESULT 1160

ID AAE36880 standard; protein; 399 AA.  
DE Latrodectus geometricus major ampullate spidroin 2 (MasP2) protein #2.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.

Query Match 11.0%; Score 259.5; DB 6; Length 399;  
Best Local Similarity 27.3%; Pred. No. 3.5e-08;

## RESULT 1161

ID ADP31162 standard; protein; 537 AA.  
DE Human secreted protein SEQ ID #1929.  
PN WO2004035732-A2.  
PD 29-APR-2004.

Query Match 11.0%; Score 259; DB 8; Length 537;  
Best Local Similarity 25.9%; Pred. No. 5e-08;

## RESULT 1162

ID ABG95083 standard; protein; 462 AA.  
DE Human translocation (12; 16)(q13; p11) protein #4.  
PN WO200269900-A2.  
PD 12-SEP-2002.  
PA (CONF-) CONFORMA THERAPEUTICS CORP.

Query Match 10.9%; Score 258.5; DB 5; Length 462;  
Best Local Similarity 32.7%; Pred. No. 4.7e-08;

## RESULT 1163

ID ADP31163 standard; protein; 594 AA.  
DE Human secreted protein SEQ ID #1930.  
PN WO2004035732-A2.  
PD 29-APR-2004.

Query Match 10.9%; Score 258; DB 8; Length 594;  
Best Local Similarity 26.2%; Pred. No. 6.4e-08;

## RESULT 1164

ID AAR37751 standard; protein; 1077 AA.  
DE CLIP 3.1 monomer containing peptide.  
PN WO9310154-A1.  
PD 27-MAY-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 10.9%; Score 258; DB 2; Length 1077;  
Best Local Similarity 28.7%; Pred. No. 1.1e-07;

## RESULT 1165

ID ADI26113 standard; protein; 518 AA.  
DE Human protein that promotes STAT6 activation #39.  
PN WO2003104277-A2.  
PD 18-DEC-2003.  
PA (ASAH ) ASAH KASEI KK.

Query Match 10.9%; Score 257.5; DB 8; Length 518;  
Best Local Similarity 26.2%; Pred. No. 6e-08;

## RESULT 1166

ID ABB71788 standard; protein; 385 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 42156.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.

Query Match 10.9%; Score 257; DB 4; Length 385;  
Best Local Similarity 35.4%; Pred. No. 4.9e-08;

## RESULT 1167

ID ADP31164 standard; protein; 534 AA.  
DE Human secreted protein SEQ ID #1931.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

Query Match 10.9%; Score 257; DB 8; Length 534;  
Best Local Similarity 26.0%; Pred. No. 6.7e-08;

## RESULT 1168

ID AAR37746 standard; protein; 633 AA.  
DE Collagen-like polymer DCP5 encoded by clone pPT 0232.  
PN WO9310154-A1.  
PD 27-MAY-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 10.9%; Score 257; DB 2; Length 633;  
Best Local Similarity 30.4%; Pred. No. 7.8e-08;

## RESULT 1169

ID AAR93257 standard; protein; 633 AA.  
DE Collagen-like polymer sequence D gene 5 polymer protein (pPT0232).  
PN US5496712-A.  
PD 05-MAR-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 10.9%; Score 257; DB 2; Length 633;  
Best Local Similarity 30.4%; Pred. No. 7.8e-08;

## RESULT 1170

ID AAW57655 standard; peptide; 633 AA.  
DE Collagen-like polymer.  
PN US5773249-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 10.9%; Score 257; DB 2; Length 633;  
Best Local Similarity 30.4%; Pred. No. 7.8e-08;

## RESULT 1171

ID ABU17075 standard; protein; 974 AA.  
DE Protein encoded by Prokaryotic essential gene #2602.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.

Query Match 10.9%; Score 257; DB 6; Length 974;  
Best Local Similarity 24.1%; Pred. No. 1.2e-07;

## RESULT 1172

ID AAR37745 standard; protein; 1065 AA.  
DE Collagen-like polymer DCP4 encoded by clone pPT 0249.  
PN WO9310154-A1.  
PD 27-MAY-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 10.9%; Score 257; DB 2; Length 1065;  
Best Local Similarity 28.0%; Pred. No. 1.3e-07;

## RESULT 1173



ID AAR93256 standard; protein; 1065 AA.  
 DE Collagen-like polymer sequence D gene 4 polymer protein (pPT0249).  
 PN US5496712-A.  
 PD 05-MAR-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 10.9%; Score 257; DB 2; Length 1065;  
 Best Local Similarity 28.0%; Pred. No. 1.3e-07;  
 RESULT 1174  
 ID AAW57654 standard; peptide; 1065 AA.  
 DE Collagen-like polymer.  
 PN US5773249-A.  
 PD 30-JUN-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 10.9%; Score 257; DB 2; Length 1065;  
 Best Local Similarity 28.0%; Pred. No. 1.3e-07;  
 RESULT 1175  
 ID AAM50035 standard; protein; 230 AA.  
 DE N. clavipes spidroin synthetic homologue SE1 protein.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 10.8%; Score 255.5; DB 5; Length 230;  
 Best Local Similarity 30.0%; Pred. No. 3.7e-08;  
 RESULT 1176  
 ID ADI26207 standard; protein; 589 AA.  
 DE Human protein that promotes STAT6 activation #86.  
 PN WO2003104277-A2.  
 PD 18-DEC-2003.  
 PA (ASAH) ASAHI KASEI KK.  
 Query Match 10.8%; Score 255.5; DB 8; Length 589;  
 Best Local Similarity 26.0%; Pred. No. 9e-08;  
 RESULT 1177  
 ID ABO53050 standard; protein; 592 AA.  
 DE Human putative spliceosome associated protein (SAP) #26.  
 PN US2003068803-A1.  
 PD 10-APR-2003.  
 PA (REED/) REED R.  
 PA (ZHOU/) ZHOU Z.  
 Query Match 10.8%; Score 255.5; DB 6; Length 592;  
 Best Local Similarity 26.0%; Pred. No. 9.1e-08;  
 RESULT 1178  
 ID ADI26209 standard; protein; 592 AA.  
 DE Human protein that promotes STAT6 activation #87.  
 PN WO2003104277-A2.  
 PD 18-DEC-2003.  
 PA (ASAH) ASAHI KASEI KK.  
 Query Match 10.8%; Score 255.5; DB 8; Length 592;  
 Best Local Similarity 26.0%; Pred. No. 9.1e-08;  
 RESULT 1179  
 ID ABB66654 standard; protein; 499 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 26754.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 10.8%; Score 254.5; DB 4; Length 499;  
 Best Local Similarity 26.3%; Pred. No. 8.9e-08;  
 RESULT 1180  
 ID ADN99871 standard; protein; 632 AA.  
 DE Novel human protein sequence #687.  
 PN WO2004038003-A2.  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 10.7%; Score 254; DB 8; Length 632;  
 Best Local Similarity 34.2%; Pred. No. 1.2e-07;  
 RESULT 1181  
 ID ABF53478 standard; protein; 1040 AA.  
 DE Protein polymer SELP6 polymer block amino acid sequence.  
 PN US2002045567-A1.  
 PD 18-APR-2002.  
 PA (CAPP/) CAPPELLO J.  
 PA (STED/) STEDRONSKY E R.  
 Query Match 10.7%; Score 254; DB 5; Length 1040;  
 Best Local Similarity 22.9%; Pred. No. 1.9e-07;

RESULT 1182  
 ID ABM83560 standard; protein; 1417 AA.  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3809.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 10.7%; Score 254; DB 8; Length 1417;  
 Best Local Similarity 27.4%; Pred. No. 2.6e-07;  
 RESULT 1183  
 ID ADE55694 standard; protein; 1419 AA.  
 DE Rat protein AAA79780, SEQ ID NO 1513.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 Query Match 10.7%; Score 254; DB 7; Length 1419;  
 Best Local Similarity 26.4%; Pred. No. 2.6e-07;  
 RESULT 1184  
 ID ABG61861 standard; protein; 1487 AA.  
 DE Prostate cancer-associated protein #62.  
 PN WO200230268-A2.  
 PD 18-APR-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 10.7%; Score 254; DB 5; Length 1487;  
 Best Local Similarity 27.4%; Pred. No. 2.7e-07;  
 RESULT 1185  
 ID ABP56769 standard; protein; 1487 AA.  
 DE Collagen IIA protein.  
 PN WO2002100426-A1.  
 PD 19-DEC-2002.  
 PA (SMIN) SMITH & NEPHEW PLC.  
 Query Match 10.7%; Score 254; DB 6; Length 1487;  
 Best Local Similarity 27.4%; Pred. No. 2.7e-07;  
 RESULT 1186  
 ID AAG77793 standard; protein; 1745 AA.  
 DE Human pro-alpha-3(V) fibrillar procollagen polypeptide.  
 PN WO200164871-A2.  
 PD 07-SEP-2001.  
 PA (WISC) WISCONSIN ALUMNI RES FOUND.  
 Query Match 10.7%; Score 254; DB 4; Length 1745;  
 Best Local Similarity 27.6%; Pred. No. 3.2e-07;  
 RESULT 1187  
 ID ABB97234 standard; protein; 1745 AA.  
 DE Novel human protein SEQ ID NO: 502.  
 PN WO200222660-A2.  
 PD 21-MAR-2002.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 10.7%; Score 254; DB 5; Length 1745;  
 Best Local Similarity 27.6%; Pred. No. 3.2e-07;  
 RESULT 1188  
 ID ADQ19841 standard; protein; 1745 AA.  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2660.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 10.7%; Score 254; DB 8; Length 1745;  
 Best Local Similarity 27.6%; Pred. No. 3.2e-07;  
 RESULT 1189  
 ID AAM50048 standard; protein; 264 AA.  
 DE N. clavipes spidroin synthetic homologue FA2 protein #2.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 10.7%; Score 253; DB 5; Length 264;  
 Best Local Similarity 30.7%; Pred. No. 6e-08;  
 RESULT 1190  
 ID ADK51957 standard; protein; 780 AA.  
 DE Repeat protein polymer repeat sequence, SEQ ID 25.  
 PN WO2003099465-A1.  
 PD 04-DEC-2003.  
 PA (DOWO) DOW CORNING CORP.  
 PA (GEMV) GENENCOR INT INC.  
 Query Match 10.7%; Score 253; DB 8; Length 780;  
 Best Local Similarity 10.7%;

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Best Local Similarity 29.2%; Pred. No. 1.7e-07;
RESULT 1191
ID ADC21544 standard; protein; 1014 AA.
DE Human type II collagen protein sequence.
PN WO2003006603-A2.
PD 23-JAN-2003.
PA (AREX-) AREXIS AB.
Query Match 10.7%; Score 253; DB 7; Length 1014;
Best Local Similarity 27.4%; Pred. No. 2.2e-07;
RESULT 1192
ID AAE18321 standard; protein; 1020 AA.
DE Collagen like protein, CLP3.1.
PN WO200200016-A1.
PD 03-JAN-2002.
PA (LUMI-) LUMINIS PTY LTD.
PA (SAUR-) SOUTH AUSTRALIAN RES & DEV INST.
Query Match 10.7%; Score 253; DB 5; Length 1020;
Best Local Similarity 29.2%; Pred. No. 2.2e-07;
RESULT 1193
ID AAR93261 standard; protein; 1077 AA.
DE CLP 3.1 polymer sequence (pPT0297).
PN US5496712-A.
PD 05-MAR-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.7%; Score 253; DB 2; Length 1077;
Best Local Similarity 29.2%; Pred. No. 2.3e-07;
RESULT 1194
ID RAW57657 standard; peptide; 1077 AA.
DE Collagen-like polymer.
PN US5773249-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.7%; Score 253; DB 2; Length 1077;
Best Local Similarity 29.2%; Pred. No. 2.3e-07;
RESULT 1195
ID ABP60377 standard; peptide; 1217 AA.
DE Bombyx mori sericin SEQ ID NO 2.
PN WO200286133-A1.
PD 31-OCT-2002.
PA (SEIR-) SEIREN CO LTD.
Query Match 10.7%; Score 253; DB 6; Length 1217;
Best Local Similarity 27.0%; Pred. No. 2.6e-07;
RESULT 1196
ID AAR59751 standard; protein; 1418 AA.
DE Type II collagen.
PN WO9414070-A1.
PD 23-JUN-1994.
PA (SHRI-) SHRINERS HOSPITALS FOR CRIPPLED CHILDREN.
Query Match 10.7%; Score 253; DB 2; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1197
ID AAR71703 standard; protein; 1418 AA.
DE Collagen alpha 1 (II) chain precursor.
PN WO9508115-A1.
PD 23-MAR-1995.
PA (OSTE-) OSTEOMETER AS.
Query Match 10.7%; Score 253; DB 2; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1198
ID RAY96124 standard; peptide; 1418 AA.
DE Collagen type II alpha-1.
PN US6110689-A.
PD 29-AUG-2000.
PA (OSTE-) OSTEOMETER AS.
Query Match 10.7%; Score 253; DB 3; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1199
ID AAB35624 standard; protein; 1418 AA.
DE Human type II collagen.
PN US6132976-A.
PD 17-OCT-2000.
PA (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
Query Match 10.7%; Score 253; DB 4; Length 1418;

Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1200
ID AAE16477 standard; protein; 1418 AA.
DE Human collagen alpha (II) protein.
PN US6323314-B1.
PD 27-NOV-2001.
PA (OSTE-) OSTEOMETER AS.
Query Match 10.7%; Score 253; DB 5; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1201
ID ABB80735 standard; protein; 1418 AA.
DE Collagen type II-alpha1 protein.
PN US6355442-B1.
PD 12-MAR-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match 10.7%; Score 253; DB 5; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1202
ID ABG91927 standard; protein; 1418 AA.
DE Human polypeptide orthologous to DACC-2.
PN WO200264625-A1.
PD 22-AUG-2002.
PA (ADPP-) ADP PHARM PTY LTD.
PA (UNSY) UNIV SYDNEY.
Query Match 10.7%; Score 253; DB 5; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1203
ID ABB09627 standard; peptide; 1418 AA.
DE Amino acid sequence of human collagen type II alpha1.
PN US6342361-B1.
PD 29-JAN-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match 10.7%; Score 253; DB 5; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1204
ID ADF13077 standard; protein; 1418 AA.
DE Human collagen alpha(II) chain precursor.
PN US2003119058-A1.
PD 26-JUN-2003.
PA (OSTE-) OSTEOMETER AS.
Query Match 10.7%; Score 253; DB 7; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1205
ID ADP31446 standard; protein; 1755 AA.
DE Human secreted protein SEQ ID #2213.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 10.7%; Score 252.5; DB 8; Length 1755;
Best Local Similarity 24.2%; Pred. No. 3.9e-07;
RESULT 1206
ID AAO16498 standard; protein; 227 AA.
DE Argiope trifasciata spider silk protein #2.
PN WO200299082-A2.
PD 12-DEC-2002.
PA (UYWY-) UNIV WYOMING.
Query Match 10.7%; Score 252; DB 6; Length 227;
Best Local Similarity 29.2%; Pred. No. 6e-08;
RESULT 1207
ID AAP90064 standard; protein; 429 AA.
DE Antigenic protein for malaria vaccination.
PN USN7238746-N.
PD 21-MAR-1989.
PA (USSH-) NAT INST OF HEALTH.
Query Match 10.7%; Score 252; DB 1; Length 429;
Best Local Similarity 19.9%; Pred. No. 1.1e-07;
RESULT 1208
ID RAAW61562 standard; protein; 1487 AA.
DE Human type II collagen alpha-chain protein.
PN WO9835235-A1.
PD 13-AUG-1998.
PA (UYSH-) UNIV SHEFFIELD.
Query Match 10.7%; Score 252; DB 2; Length 1487;
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Best Local Similarity 27.1%; Pred. No. 3.6e-07;  
RESULT 1209  
ID AEG3945 standard; protein; 1497 AA.  
DE Mouse polypeptide orthologous to DACC-10.  
PN WO200264625-A1.  
PD 22-AUG-2002.  
PA (ADPP-) ADP PHARM PTY LTD.  
PA (UNSY ) UNIV SYDNEY.  
Query Match 10.7%; Score 252; DB 5; Length 1497;  
Best Local Similarity 26.0%; Pred. No. 3.6e-07;  
RESULT 1210  
ID ADE77159 standard; protein; 462 AA.  
DE Human protein expressed in a liver disorder #83.  
PN US2003108871-A1.  
PD 12-JUN-2003.  
PA (KASE/) KASER M R.  
Query Match 10.6%; Score 251.5; DB 8; Length 462;  
Best Local Similarity 29.9%; Pred. No. 1.3e-07;  
RESULT 1211  
ID ADF31648 standard; protein; 889 AA.  
DE Human secreted protein SEQ ID #2415.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 10.6%; Score 251.5; DB 8; Length 889;  
Best Local Similarity 26.6%; Pred. No. 2.4e-07;  
RESULT 1212  
ID AAP70709 standard; protein; 402 AA.  
DE Plasmodium cynomolgi sporozoite circumsporozoite protein.  
PN WO8700533-A.  
PD 29-JAN-1987.  
PA (UYNY ) UNIV NEW YORK STATE.  
PA (ARNO/) ARNOT D E.  
Query Match 10.6%; Score 251; DB 1; Length 402;  
Best Local Similarity 25.5%; Pred. No. 1.2e-07;  
RESULT 1213  
ID ADD45053 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 10485.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 4.1e-07;  
RESULT 1214  
ID ADD45057 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 10489.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 4.1e-07;  
RESULT 1215  
ID ADD48341 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 14041.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 4.1e-07;  
RESULT 1216  
ID ADD45049 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 10481.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 4.1e-07;  
RESULT 1217  
ID ADD48337 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 14037.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 4.1e-07;  
RESULT 1218  
ID ADD48345 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 14045.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 4.1e-07;  
RESULT 1219  
ID AAM50040 standard; protein; 219 AA.  
DE N. clavipes spidroin synthetic homologue FA2 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 10.6%; Score 250.5; DB 5; Length 219;  
Best Local Similarity 32.8%; Pred. No. 7.1e-08;  
RESULT 1220  
ID ADC35282 standard; protein; 360 AA.  
DE ADF-1 silk protein.  
PN WO2003057727-A1.  
PD 17-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 10.6%; Score 250.5; DB 7; Length 360;  
Best Local Similarity 25.7%; Pred. No. 1.1e-07;  
RESULT 1221  
ID AAG92278 standard; protein; 585 AA.  
DE C glutamicum protein fragment SEQ ID NO: 6032.  
PN EPI108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 10.6%; Score 250.5; DB 4; Length 585;  
Best Local Similarity 24.9%; Pred. No. 1.8e-07;  
RESULT 1222  
ID AAG28100 standard; protein; 274 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33192.  
PN EPI33405-A2.  
PD 06-SEP-2000.  
Query Match 10.6%; Score 250; DB 3; Length 274;  
Best Local Similarity 30.2%; Pred. No. 9.5e-08;  
RESULT 1223  
ID AAU08231 standard; protein; 597 AA.  
DE Polypeptide encoded by Mycobacterium tuberculosis clone mTCC#3.  
PN WO200162893-A2.  
PD 30-AUG-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 10.6%; Score 250; DB 4; Length 597;  
Best Local Similarity 26.7%; Pred. No. 2e-07;  
RESULT 1224  
ID ABU25538 standard; protein; 669 AA.  
DE Protein encoded by Prokaryotic essential gene #11065.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 10.6%; Score 249.5; DB 6; Length 669;  
Best Local Similarity 43.6%; Pred. No. 2.4e-07;  
RESULT 1225  
ID ADJ67574 standard; protein; 702 AA.  
DE Human ovarian specific polypeptide SEQ ID NO:288.  
PN WO200401311-A2.  
PD 12-FEB-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.6%; Score 249.5; DB 8; Length 702;  
Best Local Similarity 27.8%; Pred. No. 2.5e-07;  
RESULT 1226  
ID ABB60516 standard; protein; 1190 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 8340.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 10.5%; Score 249; DB 4; Length 1190;  
Best Local Similarity 29.1%; Pred. No. 4.4e-07;  
RESULT 1227  
ID AAR79480 standard; protein; 1442 AA.  
DE Rat type II collagen.  
PN WO9522611-A2.  
PD 24-AUG-1995.  
PA (UNMI ) UNIV MICHIGAN.  
Query Match 10.5%; Score 248.5; DB 2; Length 1442;  
Best Local Similarity 24.3%; Pred. No. 5.7e-07;  
RESULT 1228  
ID AAU79906 standard; protein; 267 AA.  
DE Fragment for resistance against dehydration stress, protein #4.  
PN WO200226800-A1.  
PD 04-APR-2002.  
PA (SEIR-) SEIREN CO LTD.  
Query Match 10.5%; Score 247.5; DB 5; Length 267;  
Best Local Similarity 33.6%; Pred. No. 1.3e-07;  
RESULT 1229  
ID ABB60010 standard; protein; 399 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 6822.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 10.5%; Score 247.5; DB 4; Length 399;  
Best Local Similarity 25.0%; Pred. No. 1.9e-07;  
RESULT 1230  
ID AAY50936 standard; protein; 590 AA.  
DE Human adult skin cDNA clone vdl\_1 derived protein #1.  
PN WO955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 10.5%; Score 247.5; DB 3; Length 590;  
Best Local Similarity 24.3%; Pred. No. 2.8e-07;  
RESULT 1231  
ID ABP75534 standard; protein; 601 AA.  
DE Human secretory polypeptide SPTM SEQ ID NO 718.  
PN WO200283876-A2.  
PD 24-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 10.5%; Score 247.5; DB 6; Length 601;  
Best Local Similarity 24.3%; Pred. No. 2.9e-07;  
RESULT 1232  
ID AAG77792 standard; protein; 1739 AA.  
DE Murine pro-alpha-3(V) fibrillar procollagen polypeptide.  
PN WO200164871-A2.  
PD 07-SEP-2001.  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
Query Match 10.5%; Score 247.5; DB 4; Length 1739;  
Best Local Similarity 26.6%; Pred. No. 7.9e-07;  
RESULT 1233  
ID ABU36445 standard; protein; 3300 AA.  
DE Protein encoded by Prokaryotic essential gene #21972.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 10.5%; Score 247.5; DB 6; Length 3300;  
Best Local Similarity 24.0%; Pred. No. 1.5e-06;  
RESULT 1234  
ID ADA33477 standard; protein; 975 AA.  
DE Acinetobacter baumannii protein #638.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.5%; Score 247; DB 6; Length 975;  
Best Local Similarity 24.3%; Pred. No. 4.9e-07;  
RESULT 1235  
ID ADO08789 standard; protein; 338 AA.  
DE Novel surgical dressing-related protein SeqID76.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN ) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 10.4%; Score 246.5; DB 8; Length 338;  
Best Local Similarity 28.5%; Pred. No. 1.9e-07;  
RESULT 1236  
ID AAY06239 standard; protein; 595 AA.  
DE Mouse recombinant type I collagen COL1A1-2.  
PN EP926543-A1.  
PD 30-JUN-1999.  
PA (FUJF ) FUJII PHOTO FILM BV.  
Query Match 10.4%; Score 246.5; DB 2; Length 595;  
Best Local Similarity 28.6%; Pred. No. 3.3e-07;  
RESULT 1237  
ID AAY06240 standard; protein; 822 AA.  
DE Mouse recombinant type I collagen COL1A1-3.  
PN EP926543-A1.  
PD 30-JUN-1999.  
PA (FUJF ) FUJII PHOTO FILM BV.  
Query Match 10.4%; Score 246.5; DB 2; Length 822;  
Best Local Similarity 28.6%; Pred. No. 4.4e-07;  
RESULT 1238  
ID AAR71701 standard; protein; 1341 AA.  
DE Collagen alpha 1 (I) chain precursor.  
PN WO9508115-A1.  
PD 23-MAR-1995.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 10.4%; Score 246.5; DB 2; Length 1341;  
Best Local Similarity 27.8%; Pred. No. 7.1e-07;  
RESULT 1239  
ID AAY96122 standard; peptide; 1341 AA.  
DE Collagen type I alpha-1.  
PN US6110689-A.  
PD 29-AUG-2000.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 10.4%; Score 246.5; DB 3; Length 1341;  
Best Local Similarity 27.8%; Pred. No. 7.1e-07;  
RESULT 1240  
ID AAE16475 standard; protein; 1341 AA.  
DE Human collagen alphas (I) protein.  
PN US6323314-B1.  
PD 27-NOV-2001.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 10.4%; Score 246.5; DB 5; Length 1341;  
Best Local Similarity 27.8%; Pred. No. 7.1e-07;  
RESULT 1241  
ID ABB80733 standard; protein; 1341 AA.  
DE Collagen type I-alpha protein.  
PN US6355442-B1.  
PD 12-MAR-2002.  
PA (OSTE-) OSTEOMETER BIOTECH AS.  
Query Match 10.4%; Score 246.5; DB 5; Length 1341;  
Best Local Similarity 27.8%; Pred. No. 7.1e-07;  
RESULT 1242  
ID ABB09625 standard; peptide; 1341 AA.  
DE Amino acid sequence of human collagen type I alpha1.  
PN US6342361-B1.  
PD 29-JAN-2002.  
PA (OSTE-) OSTEOMETER BIOTECH AS.  
Query Match 10.4%; Score 246.5; DB 5; Length 1341;  
Best Local Similarity 27.8%; Pred. No. 7.1e-07;  
RESULT 1243  
ID ADF13075 standard; protein; 1341 AA.  
DE Human collagen alpha(I) chain precursor.  
PN US2003119058-A1.  
PD 26-JUN-2003.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 10.4%; Score 246.5; DB 7; Length 1341;  
Best Local Similarity 27.8%; Pred. No. 7.1e-07;  
RESULT 1244  
ID ABG93948 standard; protein; 1453 AA.  
DE Mouse polypeptide orthologous to DACC-11.

PN WO200264625-A1.  
PD 22-AUG-2002.  
PA (ADPP-) ADP PHARM PTY LTD.  
PA (UNSY ) UNIV SYDNEY.  
Query Match 10.4%; Score 246.5; DB 5; Length 1453;  
Best Local Similarity 28.6%; Pred. No. 7.7e-07;  
RESULT 1245  
ID AAR60620 standard; protein; 1958 AA.  
DE Protein from ORF2 of Pseudorabies virus large latency transcript.  
PN US5352596-A.  
PD 04-OCT-1994.  
PA (USDA ) US SEC OF AGRIC.  
Query Match 10.4%; Score 246.5; DB 2; Length 1958;  
Best Local Similarity 23.7%; Pred. No. 1e-06;  
RESULT 1246  
ID ABO23520 standard; protein; 354 AA.  
DE Mycobacterium tuberculosis outlier protein #4.  
PN US2003039963-A1.  
PD 27-FEB-2003.  
PA (BRAH/) BRAHMACHARI S K.  
PA (RAMA/) RAMACHANDRAN S.  
PA (NAND/) NANDI T.  
PA (BHIM/) BHIMARAO C.  
Query Match 10.4%; Score 245.5; DB 7; Length 354;  
Best Local Similarity 26.0%; Pred. No. 2.3e-07;  
RESULT 1247  
ID ADC21591 standard; protein; 1014 AA.  
DE Mouse type II collagen protein sequence.  
PN WO2003006603-A2.  
PD 23-JAN-2003.  
PA (AREX-) AREXIS AB.  
Query Match 10.4%; Score 245.5; DB 7; Length 1014;  
Best Local Similarity 24.9%; Pred. No. 6.3e-07;  
RESULT 1248  
ID AAE02535 standard; protein; 1449 AA.  
DE Porcine alpha1(I) collagen.  
PN WO200134647-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 10.4%; Score 245.5; DB 4; Length 1449;  
Best Local Similarity 28.9%; Pred. No. 8.8e-07;  
RESULT 1249  
ID ABG93928 standard; protein; 1487 AA.  
DE Mouse polypeptide orthologous to DACC-2.  
PN WO200264625-A1.  
PD 22-AUG-2002.  
PA (ADPP-) ADP PHARM PTY LTD.  
PA (UNSY ) UNIV SYDNEY.  
Query Match 10.4%; Score 245.5; DB 5; Length 1487;  
Best Local Similarity 24.9%; Pred. No. 9e-07;  
RESULT 1250  
ID AAG28101 standard; protein; 267 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33193.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 10.4%; Score 245; DB 3; Length 267;  
Best Local Similarity 30.2%; Pred. No. 1.9e-07;  
RESULT 1251  
ID AAB35148 standard; protein; 894 AA.  
DE Human NFAR-2 SEQ ID NO: 4.  
PN WO200077205-A1.  
PD 21-DEC-2000.  
PA (BARB/) BARBER G N.  
PA (SAUN/) SAUNDERS L.  
PA (PERK/) PERKINS D J.  
Query Match 10.4%; Score 245; DB 4; Length 894;  
Best Local Similarity 28.3%; Pred. No. 6e-07;  
RESULT 1252  
ID ADA03105 standard; protein; 894 AA.  
DE Nucleotide therapy testing protein #11.  
PN WO2003023031-A1.  
PD 20-MAR-2003.  
PA (NNSH ) NIPPON SHINYAKU CO LTD.

Query Match 10.4%; Score 245; DB 6; Length 894;  
Best Local Similarity 28.3%; Pred. No. 6e-07;  
RESULT 1253  
ID ADJ66639 standard; protein; 894 AA.  
DE Interleukin enhancer binding factor 3 for anti-cancer protein complex.  
PN WO2004009622-A2.  
PD 29-JAN-2004.  
PA (CELL-) CELLZOME AG.  
Query Match 10.4%; Score 245; DB 8; Length 894;  
Best Local Similarity 28.3%; Pred. No. 6e-07;  
RESULT 1254  
ID ADL56761 standard; protein; 894 AA.  
DE Human cell derived viral RNA binding protein 110.  
PN WO2004029199-A2.  
PD 08-APR-2004.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match 10.4%; Score 245; DB 8; Length 894;  
Best Local Similarity 28.3%; Pred. No. 6e-07;  
RESULT 1255  
ID ADQ20794 standard; protein; 894 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3614.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 10.4%; Score 245; DB 8; Length 894;  
Best Local Similarity 28.3%; Pred. No. 6e-07;  
RESULT 1256  
ID ADE31110 standard; protein; 906 AA.  
DE Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID NO 242.  
PN WO2003062376-A2.  
PD 31-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 10.4%; Score 245; DB 7; Length 906;  
Best Local Similarity 28.3%; Pred. No. 6e-07;  
RESULT 1257  
ID AAG41604 standard; protein; 1424 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51784.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 10.4%; Score 245; DB 3; Length 1424;  
Best Local Similarity 32.9%; Pred. No. 9.3e-07;  
RESULT 1258  
ID AAG41603 standard; protein; 1457 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51783.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 10.4%; Score 245; DB 3; Length 1457;  
Best Local Similarity 32.9%; Pred. No. 9.5e-07;  
RESULT 1259  
ID AAG30466 standard; protein; 1598 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36428.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 10.4%; Score 245; DB 3; Length 1598;  
Best Local Similarity 32.9%; Pred. No. 1e-06;  
RESULT 1260  
ID AAG30465 standard; protein; 1599 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36427.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 10.4%; Score 245; DB 3; Length 1599;  
Best Local Similarity 32.9%; Pred. No. 1e-06;  
RESULT 1261  
ID AAG41602 standard; protein; 1637 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51782.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 10.4%; Score 245; DB 3; Length 1637;  
Best Local Similarity 32.9%; Pred. No. 1.1e-06;  
RESULT 1262  
ID AAG30464 standard; protein; 1684 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36426.  
PN EP1033405-A2.

PD 06-SEP-2000.  
Query Match 10.4%; Score 245; DB 3; Length 1684;  
Best Local Similarity 32.9%; Pred. No. 1.1e-06;  
RESULT 1263  
ID ADJ69005 standard; protein; 1684 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID811.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 10.4%; Score 245; DB 7; Length 1684;  
Best Local Similarity 32.9%; Pred. No. 1.1e-06;  
RESULT 1264  
ID ADE87052 standard; protein; 886 AA.  
DE Human pancreatic cell protein sequence SeqID512.  
PN WO2003060145-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.3%; Score 244.5; DB 7; Length 886;  
Best Local Similarity 27.8%; Pred. No. 6.3e-07;  
RESULT 1265  
ID AAW09218 standard; protein; 1002 AA.  
DE SELPOK polymer.  
PN WO9634618-A1.  
PD 07-NOV-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.3%; Score 244.5; DB 2; Length 1002;  
Best Local Similarity 29.2%; Pred. No. 7.1e-07;  
RESULT 1266  
ID AAW53544 standard; protein; 1002 AA.  
DE Amino acid sequence of SELPOK peptide 2.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.3%; Score 244.5; DB 2; Length 1002;  
Best Local Similarity 29.2%; Pred. No. 7.1e-07;  
RESULT 1267  
ID AAY51888 standard; protein; 1002 AA.  
DE Plasmid pPT0364 protein fragment containing SELPOK polymer units.  
PN US6033654-A.  
PD 07-MAR-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.3%; Score 244.5; DB 3; Length 1002;  
Best Local Similarity 29.2%; Pred. No. 7.1e-07;  
RESULT 1268  
ID ABG31418 standard; protein; 1002 AA.  
DE SELPOK protein encoded by plasmid pPT0364.  
PN US6423333-B1.  
PD 23-JUL-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.3%; Score 244.5; DB 5; Length 1002;  
Best Local Similarity 29.2%; Pred. No. 7.1e-07;  
RESULT 1269  
ID ABW01634 standard; protein; 1002 AA.  
DE Plasmid pPT0364 SELPOK polymer protein.  
PN US2003104589-A1.  
PD 05-JUN-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.3%; Score 244.5; DB 7; Length 1002;  
Best Local Similarity 29.2%; Pred. No. 7.1e-07;  
RESULT 1270  
ID AAY84544 standard; protein; 1057 AA.  
DE A human collagen 1 (alpha) protein helical region.  
PN EP992586-A2.  
PD 12-APR-2000.  
PA (USSU) US SURGICAL CORP.  
Query Match 10.3%; Score 244.5; DB 3; Length 1057;  
Best Local Similarity 27.8%; Pred. No. 7.5e-07;  
RESULT 1271  
ID AAY84403 standard; protein; 1058 AA.  
DE Amino acid sequence of human type 1 (alpha) collagen polypeptide.  
PN WO200014201-A1.  
PD 16-MAR-2000.

PA (USSU) US SURGICAL CORP.  
PA (PAOL/) PAOLELLA D N.  
PA (GRUS/) GRUSKIN E A.  
PA (BUEC/) BUECHTER D D.  
Query Match 10.3%; Score 244.5; DB 3; Length 1058;  
Best Local Similarity 27.8%; Pred. No. 7.5e-07;  
RESULT 1272  
ID RAY84540 standard; protein; 1107 AA.  
DE Amino acid sequence of a chimeric collagen 1 (alpha)/decorin protein.  
PN EP992586-A2.  
PD 12-APR-2000.  
PA (USSU) US SURGICAL CORP.  
Query Match 10.3%; Score 244.5; DB 3; Length 1107;  
Best Local Similarity 27.8%; Pred. No. 7.8e-07;  
RESULT 1273  
ID ADE87050 standard; protein; 1161 AA.  
DE Human pancreatic cell protein sequence SeqID510.  
PN WO2003060145-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.3%; Score 244.5; DB 7; Length 1161;  
Best Local Similarity 27.8%; Pred. No. 8.2e-07;  
RESULT 1274  
ID AAY84538 standard; protein; 1171 AA.  
DE A chimeric collagen 1 (alpha)/TGF-beta1 protein.  
PN EP992586-A2.  
PD 12-APR-2000.  
PA (USSU) US SURGICAL CORP.  
Query Match 10.3%; Score 244.5; DB 3; Length 1171;  
Best Local Similarity 27.8%; Pred. No. 8.3e-07;  
RESULT 1275  
ID ADE87057 standard; protein; 1211 AA.  
DE Human pancreatic cell protein sequence SeqID517.  
PN WO2003060145-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.3%; Score 244.5; DB 7; Length 1211;  
Best Local Similarity 27.8%; Pred. No. 8.5e-07;  
RESULT 1276  
ID ADE87062 standard; protein; 1226 AA.  
DE Human pancreatic cell protein sequence SeqID522.  
PN WO2003060145-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.3%; Score 244.5; DB 7; Length 1226;  
Best Local Similarity 27.8%; Pred. No. 8.6e-07;  
RESULT 1277  
ID RAY84539 standard; protein; 1388 AA.  
DE Amino acid sequence of a chimeric collagen 1 (alpha)/decorin protein.  
PN EP992586-A2.  
PD 12-APR-2000.  
PA (USSU) US SURGICAL CORP.  
Query Match 10.3%; Score 244.5; DB 3; Length 1388;  
Best Local Similarity 27.8%; Pred. No. 9.7e-07;  
RESULT 1278  
ID REG93947 standard; protein; 1461 AA.  
DE Human polypeptide orthologous to DACC-11.  
PN WO200264625-A1.  
PD 22-AUG-2002.  
PA (ADPP-) ADP PHARM PTY LTD.  
PA (UNSY) UNIV SYDNEY.  
Query Match 10.3%; Score 244.5; DB 5; Length 1461;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1279  
ID AAW68485 standard; protein; 1464 AA.  
DE Human recombinant collagen protein.  
PN WO9827202-A1.  
PD 25-JUN-1998.  
PA (BIOC-) BIOCEM SA.  
Query Match 10.3%; Score 244.5; DB 2; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1280  
ID AAU14136 standard; protein; 1464 AA.

DE Human novel protein #7.  
PN WO200155437-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC. 10.3%; Score 244.5; DB 4; Length 1464;  
Query Match 27.8%; Pred. No. 1e-06;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1281  
ID ADD45059 standard; protein; 1464 AA.  
DE Human Protein P02452, SEQ ID NO 10491.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.3%; Score 244.5; DB 7; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1282  
ID ADD45055 standard; protein; 1464 AA.  
DE Human Protein P02452, SEQ ID NO 10487.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.3%; Score 244.5; DB 7; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1283  
ID ADD45051 standard; protein; 1464 AA.  
DE Human Protein P02452, SEQ ID NO 10483.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.3%; Score 244.5; DB 7; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1284  
ID ADE87048 standard; protein; 1464 AA.  
DE Human pancreatic cell protein sequence SeqID508.  
PN WO2003060145-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.3%; Score 244.5; DB 7; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1285  
ID ADR16800 standard; protein; 1464 AA.  
DE Human collagen I alpha1 (I) chain protein.  
PN US2004151731-A1.  
PD 05-AUG-2004.  
PA (JICH/) JICHA D L.  
Query Match 10.3%; Score 244.5; DB 8; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1286  
ID ADR16425 standard; protein; 1464 AA.  
DE Human collagen I alpha1 (I) chain protein.  
PN US2004151732-A1.  
PD 05-AUG-2004.  
PA (JICH/) JICHA D L.  
PA (PELU/) PELUSE S.  
Query Match 10.3%; Score 244.5; DB 8; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1287  
ID ADR99144 standard; protein; 1464 AA.  
DE Collagen, type I, alpha 1, COL1A1, SEQ ID 150.  
PN WO2004078035-A2.  
PD 16-SEP-2004.  
PA (FARB) BAYER PHARM CORP.  
Query Match 10.3%; Score 244.5; DB 8; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1288  
ID ABG22679 standard; protein; 1518 AA.  
DE Novel human diagnostic protein #22670.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC. 10.3%; Score 244.5; DB 4; Length 1518;  
Query Match 22.9%; Pred. No. 1.2e-06;  
Best Local Similarity 22.9%; Pred. No. 1.2e-06;  
Best Local Similarity 26.1%; Pred. No. 1.1e-06;  
RESULT 1289  
ID ADE87051 standard; protein; 1536 AA.  
DE Human pancreatic cell protein sequence SeqID511.  
PN WO2003060145-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC. 10.3%; Score 244.5; DB 7; Length 1536;  
Query Match 27.8%; Pred. No. 1.1e-06;  
Best Local Similarity 27.8%; Pred. No. 1.1e-06;  
RESULT 1290  
ID ABO53065 standard; protein; 441 AA.  
DE Human putative spliceosome associated protein (SAP) #42.  
PN US2003068803-A1.  
PD 10-APR-2003.  
PA (REED/) REED R.  
PA (ZHOU/) ZHOU Z.  
Query Match 10.3%; Score 244; DB 6; Length 441;  
Best Local Similarity 28.3%; Pred. No. 3.5e-07;  
RESULT 1291  
ID ADA03117 standard; protein; 591 AA.  
DE Nucleotide therapy testing protein #23.  
PN WO2003023031-A1.  
PD 20-MAR-2003.  
PA (NNSH) NIPPON SHINYAKU CO LTD.  
Query Match 10.3%; Score 244; DB 6; Length 591;  
Best Local Similarity 29.0%; Pred. No. 4.6e-07;  
RESULT 1292  
ID ADO08795 standard; protein; 316 AA.  
DE Novel surgical dressing-related protein SeqID82.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 10.3%; Score 243.5; DB 8; Length 316;  
Best Local Similarity 25.3%; Pred. No. 2.7e-07;  
RESULT 1293  
ID AAE36862 standard; protein; 714 AA.  
DE Human collagen type II protein.  
PN WO2003021226-A2.  
PD 13-MAR-2003.  
PA (PHAA) PHARMACIA CORP.  
Query Match 10.3%; Score 243; DB 6; Length 714;  
Best Local Similarity 27.1%; Pred. No. 6.4e-07;  
RESULT 1294  
ID ADI3185 standard; protein; 714 AA.  
DE Human collagen type II-related protein.  
PN US2003219843-A1.  
PD 27-NOV-2003.  
PA (WELS/) WELSCH D J.  
PA (DUFF/) DUFFIN K L.  
PA (NEMI/) NEMIROVSKIY O V.  
PA (DUFF/) DUFFIELD D R.  
PA (SUNI/) SUNYER T.  
PA (HOWA/) HOWARD C P.  
PA (ABRA/) ABRAMS M.  
Query Match 10.3%; Score 243; DB 8; Length 714;  
Best Local Similarity 27.1%; Pred. No. 6.4e-07;  
RESULT 1295  
ID ADP31573 standard; protein; 906 AA.  
DE Human secreted protein SEQ ID #2340.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 10.3%; Score 243; DB 8; Length 906;  
Best Local Similarity 25.8%; Pred. No. 8e-07;  
RESULT 1296  
ID ABB70775 standard; protein; 1357 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39117.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 10.3%; Score 243; DB 4; Length 1357;  
Best Local Similarity 22.9%; Pred. No. 1.2e-06;

RESULT 1297  
ID AAU28194 standard; protein; 940 AA.  
DE Novel human secretory protein, Seq ID No 363.  
PN WO200166689-A2.  
PD 13-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.3%; Score 242.5; DB 4; Length 940;  
Best Local Similarity 27.0%; Pred. No. 8.9e-07;  
RESULT 1298  
ID ABG93944 standard; protein; 1496 AA.  
DE Human polypeptide orthologous to DACC-10.  
PN WO200264625-A1.  
PD 22-AUG-2002.  
PA (ADPP-) ADP PHARM PTY LTD.  
PA (UNSY-) UNIV SYDNEY.  
Query Match 10.3%; Score 242.5; DB 5; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1299  
ID ABR47419 standard; protein; 1496 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:70.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 10.3%; Score 242.5; DB 6; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1300  
ID ADB70382 standard; protein; 1496 AA.  
DE Procollagen alpha 2(V) SEQ ID NO:74.  
PN WO2003021229-A2.  
PD 13-MAR-2003.  
PA (BGM-) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 10.3%; Score 242.5; DB 7; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1301  
ID ADE61180 standard; protein; 1496 AA.  
DE Human NP\_000384, SEQ ID NO 7098.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GHEO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match 10.3%; Score 242.5; DB 7; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1302  
ID ADP65253 standard; protein; 1496 AA.  
DE Human alpha 2 type V collagen preproprotein, collagen V, alpha-2.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 10.3%; Score 242.5; DB 7; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1303  
ID ADJ37161 standard; protein; 1496 AA.  
DE Human malignant pleural mesothelioma (MPM) protein #33.  
PN US2003219760-A1.  
PD 27-NOV-2003.  
PA (BGM-) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 10.3%; Score 242.5; DB 8; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1304  
ID ADP99242 standard; protein; 1496 AA.  
DE Collagen, type V, alpha 2, COL5A2, SEQ ID 248.  
PN WO2004078035-A2.  
PD 16-SEP-2004.  
PA (FARB-) BAYER PHARM CORP.  
Query Match 10.3%; Score 242.5; DB 8; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1305  
ID ABB60207 standard; protein; 1779 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7413.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 10.3%; Score 242.5; DB 4; Length 1779;

Best Local Similarity 25.1%; Pred. No. 1.6e-06;  
RESULT 1306  
ID ABU34499 standard; protein; 319 AA.  
DE Protein encoded by Prokaryotic essential gene #20026.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 10.2%; Score 242; DB 6; Length 319;  
Best Local Similarity 28.9%; Pred. No. 3.4e-07;  
RESULT 1307  
ID AAU28382 standard; protein; 968 AA.  
DE Novel human secretory protein, Seq ID NO 739.  
PN WO200166689-A2.  
PD 13-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.2%; Score 241.5; DB 4; Length 968;  
Best Local Similarity 27.6%; Pred. No. 1.1e-06;  
RESULT 1308  
ID AAY56800 standard; protein; 1411 AA.  
DE Human preproalpha 1 (I) collagen.  
PN EP967226-A2.  
PD 29-DEC-1999.  
PA (COHE-) COHESION TECHNOLOGIES INC.  
Query Match 10.2%; Score 241.5; DB 3; Length 1411;  
Best Local Similarity 27.4%; Pred. No. 1.5e-06;  
RESULT 1309  
ID AAE36878 standard; protein; 342 AA.  
DE Gasteracantha mammosa major ampullate spidroin 2 (MaSp2) protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 10.2%; Score 241; DB 6; Length 342;  
Best Local Similarity 28.5%; Pred. No. 4.2e-07;  
RESULT 1310  
ID ADN23179 standard; protein; 1744 AA.  
DE Bacterial polypeptide #5832.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 10.2%; Score 241; DB 8; Length 1744;  
Best Local Similarity 30.4%; Pred. No. 2e-06;  
RESULT 1311  
ID AAW64378 standard; protein; 943 AA.  
DE Mycobacterium tuberculosis antigen DIF2-1.  
PN WO9816645-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 10.2%; Score 240.5; DB 2; Length 943;  
Best Local Similarity 24.5%; Pred. No. 1.2e-06;  
RESULT 1312  
ID AAW81745 standard; protein; 943 AA.  
DE M. tuberculosis immunogenic polypeptide DIF2-1.  
PN WO9816646-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 10.2%; Score 240.5; DB 2; Length 943;  
Best Local Similarity 24.5%; Pred. No. 1.2e-06;  
RESULT 1313  
ID AAY39032 standard; protein; 943 AA.  
DE M. tuberculosis recombinant antigen protein DIF2-1.  
PN WO9421118-A2.  
PD 26-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 10.2%; Score 240.5; DB 2; Length 943;  
Best Local Similarity 24.5%; Pred. No. 1.2e-06;  
RESULT 1314  
ID AAY39175 standard; protein; 943 AA.  
DE M. tuberculosis antigen DIF2-1 amino acid sequence.  
PN WO9942076-A2.



PD 26-AUG-1999.  
 PA (CORI-) CORIXA CORP.  
 Query Match 10.2%; Score 240.5; DB 2; Length 943;  
 Best Local Similarity 24.5%; Pred. No. 1.2e-06;  
 RESULT 1315  
 ID AAR89472 standard; protein; 1107 AA.  
 DE Collagen/decortin(aa46-93) fusion protein.  
 PN CA2151547-A.  
 PD 11-DEC-1995.  
 PA (USSU) US SURGICAL CORP.  
 Query Match 10.2%; Score 240.5; DB 2; Length 1107;  
 Best Local Similarity 27.6%; Pred. No. 1.4e-06;  
 RESULT 1316  
 ID AAR89469 standard; protein; 1169 AA.  
 DE Collagen/BMP-2B fusion protein.  
 PN CA2151547-A.  
 PD 11-DEC-1995.  
 PA (USSU) US SURGICAL CORP.  
 Query Match 10.2%; Score 240.5; DB 2; Length 1169;  
 Best Local Similarity 27.6%; Pred. No. 1.5e-06;  
 RESULT 1317  
 ID AAY84537 standard; protein; 1169 AA.  
 DE Amino acid sequence of a chimeric collagen 1 (alpha1)/BMP-2B protein.  
 PN EF992586-A2.  
 PD 12-APR-2000.  
 PA (USSU) US SURGICAL CORP.  
 Query Match 10.2%; Score 240.5; DB 3; Length 1169;  
 Best Local Similarity 27.6%; Pred. No. 1.5e-06;  
 RESULT 1318  
 ID AAR89470 standard; protein; 1171 AA.  
 DE Collagen/TGF-beta-1 fusion protein.  
 PN CA2151547-A.  
 PD 11-DEC-1995.  
 PA (USSU) US SURGICAL CORP.  
 Query Match 10.2%; Score 240.5; DB 2; Length 1171;  
 Best Local Similarity 27.6%; Pred. No. 1.5e-06;  
 RESULT 1319  
 ID AAR89471 standard; protein; 1388 AA.  
 DE Collagen/decortin fusion protein.  
 PN CA2151547-A.  
 PD 11-DEC-1995.  
 PA (USSU) US SURGICAL CORP.  
 Query Match 10.2%; Score 240.5; DB 2; Length 1388;  
 Best Local Similarity 27.6%; Pred. No. 1.7e-06;  
 RESULT 1320  
 ID AAO16358 standard; protein; 7339 AA.  
 DE Human translocated promoter region (TPR) protein, SEQ ID NO 6.  
 PN WO200299050-A2.  
 PD 12-DEC-2002.  
 PA (EXEL-) EXELIXIS INC.  
 Query Match 10.2%; Score 240.5; DB 6; Length 7339;  
 Best Local Similarity 24.3%; Pred. No. 8.4e-06;  
 RESULT 1321  
 ID AAR80350 standard; protein; 338 AA.  
 DE Protein polymeric adhesion substrate 2-F.  
 PN WO9523611-A1.  
 PD 08-SEP-1995.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 10.2%; Score 240; DB 2; Length 338;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-07;  
 RESULT 1322  
 ID ABU36649 standard; protein; 678 AA.  
 DE Protein encoded by Prokaryotic essential gene #22176.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 10.2%; Score 240; DB 6; Length 678;  
 Best Local Similarity 27.5%; Pred. No. 9.3e-07;  
 RESULT 1323  
 ID ADD89022 standard; protein; 1212 AA.  
 DE TAT282.  
 PN WO2003057160-A2.  
 PD 17-JUL-2003.

PA (GETH) GENENTECH INC.  
 Query Match 10.2%; Score 240; DB 7; Length 1212;  
 Best Local Similarity 26.2%; Pred. No. 1.6e-06;  
 RESULT 1324  
 ID AAM40863 standard; protein; 1669 AA.  
 DE Human polypeptide SEQ ID NO 5794.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 10.2%; Score 240; DB 4; Length 1669;  
 Best Local Similarity 26.2%; Pred. No. 2.2e-06;  
 RESULT 1325  
 ID AAB70178 standard; peptide; 183 AA.  
 DE Peptide dendrimer carrier #3.  
 PN WO200107469-A2.  
 PD 01-FEB-2001.  
 PA (VERD/) VERDINI A.  
 Query Match 10.1%; Score 239.5; DB 4; Length 183;  
 Best Local Similarity 29.7%; Pred. No. 2.8e-07;  
 RESULT 1326  
 ID ADP31574 standard; protein; 366 AA.  
 DE Human secreted protein SEQ ID #2341.  
 PN WO2004035732-A2.  
 PD 23-APR-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 10.1%; Score 239.5; DB 8; Length 366;  
 Best Local Similarity 26.3%; Pred. No. 5.5e-07;  
 RESULT 1327  
 ID ADP31575 standard; protein; 384 AA.  
 DE Human secreted protein SEQ ID #2342.  
 PN WO2004035732-A2.  
 PD 29-APR-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 10.1%; Score 239.5; DB 8; Length 384;  
 Best Local Similarity 26.3%; Pred. No. 5.8e-07;  
 RESULT 1328  
 ID ABU17351 standard; protein; 469 AA.  
 DE Protein encoded by Prokaryotic essential gene #2878.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 10.1%; Score 239.5; DB 6; Length 469;  
 Best Local Similarity 28.2%; Pred. No. 7e-07;  
 RESULT 1329  
 ID AAY84541 standard; protein; 1057 AA.  
 DE Amino acid sequence of a human collagen 1 (alpha1) protein.  
 PN EF992586-A2.  
 PD 12-APR-2000.  
 PA (USSU) US SURGICAL CORP.  
 Query Match 10.1%; Score 239.5; DB 3; Length 1057;  
 Best Local Similarity 26.7%; Pred. No. 1.5e-06;  
 RESULT 1330  
 ID AAB82454 standard; protein; 1464 AA.  
 DE Human pro-alpha-1 chain of type I procollagen.  
 PN WO200144455-A2.  
 PD 21-JUN-2001.  
 PA (ASTR) ASTRAZENECA AB.  
 Query Match 10.1%; Score 239.5; DB 4; Length 1464;  
 Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
 RESULT 1331  
 ID ABB90764 standard; protein; 1464 AA.  
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 261.  
 PN WO200210217-A2.  
 PD 07-FEB-2002.  
 PA (UJO) UNIV JOHNS HOPKINS.  
 Query Match 10.1%; Score 239.5; DB 5; Length 1464;  
 Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
 RESULT 1332  
 ID ABP68610 standard; protein; 1464 AA.  
 DE Human pancreatic cancer expressed protein SEQ ID NO 159.  
 PN WO200260317-A2.  
 PD 08-AUG-2002.

PA (CORI-) CORIXA CORP.  
Query Match 10.1%; Score 239.5; DB 5; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1333  
ID ABUS4471 standard; protein; 1464 AA.  
DE Human tumour endothelial marker TEM 38.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO-) UNIV JOHNS HOPKINS.  
Query Match 10.1%; Score 239.5; DB 6; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1334  
ID ABR47417 standard; protein; 1464 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:65.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.1%; Score 239.5; DB 6; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1335  
ID ABR92064 standard; protein; 1464 AA.  
DE Human cervical cancer cell marker protein SEQ ID NO:36.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.1%; Score 239.5; DB 6; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1336  
ID ADD14142 standard; protein; 1464 AA.  
DE Human src biomarker polypeptide SEQ ID NO:331.  
PN WO2003062395-A2.  
PD 31-JUL-2003.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
Query Match 10.1%; Score 239.5; DB 7; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1337  
ID ADP65246 standard; protein; 1464 AA.  
DE Human alpha 1 type I collagen preproprotein, Collagen I, alpha-1.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 10.1%; Score 239.5; DB 7; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1338  
ID ADQ19470 standard; protein; 1464 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2289.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 10.1%; Score 239.5; DB 8; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1339  
ID ADQ29653 standard; protein; 1464 AA.  
DE Human colorectal cancer-associated protein #8.  
PN EP1439393-A2.  
PD 21-JUL-2004.  
PA (FARB-) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 10.1%; Score 239.5; DB 8; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1340  
ID ADP65203 standard; protein; 1629 AA.  
DE Human alpha 2 type XI collagen, isoform 3 preproprotein.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 10.1%; Score 239.5; DB 7; Length 1629;  
Best Local Similarity 25.7%; Pred. No. 2.3e-06;  
RESULT 1341  
ID ABB57334 standard; protein; 1669 AA.  
DE Mouse ischaemic condition related protein sequence SEQ ID NO:933.  
PN WO200188188-A2.  
PD 22-NOV-2001.

PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Query Match 10.1%; Score 239.5; DB 5; Length 1669;  
Best Local Similarity 27.7%; Pred. No. 2.4e-06;  
RESULT 1342  
ID ABU22680 standard; protein; 584 AA.  
DE Protein encoded by Prokaryotic essential gene #8207.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 10.1%; Score 239; DB 6; Length 584;  
Best Local Similarity 26.2%; Pred. No. 9.3e-07;  
RESULT 1343  
ID AAB68072 standard; protein; 662 AA.  
DE Amino acid sequence of a recombinant human gelatin.  
PN WO200134801-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 10.1%; Score 239; DB 4; Length 662;  
Best Local Similarity 27.6%; Pred. No. 1e-06;  
RESULT 1344  
ID AAE02718 standard; protein; 662 AA.  
DE Human alpha (I) type I collagen helical domain (residues 531-1192).  
PN WO200134646-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 10.1%; Score 239; DB 4; Length 662;  
Best Local Similarity 27.6%; Pred. No. 1e-06;  
RESULT 1345  
ID ADB84306 standard; protein; 662 AA.  
DE Recombinant gelatin #18.  
PN US2003064074-A1.  
PD 03-APR-2003.  
PA (CHAN-) CHANG R C.  
PA (KIVI-) KIVIRIKKO K I.  
PA (NEFF-) NEFF T B.  
PA (OLSE-) OLSEN D R.  
PA (POLA-) POLAREK J W.  
Query Match 10.1%; Score 239; DB 7; Length 662;  
Best Local Similarity 27.6%; Pred. No. 1e-06;  
RESULT 1346  
ID AAE02532 standard; protein; 1463 AA.  
DE Bovine alpha (I) collagen.  
PN WO200134647-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 10.1%; Score 239; DB 4; Length 1463;  
Best Local Similarity 27.7%; Pred. No. 2.2e-06;  
RESULT 1347  
ID AAU84266 standard; protein; 1806 AA.  
DE Human endometrial cancer related protein, COL1A1.  
PN WO200209573-A2.  
PD 07-FEB-2002.  
PA (BGHM-) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 10.1%; Score 239; DB 5; Length 1806;  
Best Local Similarity 24.7%; Pred. No. 2.7e-06;  
RESULT 1348  
ID ABJ05596 standard; protein; 1806 AA.  
DE Breast cancer-associated protein 61.  
PN WO200259377-A2.  
PD 01-AUG-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.1%; Score 239; DB 5; Length 1806;  
Best Local Similarity 24.7%; Pred. No. 2.7e-06;  
RESULT 1349  
ID ABR58545 standard; protein; 1806 AA.  
DE Human cancer related protein SEQ ID NO:202.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.1%; Score 239; DB 6; Length 1806;  
Best Local Similarity 24.7%; Pred. No. 2.7e-06;  
RESULT 1350  
ID ABU56581 standard; protein; 1806 AA.



DE EBSI multimeric protein.  
PN US5243038-A.  
PD 07-SEP-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.0%; Score 236.5; DB 2; Length 1413;  
Best Local Similarity 28.0%; Pred. No. 3.1e-06;  
RESULT 1369  
ID AAM26343 standard; protein; 1413 AA.  
DE EBSI synthetic elastomeric protein.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.0%; Score 236.5; DB 2; Length 1413;  
Best Local Similarity 28.0%; Pred. No. 3.1e-06;  
RESULT 1370  
ID AAY78278 standard; protein; 1464 AA.  
DE EBSI protein sequence SEQ ID NO:74.  
PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.0%; Score 236.5; DB 3; Length 1464;  
Best Local Similarity 28.0%; Pred. No. 3.2e-06;  
RESULT 1371  
ID ABG59268 standard; protein; 1465 AA.  
DE Elastin-like protein EBSI (not defined).  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.0%; Score 236.5; DB 5; Length 1465;  
Best Local Similarity 28.0%; Pred. No. 3.2e-06;  
RESULT 1372  
ID ABE44969 standard; protein; 1465 AA.  
DE Recombinant structural protein EBSI protein seq id 74.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.0%; Score 236.5; DB 7; Length 1465;  
Best Local Similarity 28.0%; Pred. No. 3.2e-06;  
RESULT 1373  
ID ABG74869 standard; protein; 643 AA.  
DE Human cytokerin-1 protein.  
PN WO2003002600-A1.  
PD 09-JAN-2003.  
PA (BRAH-) BRAHMS AG.  
Query Match 10.0%; Score 235.5; DB 6; Length 643;  
Best Local Similarity 39.8%; Pred. No. 1.7e-06;  
RESULT 1374  
ID ADQ17549 standard; protein; 644 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 366.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 10.0%; Score 235.5; DB 8; Length 644;  
Best Local Similarity 39.8%; Pred. No. 1.7e-06;  
RESULT 1375  
ID ABB65175 standard; protein; 1180 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 22317.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 10.0%; Score 235.5; DB 4; Length 1180;  
Best Local Similarity 26.1%; Pred. No. 3e-06;  
RESULT 1376  
ID AAM39077 standard; protein; 1672 AA.  
DE Human polypeptide SEQ ID NO 2222.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.0%; Score 235.5; DB 4; Length 1672;  
Best Local Similarity 26.0%; Pred. No. 4.2e-06;  
RESULT 1377  
ID AAB70107 standard; protein; 936 AA.  
DE Gelatin protein.

PN JP2000325095-A.  
PD 28-NOV-2000.  
PA (MIYA-) MIYAGI KAGAKU KOGYO KK.  
PA (DAII-) DAIICHI KAKAGU YAKUHIN KK.  
Query Match 9.9%; Score 235; DB 4; Length 936;  
Best Local Similarity 23.9%; Pred. No. 2.6e-06;  
RESULT 1378  
ID ABP56960 standard; protein; 2189 AA.  
DE E. maxima 250 kDa antigen homologous protein sequence SEQ ID NO:7.  
PN WO2003004684-A2.  
PD 16-JAN-2003.  
PA (WITC/) WITCOMBE D.  
PA (SMIT/) SMITH N C.  
PA (WALL/) WALLACH M.  
Query Match 9.9%; Score 235; DB 6; Length 2189;  
Best Local Similarity 27.6%; Pred. No. 5.8e-06;  
RESULT 1379  
ID AAB68066 standard; protein; 510 AA.  
DE Amino acid sequence of a recombinant human gelatin.  
PN WO200134801-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 9.9%; Score 234.5; DB 4; Length 510;  
Best Local Similarity 26.9%; Pred. No. 1.5e-06;  
RESULT 1380  
ID AAE02712 standard; protein; 510 AA.  
DE Recombinant human gelatin #1.  
PN WO200134646-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 9.9%; Score 234.5; DB 4; Length 510;  
Best Local Similarity 26.9%; Pred. No. 1.5e-06;  
RESULT 1381  
ID ADB84299 standard; protein; 510 AA.  
DE Recombinant gelatin #12.  
PN US2003064074-A1.  
PD 03-APR-2003.  
PA (CHAN/) CHANG R C.  
PA (KIVI/) KIVIRIKKO K I.  
PA (NEFF/) NEFF T B.  
PA (OLSE/) OLSEN D R.  
PA (POLA/) POLAREK J W.  
Query Match 9.9%; Score 234.5; DB 7; Length 510;  
Best Local Similarity 26.9%; Pred. No. 1.5e-06;  
RESULT 1382  
ID AAR80251 standard; peptide; 936 AA.  
DE Polymer SELP0.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.9%; Score 234.5; DB 2; Length 936;  
Best Local Similarity 28.5%; Pred. No. 2.7e-06;  
RESULT 1383  
ID ABP53472 standard; protein; 936 AA.  
DE Protein polymer SELP0 polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY B R.  
Query Match 9.9%; Score 234.5; DB 5; Length 936;  
Best Local Similarity 28.5%; Pred. No. 2.7e-06;  
RESULT 1384  
ID ABU56436 standard; protein; 2944 AA.  
DE Lung cancer-associated polypeptide #29.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (BOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 9.9%; Score 234.5; DB 6; Length 2944;  
Best Local Similarity 26.2%; Pred. No. 8.2e-06;  
RESULT 1385  
ID ADQ18966 standard; protein; 2944 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1785.  
PN WO2004048938-A2.

PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.9%; Score 234.5; DB 8; Length 2944;  
Best Local Similarity 26.2%; Pred. No. 8.2e-06;  
RESULT 1386  
ID AAO39966 standard; protein; 2944 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1629.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.9%; Score 234.5; DB 8; Length 2944;  
Best Local Similarity 26.2%; Pred. No. 8.2e-06;  
RESULT 1387  
ID ADN23131 standard; protein; 3507 AA.  
DE Bacterial polypeptide #5784.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 9.9%; Score 234.5; DB 8; Length 3507;  
Best Local Similarity 22.6%; Pred. No. 9.7e-06;  
RESULT 1388  
ID ABR40001 standard; protein; 1626 AA.  
DE Human collagen XXII.  
PD 13-FEB-2003.  
PA (GEOH) GEN HOSPITAL CORP.  
Query Match 9.9%; Score 234; DB 6; Length 1626;  
Best Local Similarity 26.1%; Pred. No. 5e-06;  
RESULT 1389  
ID AAG36620 standard; protein; 263 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44904.  
PD 06-SEP-2000.  
PA (GEOH) GEN HOSPITAL CORP.  
Query Match 9.9%; Score 233.5; DB 3; Length 263;  
Best Local Similarity 34.9%; Pred. No. 9.4e-07;  
RESULT 1390  
ID AGS51723 standard; protein; 258 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65674.  
PD 06-SEP-2000.  
PA (GEOH) GEN HOSPITAL CORP.  
Query Match 9.9%; Score 233; DB 3; Length 258;  
Best Local Similarity 30.0%; Pred. No. 9.9e-07;  
RESULT 1391  
ID AAE36929 standard; protein; 387 AA.  
DE Nephila clavipes flagelliform (flag) consensus protein.  
PD 13-MAR-2003.  
PA (UYWV-) UNIV WYOMING.  
Query Match 9.9%; Score 233; DB 6; Length 387;  
Best Local Similarity 27.1%; Pred. No. 1.5e-06;  
RESULT 1392  
ID AAB70182 standard; peptide; 564 AA.  
DE Peptide dendrimer carrier #7.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 9.9%; Score 233; DB 4; Length 564;  
Best Local Similarity 22.9%; Pred. No. 2.1e-06;  
RESULT 1393  
ID ADE56670 standard; protein; 864 AA.  
DE Rat Protein Q99372, SEQ ID NO 2524.  
PD 27-FEB-2003.  
PA (GEOH) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 9.9%; Score 233; DB 7; Length 864;  
Best Local Similarity 26.0%; Pred. No. 3.1e-06;  
RESULT 1394  
ID AAB68065 standard; protein; 416 AA.

DE Amino acid sequence of a recombinant human gelatin.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 9.8%; Score 232.5; DB 4; Length 416;  
Best Local Similarity 28.3%; Pred. No. 1.7e-06;  
RESULT 1395  
ID AAE02711 standard; protein; 416 AA.  
DE Human alpha1 (I) type I collagen helical domain (residues 615-1030).  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 9.8%; Score 232.5; DB 4; Length 416;  
Best Local Similarity 28.3%; Pred. No. 1.7e-06;  
RESULT 1396  
ID ADB84298 standard; protein; 416 AA.  
DE Recombinant gelatin #11.  
PD 03-APR-2003.  
PA (CHAN/) CHANG R C.  
PA (KIVI/) KIVIRIKKO K I.  
PA (NEFF/) NEFF T B.  
PA (OLSE/) OLSEN D R.  
PA (POLA/) POLAREK J W.  
Query Match 9.8%; Score 232.5; DB 7; Length 416;  
Best Local Similarity 28.3%; Pred. No. 1.7e-06;  
RESULT 1397  
ID ADP31594 standard; protein; 2542 AA.  
DE Human secreted protein SEQ ID #2361.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 9.8%; Score 232.5; DB 8; Length 2542;  
Best Local Similarity 25.1%; Pred. No. 9.5e-06;  
RESULT 1398  
ID AAB68057 standard; protein; 501 AA.  
DE Amino acid sequence of a recombinant human gelatin.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 9.8%; Score 232; DB 4; Length 501;  
Best Local Similarity 29.7%; Pred. No. 2.2e-06;  
RESULT 1399  
ID AAE02703 standard; protein; 501 AA.  
DE Human alpha1 (I) type I collagen helical domain (residues 179-679).  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 9.8%; Score 232; DB 4; Length 501;  
Best Local Similarity 29.7%; Pred. No. 2.2e-06;  
RESULT 1400  
ID ADB84290 standard; protein; 501 AA.  
DE Recombinant gelatin #3.  
PD 03-APR-2003.  
PA (CHAN/) CHANG R C.  
PA (KIVI/) KIVIRIKKO K I.  
PA (NEFF/) NEFF T B.  
PA (OLSE/) OLSEN D R.  
PA (POLA/) POLAREK J W.  
Query Match 9.8%; Score 232; DB 7; Length 501;  
Best Local Similarity 29.7%; Pred. No. 2.2e-06;  
RESULT 1401  
ID ADQ39813 standard; protein; 1767 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1476.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.8%; Score 232; DB 8; Length 1767;  
Best Local Similarity 24.5%; Pred. No. 7.2e-06;  
RESULT 1402  
ID ADQ39817 standard; protein; 1767 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1480.

PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1767;  
Query Match Best Local Similarity 24.5%; Pred. No. 7.2e-06;  
RESULT 1403  
ID ADP65251 standard; protein; 1806 AA.  
DE Human alpha 1 type XI collagen, isoform A preproprotein.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match Best Local Similarity 24.5%; Pred. No. 7.3e-06;  
RESULT 1404  
ID ADQ39816 standard; protein; 1806 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1479.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1806;  
Query Match Best Local Similarity 24.5%; Pred. No. 7.3e-06;  
RESULT 1405  
ID ADQ39815 standard; protein; 1806 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1478.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1806;  
Query Match Best Local Similarity 24.5%; Pred. No. 7.3e-06;  
RESULT 1406  
ID ADQ39812 standard; protein; 1818 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1475.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1818;  
Query Match Best Local Similarity 24.5%; Pred. No. 7.4e-06;  
RESULT 1407  
ID ADQ39814 standard; protein; 1818 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1477.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1818;  
Query Match Best Local Similarity 24.5%; Pred. No. 7.4e-06;  
RESULT 1408  
ID ADJ72165 standard; protein; 562 AA.  
DE Elastic polypeptide copolymer sequence #11.  
PN WO200309835-A1.  
PD 04-DEC-2003.  
PA (UYEM-) UNIV EMORY. 9.8%; Score 231.5; DB 8; Length 562;  
Query Match Best Local Similarity 29.8%; Pred. No. 2.6e-06;  
RESULT 1409  
ID ADO08545 standard; protein; 562 AA.  
DE Elastomeric hydrophilic middle block protein SeqID 33.  
PN EP1422242-A1.  
PD 26-MAY-2004.  
PA (UYEM-) UNIV EMORY. 9.8%; Score 231.5; DB 8; Length 562;  
Query Match Best Local Similarity 29.8%; Pred. No. 2.6e-06;  
RESULT 1410  
ID ADJ72166 standard; protein; 730 AA.  
DE Elastic polypeptide copolymer sequence #12.  
PN WO200309835-A1.  
PD 04-DEC-2003.  
PA (UYEM-) UNIV EMORY. 9.8%; Score 231.5; DB 8; Length 730;  
Query Match Best Local Similarity 29.8%; Pred. No. 3.3e-06;  
RESULT 1411  
ID ADO08547 standard; protein; 730 AA.  
DE Elastomeric hydrophilic middle block protein SeqID 35.  
PN EP1422242-A1.

PD 26-MAY-2004.  
PA (UYEM-) UNIV EMORY. 9.8%; Score 231.5; DB 8; Length 730;  
Query Match Best Local Similarity 29.8%; Pred. No. 3.3e-06;  
RESULT 1412  
ID ADO08572 standard; protein; 1382 AA.  
DE Multi-block copolymer PHP comprising elastic & plastic peptides SeqID 60.  
PN EP1422242-A1.  
PD 26-MAY-2004.  
PA (UYEM-) UNIV EMORY. 9.8%; Score 231.5; DB 8; Length 1382;  
Query Match Best Local Similarity 29.8%; Pred. No. 6.1e-06;  
RESULT 1413  
ID ADO08566 standard; protein; 1550 AA.  
DE Multi-block copolymer comprising elastomeric and plastic peptides Seq 54.  
PN EP1422242-A1.  
PD 26-MAY-2004.  
PA (UYEM-) UNIV EMORY. 9.8%; Score 231.5; DB 8; Length 1550;  
Query Match Best Local Similarity 29.8%; Pred. No. 6.8e-06;  
RESULT 1414  
ID ABG30822 standard; protein; 378 AA.  
DE Chicken hmrNP1 protein.  
PN US2002068321-A1.  
PD 06-JUN-2002.  
PA (NEWM/) NEWMAN S. A.  
PA (BRON/) BRONSTEIN N. B. 9.8%; Score 230.5; DB 5; Length 378;  
Query Match Best Local Similarity 33.5%; Pred. No. 2e-06;  
RESULT 1415  
ID AAM09221 standard; protein; 936 AA.  
DE SELPOK-CS1 polymer.  
PN WO9634618-A1.  
PD 07-NOV-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.8%; Score 230.5; DB 2; Length 936;  
Query Match Best Local Similarity 27.5%; Pred. No. 4.8e-06;  
RESULT 1416  
ID AAY51891 standard; protein; 936 AA.  
DE Plasmid pPT0370 protein fragment containing SELPOK-CS1 polymer units.  
PN US6033654-A.  
PD 07-MAR-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.8%; Score 230.5; DB 3; Length 936;  
Query Match Best Local Similarity 27.5%; Pred. No. 4.8e-06;  
RESULT 1417  
ID ABG31421 standard; protein; 936 AA.  
DE SELPOK-CS1 protein encoded by plasmid pPT0370.  
PN US6423333-B1.  
PD 23-JUL-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.8%; Score 230.5; DB 5; Length 936;  
Query Match Best Local Similarity 27.5%; Pred. No. 4.8e-06;  
RESULT 1418  
ID ABW01637 standard; protein; 936 AA.  
DE Plasmid pPT0370 SELPOK-CS1 polymer protein.  
PN US2003104589-A1.  
PD 05-JUN-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.8%; Score 230.5; DB 7; Length 936;  
Query Match Best Local Similarity 27.5%; Pred. No. 4.8e-06;  
RESULT 1419  
ID AAW35547 standard; protein; 937 AA.  
DE Amino acid sequence of SELPOK-CS1 protein.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.8%; Score 230.5; DB 2; Length 937;  
Query Match Best Local Similarity 27.5%; Pred. No. 4.8e-06;  
RESULT 1420  
ID AAE36928 standard; protein; 200 AA.  
DE Araneus diadematus minor ampullate spidroin 1 consensus protein.  
PN WO2003020916-A2.

PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 9.7%; Score 230; DB 6; Length 200;  
Best Local Similarity 29.2%; Pred. No. 1.2e-06;  
RESULT 1421  
ID ADP31572 standard; protein; 279 AA.  
DE Human secreted protein SEQ ID #2339.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 9.7%; Score 229.5; DB 8; Length 279;  
Best Local Similarity 26.1%; Pred. No. 1.8e-06;  
RESULT 1422  
ID ADC35283 standard; protein; 294 AA.  
DE ADF-2 silk protein.  
PN WO2003057727-A1.  
PD 17-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 9.7%; Score 229.5; DB 7; Length 294;  
Best Local Similarity 27.5%; Pred. No. 1.8e-06;  
RESULT 1423  
ID ABU19388 standard; protein; 827 AA.  
DE Protein encoded by Prokaryotic essential gene #4915.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 9.7%; Score 229.5; DB 6; Length 827;  
Best Local Similarity 28.7%; Pred. No. 5e-06;  
RESULT 1424  
ID AAY30680 standard; protein; 1574 AA.  
DE Splice variant ZAP-1A protein of the human tumor suppressor gene ZAP-1.  
PN WO9946276-A1.  
PD 16-SEP-1999.  
PA (GENO-) GENOS BIOSCIENCES INC.  
Query Match 9.7%; Score 229.5; DB 2; Length 1574;  
Best Local Similarity 27.9%; Pred. No. 9.2e-06;  
RESULT 1425  
ID ADL18527 standard; protein; 391 AA.  
DE Wheat dehydrin protein SEQ ID NO:36.  
PN WO2003027249-A2.  
PD 03-APR-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 9.7%; Score 229; DB 7; Length 391;  
Best Local Similarity 26.8%; Pred. No. 2.6e-06;  
RESULT 1426  
ID ADP31595 standard; protein; 3036 AA.  
DE Human secreted protein SEQ ID #2362.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 9.7%; Score 229; DB 8; Length 3036;  
Best Local Similarity 24.1%; Pred. No. 1.8e-05;  
RESULT 1427  
ID ABG93178 standard; protein; 430 AA.  
DE S. cerevisiae BAX-associated protein fragment SEQ ID 314.  
PN WO200264766-A2.  
PD 22-AUG-2002.  
PA (JANC) JANSSEN PHARM NV.  
Query Match 9.7%; Score 228.5; DB 5; Length 430;  
Best Local Similarity 22.8%; Pred. No. 3.1e-06;  
RESULT 1428  
ID ABU69145 standard; protein; 733 AA.  
DE Human NOVX polypeptide #20.  
PN WO200290504-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.7%; Score 228.5; DB 6; Length 733;  
Best Local Similarity 27.0%; Pred. No. 5.1e-06;  
RESULT 1429  
ID ABB63723 standard; protein; 5002 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 17961.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 9.6%; Score 227; DB 6; Length 717;  
Best Local Similarity 26.8%; Pred. No. 6e-06;  
RESULT 1430  
ID AAG84989 standard; protein; 1389 AA.  
DE Shrimp white spot Bacilliform virus (WSBV) protein 80.  
PN WO200138351-A2.  
PD 31-MAY-2001.  
PA (PENY-) PE CORP NY.  
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.  
PA (SINO-) SINOGENOMAX CO LTD.  
Query Match 9.6%; Score 228; DB 4; Length 1389;  
Best Local Similarity 25.9%; Pred. No. 1e-05;  
RESULT 1431  
ID AAW65462 standard; protein; 485 AA.  
DE Neocallimastix patriciarum endo-xylanase.  
PN CA2190194-A.  
PD 13-MAY-1998.  
PA (LIUJ/) LIU J H.  
PA (SELI/) SELINGER L B.  
PA (MOLO/) MOLONEY M M.  
PA (FORS/) FORSBERG C W.  
PA (CHEN/) CHENG K.  
PA (HUY/) HU Y.  
Query Match 9.6%; Score 227.5; DB 2; Length 485;  
Best Local Similarity 28.4%; Pred. No. 3.9e-06;  
RESULT 1432  
ID AAY27283 standard; protein; 485 AA.  
DE N. patriciarum xylanase.  
PN US948667-A.  
PD 07-SEP-1999.  
PA (MIAC) CANADA DEPT AGRICULTURE.  
Query Match 9.6%; Score 227.5; DB 2; Length 485;  
Best Local Similarity 28.4%; Pred. No. 3.9e-06;  
RESULT 1433  
ID AAB35588 standard; protein; 485 AA.  
DE N. patriciarum endo-xylanase xynC.  
PN US6137032-A.  
PD 24-OCT-2000.  
PA (MIAC) CANADA DEPT AGRICULTURE.  
Query Match 9.6%; Score 227.5; DB 4; Length 485;  
Best Local Similarity 28.4%; Pred. No. 3.9e-06;  
RESULT 1434  
ID ADJ72170 standard; protein; 528 AA.  
DE Elastic polypeptide copolymer sequence #16.  
PN WO2003099835-A1.  
PD 04-DEC-2003.  
PA (UYEN-) UNIV EMORY.  
Query Match 9.6%; Score 227.5; DB 8; Length 528;  
Best Local Similarity 29.7%; Pred. No. 4.3e-06;  
RESULT 1435  
ID ADO08555 standard; protein; 528 AA.  
DE Elastomeric hydrophilic middle block protein SeqID 43.  
PN EPI422242-A1.  
PD 26-MAY-2004.  
PA (UYEN-) UNIV EMORY.  
Query Match 9.6%; Score 227.5; DB 8; Length 528;  
Best Local Similarity 29.7%; Pred. No. 4.3e-06;  
RESULT 1436  
ID ABP96315 standard; protein; 703 AA.  
DE Human collagen protein SEQ ID NO:4.  
PN WO2003016481-A2.  
PD 27-FEB-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 9.6%; Score 227; DB 6; Length 703;  
Best Local Similarity 26.8%; Pred. No. 6e-06;  
RESULT 1437  
ID ABP96314 standard; protein; 717 AA.  
DE Human collagen protein SEQ ID NO:2.  
PN WO2003016481-A2.  
PD 27-FEB-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 9.6%; Score 227; DB 6; Length 717;

Best Local Similarity 26.8%; Pred. No. 6.2e-06;  
RESULT 1438  
ID ADF22968 standard; protein; 1181 AA.  
DE PRO polypeptide SEQ ID NO:62.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 9.6%; Score 227; DB 8; Length 1181;  
Best Local Similarity 26.8%; Pred. No. 9.9e-06;  
RESULT 1439  
ID ABP43711 standard; protein; 1497 AA.  
DE Bullous pemphigoid autoantigen BP180 gene.  
PN WO200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.6%; Score 227; DB 5; Length 1497;  
Best Local Similarity 26.4%; Pred. No. 1.2e-05;  
RESULT 1440  
ID ADN24379 standard; protein; 1759 AA.  
DE Bacterial polypeptide #7032.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 9.6%; Score 227; DB 8; Length 1759;  
Best Local Similarity 27.9%; Pred. No. 1.5e-05;  
RESULT 1441  
ID ADQ39964 standard; protein; 2502 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1627.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.6%; Score 227; DB 8; Length 2502;  
Best Local Similarity 26.8%; Pred. No. 2e-05;  
RESULT 1442  
ID ABB69041 standard; protein; 294 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 33915.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.6%; Score 226.5; DB 4; Length 294;  
Best Local Similarity 29.2%; Pred. No. 2.8e-06;  
RESULT 1443  
ID ADM16778 standard; protein; 448 AA.  
DE N. patriciarum xylanase #1.  
PN US2004053238-A1.  
PD 18-MAR-2004.  
PA (HSEU/) HSEU R.  
PA (HUAN/) HUANG Y.  
Query Match 9.6%; Score 226.5; DB 8; Length 448;  
Best Local Similarity 28.5%; Pred. No. 4.2e-06;  
RESULT 1444  
ID AAB68959 standard; protein; 192 AA.  
DE Zea mays root cap specific protein.  
PN JP2000325081-A.  
PD 28-NOV-2000.  
PA (MITA ) MITSUI CHEM INC.  
Query Match 9.6%; Score 226; DB 4; Length 192;  
Best Local Similarity 30.2%; Pred. No. 2e-06;  
RESULT 1445  
ID ABO52977 standard; protein; 379 AA.  
DE Human spliceosome associated protein (SAP) #95.  
PN US2003068803-A1.  
PD 10-APR-2003.  
PA (REED/) REED R.  
PA (ZHOU/) ZHOU Z.  
Query Match 9.6%; Score 226; DB 6; Length 379;  
Best Local Similarity 31.1%; Pred. No. 3.9e-06;  
RESULT 1446  
ID ADE61159 standard; protein; 379 AA.  
DE Human Protein P51991, SEQ ID NO 7077.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 9.6%; Score 226; DB 7; Length 379;  
Best Local Similarity 31.1%; Pred. No. 3.9e-06;  
RESULT 1447  
ID ABB60000 standard; protein; 945 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 6792.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.6%; Score 226; DB 4; Length 945;  
Best Local Similarity 22.1%; Pred. No. 9.2e-06;  
RESULT 1448  
ID ABB90760 standard; protein; 1669 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 252.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 9.6%; Score 226; DB 5; Length 1669;  
Best Local Similarity 26.0%; Pred. No. 1.6e-05;  
RESULT 1449  
ID ABU54467 standard; protein; 1669 AA.  
DE Human tumour endothelial marker TEM 31.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 9.6%; Score 226; DB 6; Length 1669;  
Best Local Similarity 26.0%; Pred. No. 1.6e-05;  
RESULT 1450  
ID ADF90900 standard; protein; 1669 AA.  
DE Human hepatic-fibrosis disease marker protein SEQ ID 362.  
PN JP2003259877-A.  
PD 16-SEP-2003.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Query Match 9.6%; Score 226; DB 7; Length 1669;  
Best Local Similarity 26.0%; Pred. No. 1.6e-05;  
RESULT 1451  
ID ADR87604 standard; protein; 1669 AA.  
DE Human Type IV collagen alpha 1, SEQ ID 8.  
PN WO2004075835-A2.  
PD 10-SEP-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 9.6%; Score 226; DB 8; Length 1669;  
Best Local Similarity 26.0%; Pred. No. 1.6e-05;  
RESULT 1452  
ID ADQ21326 standard; protein; 1678 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4146.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.6%; Score 226; DB 8; Length 1678;  
Best Local Similarity 25.7%; Pred. No. 1.6e-05;  
RESULT 1453  
ID AAR05222 standard; protein; 2189 AA.  
DE Antigen GX540rFL encoded by Eimeria tenella genomic DNA.  
PN WO9000403-A.  
PD 25-JAN-1990.  
PA (GEMX ) GENEX CORP.  
Query Match 9.6%; Score 226; DB 2; Length 2189;  
Best Local Similarity 27.0%; Pred. No. 2.1e-05;  
RESULT 1454  
ID ABR53293 standard; protein; 1113 AA.  
DE Protein sequence #SEQ ID 1451.  
PN EP1258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Query Match 9.5%; Score 225.5; DB 6; Length 1113;  
Best Local Similarity 23.7%; Pred. No. 1.2e-05;  
RESULT 1455  
ID ADK63560 standard; protein; 1113 AA.



DE Disease treating protein complex-derived protein #873.  
PN EPI338608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZOME AG. 9.5%; Score 225.5; DB 7; Length 1113;  
Query Match  
Best Local Similarity 23.7%; Pred. No. 1.2e-05;  
RESULT 1456  
ID ABM84430 standard; protein; 1476 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4679.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP. 9.5%; Score 225.5; DB 8; Length 1476;  
Query Match  
Best Local Similarity 25.4%; Pred. No. 1.5e-05;  
RESULT 1457  
ID AAE36930 standard; protein; 329 AA.  
DE Nephila madagascariensis flagelliform (flag) consensus protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING. 9.5%; Score 225; DB 6; Length 329;  
Query Match  
Best Local Similarity 30.0%; Pred. No. 3.9e-06;  
RESULT 1458  
ID AAW53545 standard; protein; 378 AA.  
DE Amino acid sequence of SELPOK peptide 3.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.5%; Score 225; DB 2; Length 378;  
Query Match  
Best Local Similarity 28.5%; Pred. No. 4.4e-06;  
RESULT 1459  
ID AAG39747 standard; protein; 174 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49227.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 29.9%; Pred. No. 2.3e-06;  
RESULT 1460  
ID AAM78619 standard; protein; 378 AA.  
DE Human protein SEQ ID NO 1281.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC. 9.5%; Score 224.5; DB 4; Length 378;  
Query Match  
Best Local Similarity 30.3%; Pred. No. 4.7e-06;  
RESULT 1461  
ID ADE87046 standard; protein; 516 AA.  
DE Human pancreatic cell protein sequence SeqID506.  
PN WO2003060145-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC. 9.5%; Score 224.5; DB 7; Length 516;  
Query Match  
Best Local Similarity 28.6%; Pred. No. 6.4e-06;  
RESULT 1462  
ID ADP31571 standard; protein; 252 AA.  
DE Human secreted protein SEQ ID #2338.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC. 9.5%; Score 224; DB 8; Length 252;  
Query Match  
Best Local Similarity 27.3%; Pred. No. 3.5e-06;  
RESULT 1463  
ID ADA83846 standard; protein; 1497 AA.  
DE Human COL17A1 protein.  
PN WO2002103028-A2.  
PD 27-DEC-2002.  
PA (BIOM-) BIOMEDICAL CENT. 9.5%; Score 224; DB 6; Length 1497;  
Query Match  
Best Local Similarity 26.4%; Pred. No. 1.9e-05;  
RESULT 1464  
ID ABB66232 standard; protein; 2309 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 25488.  
PN WO200171042-A2.

PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY. 9.5%; Score 224; DB 4; Length 2309;  
Query Match  
Best Local Similarity 23.8%; Pred. No. 2.9e-05;  
RESULT 1465  
ID ABO84587 standard; protein; 1475 AA.  
DE Human cancer-associated protein HPI7-008.2.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC. 9.5%; Score 223.5; DB 8; Length 1475;  
Query Match  
Best Local Similarity 25.5%; Pred. No. 2e-05;  
RESULT 1466  
ID AAW09219 standard; protein; 378 AA.  
DE SELPOK polymer.  
PN WO9634618-A1.  
PD 07-NOV-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.4%; Score 223; DB 2; Length 378;  
Query Match  
Best Local Similarity 28.5%; Pred. No. 5.9e-06;  
RESULT 1467  
ID AAV51889 standard; protein; 378 AA.  
DE Plasmid pPT0375 protein fragment containing SELPOK polymer units.  
PN US6033654-A.  
PD 07-MAR-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.4%; Score 223; DB 3; Length 378;  
Query Match  
Best Local Similarity 28.5%; Pred. No. 5.9e-06;  
RESULT 1468  
ID ABG31419 standard; protein; 378 AA.  
DE SELPOK protein encoded by plasmid pPT0375.  
PN US6423333-B1.  
PD 23-JUL-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.4%; Score 223; DB 5; Length 378;  
Query Match  
Best Local Similarity 28.5%; Pred. No. 5.9e-06;  
RESULT 1469  
ID ABW01635 standard; protein; 378 AA.  
DE Plasmid pPT0375 SELPOK polymer protein.  
PN US2003104589-A1.  
PD 05-JUN-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.4%; Score 223; DB 7; Length 378;  
Query Match  
Best Local Similarity 28.5%; Pred. No. 5.9e-06;  
RESULT 1470  
ID ADR28985 standard; protein; 976 AA.  
DE Pseudomonas syringae antifreeze related protein SEQ ID NO:2.  
PN WO2004072283-A1.  
PD 26-AUG-2004.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. 9.4%; Score 223; DB 8; Length 976;  
Query Match  
Best Local Similarity 24.8%; Pred. No. 1.5e-05;  
RESULT 1471  
ID ADR28997 standard; protein; 1200 AA.  
DE Pseudomonas syringae antifreeze related protein SEQ ID NO:14.  
PN WO2004072283-A1.  
PD 26-AUG-2004.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. 9.4%; Score 223; DB 8; Length 1200;  
Query Match  
Best Local Similarity 24.8%; Pred. No. 1.8e-05;  
RESULT 1472  
ID ADM48392 standard; protein; 821 AA.  
DE Human recombinant gelatin-like polypeptide Hu-4.  
PN EPI398324-A1.  
PD 17-MAR-2004.  
PA (FUJF-) FUJI PHOTO FILM BV. 9.4%; Score 222.5; DB 8; Length 821;  
Query Match  
Best Local Similarity 24.3%; Pred. No. 1.3e-05;  
RESULT 1473  
ID AAW09223 standard; protein; 966 AA.  
DE SELPOK-CS2 polymer.  
PN WO9634618-A1.  
PD 07-NOV-1996.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.3%; Score 222.5; DB 2; Length 966;  
Best Local Similarity 26.3%; Pred. No. 1.5e-05;  
RESULT 1474  
ID AAY51893 standard; protein; 966 AA.  
DE Plasmid pPT0373 crosslinking protein SELPOK-CS2 polymer unit.  
PN US6033654-A.  
PD 07-MAR-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.4%; Score 222.5; DB 3; Length 966;  
Best Local Similarity 26.3%; Pred. No. 1.5e-05;  
RESULT 1475  
ID ABG31423 standard; protein; 966 AA.  
DE SELPOK-CS2 protein encoded by plasmid pPT0373.  
PN US6423333-B1.  
PD 23-JUL-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.4%; Score 222.5; DB 5; Length 966;  
Best Local Similarity 26.3%; Pred. No. 1.5e-05;  
RESULT 1476  
ID ABW01639 standard; protein; 966 AA.  
DE Plasmid pPT0373 SELPOK-CS2 polymer protein.  
PN US2003104589-A1.  
PD 05-JUN-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.4%; Score 222.5; DB 7; Length 966;  
Best Local Similarity 26.3%; Pred. No. 1.5e-05;  
RESULT 1477  
ID ABB54168 standard; protein; 1063 AA.  
DE Lactococcus lactis protein yihd.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 9.4%; Score 222.5; DB 5; Length 1063;  
Best Local Similarity 24.8%; Pred. No. 1.7e-05;  
RESULT 1478  
ID ABO84590 standard; protein; 1472 AA.  
DE Human cancer-associated protein HP17-008.5.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.4%; Score 222; DB 8; Length 1472;  
Best Local Similarity 25.2%; Pred. No. 2.5e-05;  
RESULT 1479  
ID AAW40109 standard; protein; 1694 AA.  
DE Human alpha-6(IV) collagen protein.  
PN US5731192-A.  
PD 24-MAR-1998.  
PA (UYVA ) UNIV YALE.  
Query Match 9.4%; Score 222; DB 2; Length 1694;  
Best Local Similarity 25.2%; Pred. No. 2.8e-05;  
RESULT 1480  
ID ABU19448 standard; protein; 979 AA.  
DE Protein encoded by Prokaryotic essential gene #4975.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 9.4%; Score 221.5; DB 6; Length 979;  
Best Local Similarity 26.3%; Pred. No. 1.8e-05;  
RESULT 1481  
ID AAB97070 standard; protein; 2058 AA.  
DE Human polypeptide #3 expressed in intraabdominal adipose tissue.  
PN JP2001008699-A.  
PD 16-JAN-2001.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match 9.4%; Score 221.5; DB 4; Length 2058;  
Best Local Similarity 29.2%; Pred. No. 3.7e-05;  
RESULT 1482  
ID ABB69088 standard; protein; 181 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 34056.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.

Query Match 9.3%; Score 220.5; DB 4; Length 181;  
Best Local Similarity 32.9%; Pred. No. 4.1e-06;  
RESULT 1483  
ID ABP98825 standard; protein; 625 AA.  
DE Human structural and cytoskeletal associated protein #16.  
PN WO2003031940-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.3%; Score 220.5; DB 6; Length 625;  
Best Local Similarity 41.2%; Pred. No. 1.4e-05;  
RESULT 1484  
ID ABG77177 standard; protein; 645 AA.  
DE Prostate adenocarcinoma associated protein #12.  
PN US2002119463-A1.  
PD 29-AUG-2002.  
PA (FARI/) FARIS M.  
PA (TURN/) TURNER C M.  
Query Match 9.3%; Score 220.5; DB 5; Length 645;  
Best Local Similarity 41.2%; Pred. No. 1.4e-05;  
RESULT 1485  
ID ADN04309 standard; protein; 645 AA.  
DE Antipsoriatic protein sequence #349.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 9.3%; Score 220.5; DB 8; Length 645;  
Best Local Similarity 41.2%; Pred. No. 1.4e-05;  
RESULT 1486  
ID ABUS2683 standard; protein; 957 AA.  
DE Human cell structure and mobility-associated protein from DKF2phfbr2\_2b5.  
PN WO200112659-A2.  
PD 22-FEB-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 9.3%; Score 220; DB 4; Length 957;  
Best Local Similarity 25.8%; Pred. No. 2.2e-05;  
RESULT 1487  
ID ADP31661 standard; protein; 1365 AA.  
DE Human secreted protein SEQ ID #2428.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 9.3%; Score 220; DB 8; Length 1365;  
Best Local Similarity 25.1%; Pred. No. 3.1e-05;  
RESULT 1488  
ID AAB37932 standard; protein; 1488 AA.  
DE Human CGDD-21 protein.  
PN WO2003050253-A2.  
PD 19-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.3%; Score 220; DB 7; Length 1488;  
Best Local Similarity 23.9%; Pred. No. 3.3e-05;  
RESULT 1489  
ID ADP31664 standard; protein; 1875 AA.  
DE Human secreted protein SEQ ID #2431.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 9.3%; Score 220; DB 8; Length 1875;  
Best Local Similarity 25.1%; Pred. No. 4.2e-05;  
RESULT 1490  
ID ADP31662 standard; protein; 1956 AA.  
DE Human secreted protein SEQ ID #2429.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 9.3%; Score 220; DB 8; Length 1956;  
Best Local Similarity 25.1%; Pred. No. 4.3e-05;  
RESULT 1491  
ID AAW26341 standard; protein; 168 AA.  
DE Silk-like protein slpi dimer.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 9.3%; Score 219.5; DB 2; Length 168;  
 Best Local Similarity 33.8%; Pred. No. 4.4e-06;  
 RESULT 1492  
 ID ABG69263 standard; protein; 168 AA.  
 DE Silk-like protein encoded by DNA clone PSY708 #2.  
 PN US635776-B1.  
 PD 12-MAR-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 9.3%; Score 219.5; DB 5; Length 168;  
 Best Local Similarity 33.8%; Pred. No. 4.4e-06;  
 RESULT 1493  
 ID ADE44947 standard; protein; 168 AA.  
 DE Silk fibroin protein repeating peptide related peptide 'seq id 52'.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 9.3%; Score 219.5; DB 7; Length 168;  
 Best Local Similarity 33.8%; Pred. No. 4.4e-06;  
 RESULT 1494  
 ID ADM48391 standard; protein; 617 AA.  
 DE Human recombinant gelatin-like polypeptide Hu-3.  
 PN EPI398324-A1.  
 PD 17-MAR-2004.  
 PA (FUJF) FUJI PHOTO FILM BV.  
 Query Match 9.3%; Score 219.5; DB 8; Length 617;  
 Best Local Similarity 26.4%; Pred. No. 1.5e-05;  
 RESULT 1495  
 ID ADO26217 standard; protein; 617 AA.  
 DE Human gelatine-like polypeptide Hu-3.  
 PN WO2004056976-A2.  
 PD 08-JUL-2004.  
 PA (FUJF) FUJI PHOTO FILM BV.  
 Query Match 9.3%; Score 219.5; DB 8; Length 617;  
 Best Local Similarity 26.4%; Pred. No. 1.5e-05;  
 RESULT 1496  
 ID ADO08293 standard; protein; 733 AA.  
 DE Human NOVX polypeptide #20.  
 PN US2004018594-A1.  
 PD 29-JAN-2004.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (ANDE/) ANDERSON D W.  
 PA (BOLD/) BOLDG F L.  
 PA (BURG/) BURGESS C E.  
 PA (CASM/) CASMAN S J.  
 PA (CHAP/) CHAPOVAL A.  
 PA (EDIN/) EDINGER S R.  
 PA (GERL/) GERLACH V.  
 PA (GORM/) GORMAN L.  
 PA (GUNT/) GUNTHER E.  
 PA (GUOX/) GUO X S.  
 PA (KEKU/) KEKUDA R.  
 PA (LEPL/) LEPLEY D M.  
 PA (LILL/) LI L.  
 PA (LIUX/) LIU X.  
 PA (MALY/) MALYANKAR U M.  
 PA (MILL/) MILLER C E.  
 PA (MILL/) MILLET I.  
 PA (PADI/) PADIGARU M.  
 PA (PATT/) PATTURAJAN M.  
 PA (PENA/) PENA C E A.  
 PA (RIEG/) RIEGER D K.  
 PA (SHEN/) SHENOY S G.  
 PA (SHIM/) SHIMKETS R A.  
 PA (SPYT/) SPYTEK K A.  
 PA (TAUP/) TAUPIER R J.  
 PA (VERN/) VERNET C A M.  
 PA (VOSS/) VOSS E Z.  
 PA (ZERH/) ZERHUSEN B D.  
 Query Match 9.3%; Score 219.5; DB 8; Length 733;  
 Best Local Similarity 26.5%; Pred. No. 1.8e-05;  
 RESULT 1497  
 ID AAR80334 standard; protein; 829 AA.  
 DE Protein polymeric adhesion substrate 1-F.

PN WO9523611-A1.  
 PD 08-SEP-1995.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 9.3%; Score 219.5; DB 2; Length 829;  
 Best Local Similarity 29.4%; Pred. No. 2e-05;  
 RESULT 1498  
 ID AAW57673 standard; peptide; 829 AA.  
 DE Collagen-like polymer.  
 PN US5773249-A.  
 PD 30-JUN-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 9.3%; Score 219.5; DB 2; Length 829;  
 Best Local Similarity 29.4%; Pred. No. 2e-05;  
 RESULT 1499  
 ID AAW49723 standard; protein; 829 AA.  
 DE Protein polymer adhesive substrate PPASI-F.  
 PN US5773577-A.  
 PD 30-JUN-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 9.3%; Score 219.5; DB 2; Length 829;  
 Best Local Similarity 29.4%; Pred. No. 2e-05;  
 RESULT 1500  
 ID ADB70380 standard; protein; 1019 AA.  
 DE Collagen VI SEQ ID NO:72.  
 PN WO2003021229-A2.  
 PD 13-MAR-2003.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
 Query Match 9.3%; Score 219.5; DB 7; Length 1019;  
 Best Local Similarity 29.3%; Pred. No. 2.5e-05;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 7, 2005, 00:03:25 ; Search time 44 Seconds  
(without alignments)  
746.491 Million cell updates/sec

Title: US-10-063-561-52

Perfect score: 2363

Sequence: 1 MKPQGLACLLALCLGSGE.....KLGFINDAINKQRRSRIP 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	669	28.3	230	4	US-09-673-395A-256
2	402.5	17.0	1136	3	US-08-806-029-9
3	402.5	17.0	1177	1	US-07-609-716-31
4	402.5	17.0	1177	1	US-08-175-155-29
5	402.5	17.0	1177	1	US-08-477-509B-64
6	402.5	17.0	1177	2	US-08-707-237A-35
7	402.5	17.0	1177	3	US-08-482-085B-64
8	402.5	17.0	1177	3	US-08-475-411A-31
9	402.5	17.0	1177	3	US-08-478-029A-31
10	402.5	17.0	1177	3	US-09-444-791A-64
11	399	16.9	1059	2	US-08-175-155-48
12	399	16.9	1059	2	US-08-707-237A-54
13	399	16.9	1059	3	US-08-806-029-10
14	399	16.9	1101	1	US-08-477-509B-83
15	399	16.9	1101	3	US-08-482-085B-83
16	399	16.9	1101	3	US-09-444-791A-83
17	383	16.2	641	4	US-09-249-585A-3
18	383	16.2	641	4	US-09-410-399-4
19	376.5	15.9	1038	1	US-07-609-716-36
20	376.5	15.9	1038	3	US-08-475-411A-36
21	376.5	15.9	1038	3	US-08-478-029A-36
22	373	15.8	745	2	US-09-010-928B-28
23	373	15.8	870	2	US-09-010-928B-2
24	371	15.7	651	3	US-08-556-978B-19
25	371	15.7	651	3	US-09-247-806-1
26	371	15.7	651	4	US-09-863-859-1
27	371	15.7	718	1	US-08-425-069-2
28	371	15.7	718	2	US-08-317-844B-2
29	371	15.7	747	3	US-09-034-177-3
30	367	15.5	1011	1	US-08-477-509B-94
31	367	15.5	1011	3	US-08-482-085B-94
32	367	15.5	1011	3	US-09-444-791A-94
33	367	15.5	1170	1	US-08-175-155-59
34	367	15.5	1170	2	US-08-707-237A-66
35	366	15.5	766	1	US-08-175-155-53
36	366	15.5	766	1	US-08-477-509B-88
37	366	15.5	766	2	US-08-707-237A-61
38	366	15.5	766	3	US-08-482-085B-88
39	366	15.5	766	3	US-09-444-791A-88
40	366	15.5	979	1	US-08-477-509B-89
41	366	15.5	979	3	US-08-482-085B-89
42	366	15.5	979	3	US-09-444-791A-89
43	366	15.5	1050	1	US-08-175-155-54
44	364.5	15.4	907	2	US-09-010-928B-4
45	364.5	15.4	2018	3	US-09-444-791A-80
46	364.5	15.4	2100	3	US-08-477-509B-80
47	364.5	15.4	2100	3	US-08-482-085B-80
48	364	15.4	649	1	US-07-609-716-49
49	364	15.4	649	3	US-08-475-411A-49
50	364	15.4	649	3	US-08-478-029A-49
51	364	15.4	784	1	US-07-609-716-48
52	364	15.4	784	3	US-08-475-411A-48
53	364	15.4	784	3	US-08-478-029A-48
54	364	15.4	1018	1	US-08-089-862-11
55	364	15.4	1018	1	US-08-587-333-18
56	364	15.4	1018	5	PCT-US94-07776-16
57	364	15.4	2107	1	US-08-175-155-45
58	364	15.4	2107	2	US-08-707-237A-51
59	362	15.3	604	3	US-08-556-978B-63
60	362	15.3	1332	1	US-07-609-716-41
61	362	15.3	1332	3	US-08-475-411A-41
62	362	15.3	1332	3	US-08-478-029A-41
63	358.5	15.2	2055	1	US-08-175-155-46
64	358.5	15.2	2055	1	US-08-477-509B-81
65	358.5	15.2	2055	2	US-08-707-237A-52
66	358.5	15.2	2055	3	US-08-482-085B-81
67	358.5	15.2	2055	3	US-09-444-791A-81
68	358	15.2	606	3	US-08-556-978B-21
69	358	15.2	606	3	US-08-556-978B-23
70	358	15.2	606	3	US-09-247-806-4
71	358	15.2	606	3	US-09-247-806-6
72	358	15.2	606	3	US-09-247-806-8
73	358	15.2	809	4	US-09-863-859-13
74	358	15.2	818	4	US-09-863-859-22
75	358	15.2	1617	4	US-09-863-859-14
76	358	15.2	1626	4	US-09-863-859-24
77	354	15.0	945	1	US-08-089-862-6
78	354	15.0	945	1	US-08-587-333-13
79	354	15.0	945	5	PCT-US94-07776-11
80	351.5	14.9	1056	1	US-08-212-237-6
81	351.5	14.9	1056	3	US-08-806-029-29
82	351.5	14.9	1056	5	PCT-US95-02772-6
83	350.5	14.8	2257	1	US-08-175-155-47
84	350.5	14.8	2257	2	US-08-477-509B-82
85	350.5	14.8	2257	2	US-08-707-237A-53
86	350.5	14.8	2257	3	US-08-482-085B-82
87	350.5	14.8	2257	3	US-09-444-791A-82
88	350	14.8	316	4	US-09-538-092-997
89	348.5	14.7	528	4	US-09-420-291-8
90	348	14.7	832	1	US-08-209-747-2
91	348	14.7	832	4	US-08-458-298-2
92	343	14.5	681	4	US-09-490-291-4
93	343	14.5	691	4	US-09-490-291-6
94	336	14.2	1169	3	US-08-806-029-33
95	327.5	13.9	334	3	US-09-060-756-728
96	327.5	13.9	334	4	US-09-670-314-728
97	327.5	13.6	972	1	US-08-212-237-7
98	322.5	13.6	972	3	US-08-806-029-30
99	322.5	13.6	972	5	PCT-US95-02772-7
100	319.5	13.5	318	3	US-09-060-756-727

Sequence 2, Appli  
Sequence 3, Appli  
Sequence 94, Appli  
Sequence 94, Appli  
Sequence 94, Appli  
Sequence 55, Appli  
Sequence 66, Appli  
Sequence 53, Appli  
Sequence 88, Appli  
Sequence 61, Appli  
Sequence 88, Appli  
Sequence 88, Appli  
Sequence 89, Appli  
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Sequence 7, Appli  
Sequence 727, Appl

101	319.5	13.5	318	4	US-09-670-314-727	Sequence 727, App	174	268	11.3	762	1	US-08-397-633A-31	Sequence 31, Appl
102	317.5	13.4	988	1	US-08-212-237-5	Sequence 5, Appl	175	267.5	11.3	1024	3	US-08-931-820-2	Sequence 2, Appl
103	317.5	13.4	988	3	US-08-806-029-28	Sequence 28, Appl	176	267.5	11.3	1366	3	US-08-963-825-19	Sequence 19, Appl
104	317.5	13.4	988	5	PCT-US95-02772-5	Sequence 5, Appl	177	267.5	11.3	1366	3	US-09-500-811-19	Sequence 19, Appl
105	309.5	13.1	200	4	US-09-989-981A-13	Sequence 13, Appl	178	267.5	11.3	1366	3	US-09-570-573-19	Sequence 19, Appl
106	309	13.1	201	3	US-09-052-995-1	Sequence 1, Appl	179	267.5	11.3	1366	3	US-09-548-608-19	Sequence 19, Appl
107	309	13.1	201	3	US-09-053-003-40	Sequence 40, Appl	180	264.5	11.2	1008	3	US-09-219-849-8	Sequence 8, Appl
108	309	13.1	201	4	US-09-054-281-22	Sequence 22, Appl	181	264.5	11.2	1065	1	US-08-642-255-80	Sequence 80, Appl
109	309	13.1	201	4	US-09-478-948-6	Sequence 6, Appl	182	264.5	11.2	1065	3	US-08-642-246-16	Sequence 16, Appl
110	309	13.1	201	4	US-09-818-094-40	Sequence 40, Appl	183	264.5	11.2	1065	3	US-09-451-206-16	Sequence 16, Appl
111	309	13.1	201	4	US-09-754-947-5	Sequence 5, Appl	184	264.5	11.2	1065	5	PCT-US96-06229-16	Sequence 16, Appl
112	308	13.0	235	2	US-08-529-1908-1	Sequence 1, Appl	185	264	11.2	269	1	US-08-452-531-4	Sequence 4, Appl
113	304.5	12.9	889	3	US-08-806-029-19	Sequence 19, Appl	186	264	11.2	269	2	US-08-460-746A-4	Sequence 4, Appl
114	302	12.8	714	3	US-08-556-978B-61	Sequence 61, Appl	187	264	11.2	269	2	US-08-460-555-4	Sequence 4, Appl
115	302	12.8	714	3	US-09-247-806-10	Sequence 10, Appl	188	264	11.2	269	3	US-08-460-066-4	Sequence 4, Appl
116	300.5	12.7	768	3	US-08-806-029-35	Sequence 35, Appl	189	257	10.9	633	1	US-08-642-255-73	Sequence 73, Appl
117	300.5	12.7	884	1	US-08-397-633A-68	Sequence 68, Appl	190	257	10.9	1065	1	US-08-642-255-72	Sequence 72, Appl
118	300.5	12.7	884	2	US-08-435-641-15	Sequence 15, Appl	191	254	10.7	1040	3	US-08-806-029-32	Sequence 32, Appl
119	300.5	12.7	884	2	US-08-707-237A-96	Sequence 96, Appl	192	254	10.7	1745	4	US-09-795-061-4	Sequence 4, Appl
120	300.5	12.7	884	3	US-08-642-246-15	Sequence 15, Appl	193	253	10.7	1060	3	US-08-931-820-3	Sequence 3, Appl
121	300.5	12.7	884	4	US-09-451-206-15	Sequence 15, Appl	194	253	10.7	1077	1	US-07-972-032-82	Sequence 82, Appl
122	300.5	12.7	884	5	PCT-US96-06229-15	Sequence 15, Appl	195	253	10.7	1077	1	US-08-642-255-95	Sequence 95, Appl
123	300	12.7	738	3	US-08-864-038A-3	Sequence 3, Appl	196	253	10.7	1418	3	US-08-963-825-20	Sequence 20, Appl
124	296.5	12.5	1024	1	US-08-212-237-8	Sequence 8, Appl	197	253	10.7	1418	3	US-09-010-999-1	Sequence 10, Appl
125	296.5	12.5	1024	3	US-08-806-029-31	Sequence 31, Appl	198	253	10.7	1418	3	US-09-500-811-20	Sequence 20, Appl
126	296.5	12.5	1024	5	PCT-US95-02772-8	Sequence 8, Appl	199	253	10.7	1418	3	US-09-570-573-20	Sequence 20, Appl
127	296	12.5	595	1	US-08-425-069-4	Sequence 4, Appl	200	251.5	10.6	462	3	US-09-548-608-20	Sequence 20, Appl
128	296	12.5	595	2	US-08-317-844B-4	Sequence 4, Appl	201	251.5	10.6	462	3	US-09-919-039-324	Sequence 324, App
129	294.5	12.5	832	1	US-08-212-237-4	Sequence 4, Appl	202	248.5	10.5	1442	2	US-08-316-650-12	Sequence 12, Appl
130	294.5	12.5	832	3	US-08-806-029-27	Sequence 27, Appl	203	248.5	10.5	1442	5	PCT-US95-02251-12	Sequence 12, Appl
131	294.5	12.5	832	5	PCT-US95-02772-4	Sequence 4, Appl	204	247.5	10.5	419	4	US-09-270-767-41767	Sequence 41767, A
132	294	12.4	493	3	US-08-556-978B-59	Sequence 59, Appl	205	247.5	10.5	943	4	US-09-477-135A-131	Sequence 131, App
133	294	12.4	529	3	US-09-247-806-2	Sequence 2, Appl	206	247.5	10.5	1739	4	US-09-795-061-2	Sequence 2, Appl
134	294	12.4	674	1	US-08-317-522A-3	Sequence 3, Appl	207	247	10.5	975	4	US-09-328-352-4764	Sequence 4764, Ap
135	294	12.4	674	1	US-08-439-818A-3	Sequence 3, Appl	208	246.5	10.4	448	4	US-09-248-796A-19135	Sequence 19135, A
136	294	12.4	674	2	US-08-751-965-3	Sequence 3, Appl	209	246.5	10.4	556	4	US-09-248-796A-22338	Sequence 22338, A
137	294	12.4	674	2	US-08-738-975-3	Sequence 3, Appl	210	246.5	10.4	595	3	US-09-219-849-48	Sequence 48, Appl
138	294	12.4	674	2	US-08-728-626-3	Sequence 3, Appl	211	246.5	10.4	595	3	US-09-219-849-50	Sequence 50, Appl
139	294	12.4	674	3	US-08-808-599A-3	Sequence 3, Appl	212	246.5	10.4	822	3	US-09-219-849-49	Sequence 49, Appl
140	290.5	12.3	749	1	US-08-317-522A-2	Sequence 2, Appl	213	246.5	10.4	1057	3	US-08-931-820-1	Sequence 1, Appl
141	290.5	12.3	749	1	US-08-439-818A-2	Sequence 2, Appl	214	246.5	10.4	1341	3	US-08-963-825-18	Sequence 18, Appl
142	290.5	12.3	749	2	US-08-751-965-2	Sequence 2, Appl	215	246.5	10.4	1341	3	US-09-500-811-18	Sequence 18, Appl
143	290.5	12.3	749	2	US-08-738-975-2	Sequence 2, Appl	216	246.5	10.4	1341	3	US-09-570-573-18	Sequence 18, Appl
144	290.5	12.3	749	2	US-08-728-626-2	Sequence 2, Appl	217	246.5	10.4	1341	3	US-09-548-608-18	Sequence 18, Appl
145	290.5	12.3	749	3	US-08-808-599A-2	Sequence 2, Appl	218	246.5	10.4	1358	1	US-07-945-283-2	Sequence 2, Appl
146	288.5	12.2	877	1	US-08-397-633A-54	Sequence 54, Appl	219	245	10.4	907	4	US-09-949-016-9750	Sequence 9750, Ap
147	288.5	12.2	953	3	US-08-806-029-14	Sequence 14, Appl	220	245	10.4	907	4	US-09-949-016-9751	Sequence 9751, Ap
148	283.5	12.0	401	3	US-09-219-849-34	Sequence 34, Appl	221	244.5	10.3	492	4	US-08-468-996-11	Sequence 11, Appl
149	283.5	12.0	599	4	US-09-602-459-22	Sequence 22, Appl	222	244.5	10.3	1002	2	US-08-707-237A-103	Sequence 103, App
150	283.5	12.0	599	4	US-09-602-459-23	Sequence 23, Appl	223	244.5	10.3	1002	3	US-08-642-246-25	Sequence 25, Appl
151	283	12.0	1160	3	US-08-808-599A-24	Sequence 24, Appl	224	244.5	10.3	1002	4	US-09-451-206-25	Sequence 25, Appl
152	280	11.8	1057	3	US-08-931-820-4	Sequence 4, Appl	225	244.5	10.3	1002	5	PCT-US96-06229-25	Sequence 25, Appl
153	278.5	11.8	526	4	US-09-538-092-1080	Sequence 1080, Ap	226	244.5	10.3	1464	4	US-09-331-347C-21	Sequence 21, Appl
154	276	11.7	231	4	US-09-248-796A-14281	Sequence 14281, A	227	244	10.3	492	4	US-08-468-996-12	Sequence 12, Appl
155	276	11.7	1078	3	US-08-963-825-21	Sequence 21, Appl	228	243	10.3	1017	4	US-08-468-996-10	Sequence 10, Appl
156	276	11.7	1078	3	US-09-500-811-21	Sequence 21, Appl	229	242.5	10.3	955	4	US-09-949-016-8369	Sequence 8369, Ap
157	276	11.7	1078	3	US-09-570-573-21	Sequence 21, Appl	230	241.5	10.2	1461	4	US-09-585-887-9	Sequence 9, Appl
158	276	11.7	1078	3	US-09-548-608-21	Sequence 21, Appl	231	241.5	10.2	1461	4	US-09-289-578-9	Sequence 9, Appl
159	276	11.7	1366	4	US-09-585-887-10	Sequence 10, Appl	232	240.5	10.2	250	4	US-09-248-796A-22487	Sequence 22487, A
160	276	11.7	1366	4	US-09-289-578-10	Sequence 10, Appl	233	240.5	10.2	943	3	US-09-056-556-204	Sequence 204, App
161	276	11.7	1366	4	US-09-949-016-5882	Sequence 5882, Ap	234	240.5	10.2	943	4	US-09-072-596-199	Sequence 199, App
162	275	11.6	482	4	US-09-302-540-14708	Sequence 14708, A	235	240.5	10.2	943	4	US-09-072-967-204	Sequence 204, App
163	274	11.6	593	4	US-09-538-092-919	Sequence 919, App	236	239	10.1	960	3	US-09-219-849-6	Sequence 6, Appl
164	273	11.6	486	1	US-08-397-633A-77	Sequence 77, Appl	237	239	10.1	1806	4	US-09-519-497-56	Sequence 56, Appl
165	272.5	11.5	479	1	US-08-397-633A-78	Sequence 78, Appl	238	237.5	10.1	682	1	US-08-642-255-136	Sequence 126, App
166	272.5	11.5	619	4	US-09-252-991A-26352	Sequence 26352, A	239	237.5	10.1	1681	1	US-08-397-633A-36	Sequence 36, Appl
167	272	11.5	291	4	US-09-490-291-2	Sequence 2, Appl	240	236.5	10.0	1413	2	US-08-175-155-39	Sequence 39, Appl
168	272	11.5	656	3	US-08-806-029-36	Sequence 36, Appl	241	236.5	10.0	1413	2	US-08-707-237A-45	Sequence 45, Appl
169	272	11.5	750	3	US-08-806-029-25	Sequence 25, Appl	242	236.5	10.0	1464	1	US-08-477-508B-74	Sequence 74, Appl
170	271	11.5	761	2	US-08-707-237A-84	Sequence 84, Appl	243	236.5	10.0	1464	1	US-08-482-085B-74	Sequence 74, Appl
171	271	11.5	762	1	US-08-642-255-114	Sequence 114, App	244	236.5	10.0	1465	3	US-08-444-791A-74	Sequence 74, Appl
172	271	11.5	762	1	US-08-397-633A-26	Sequence 26, Appl	245	236	10.0	508	4	US-09-270-767-46233	Sequence 46233, A
173	268	11.3	762	1	US-08-642-255-120	Sequence 120, App	246	236	10.0	552	3	US-09-219-849-7	Sequence 7, Appl

247	235.5	10.0	643	4	US-09-538-092-844	Sequence 844, App	320	206	8.7	417	1	US-08-477-509B-104	Sequence 104, App
248	234.5	9.9	936	1	US-08-212-237-3	Sequence 3, Appli	321	206	8.7	417	1	US-08-642-255-102	Sequence 102, App
249	234.5	9.9	936	2	US-08-806-029-26	Sequence 26, Appl	322	206	8.7	417	1	US-08-707-237A-76	Sequence 76, Appl
250	234.5	9.9	936	5	PCT-US95-02772-3	Sequence 3, Appli	323	206	8.7	417	3	US-08-482-085B-104	Sequence 104, App
251	232.5	9.8	536	1	US-09-270-767-43766	Sequence 43766, A	324	206	8.7	417	3	US-09-444-791A-104	Sequence 104, App
252	231.5	9.8	100	4	US-09-411-067C-4	Sequence 4, Appli	325	206	8.7	837	1	US-08-175-155-68	Sequence 68, Appl
253	231.5	9.8	2088	4	US-09-548-372D-13	Sequence 13, Appl	326	206	8.7	837	1	US-08-477-509B-103	Sequence 103, App
254	231.5	9.8	2088	4	US-09-548-367D-13	Sequence 13, Appl	327	206	8.7	837	1	US-08-642-255-101	Sequence 101, App
255	231.5	9.8	2088	4	US-09-551-853D-13	Sequence 13, Appl	328	206	8.7	837	2	US-08-707-237A-75	Sequence 75, Appl
256	231.5	9.8	2088	4	US-09-548-376D-13	Sequence 13, Appl	329	206	8.7	837	3	US-08-482-085B-103	Sequence 103, App
257	231.5	9.8	2088	4	US-09-548-373D-13	Sequence 13, Appl	330	206	8.7	837	3	US-08-482-085B-103	Sequence 103, App
258	231.5	9.8	2088	4	US-09-548-366P-13	Sequence 13, Appl	331	206	8.7	837	1	US-09-444-791A-103	Sequence 103, App
259	231.5	9.8	2088	4	US-09-548-368D-13	Sequence 13, Appl	332	206	8.7	837	1	US-08-397-633A-50	Sequence 50, Appl
260	230.5	9.8	936	2	US-08-707-237A-108	Sequence 108, App	333	205.5	8.7	1516	4	US-09-949-016-8209	Sequence 8209, Ap
261	230.5	9.8	936	3	US-08-642-246-30	Sequence 30, Appl	334	205.5	8.7	489	2	US-08-794-795-7	Sequence 7, Appli
262	230.5	9.8	936	4	US-09-451-206-30	Sequence 30, Appl	335	205.5	8.7	489	3	US-09-249-200-7	Sequence 2, Appli
263	230.5	9.8	936	5	PCT-US96-06229-30	Sequence 30, Appl	336	205.5	8.7	518	1	US-08-392-367B-2	Sequence 2, Appli
264	229.5	9.7	857	4	US-09-902-404-12312	Sequence 12312, A	337	205	8.7	518	3	US-08-893-467A-2	Sequence 2, Appli
265	227.5	9.6	485	2	US-08-749-391-2	Sequence 2, Appli	338	205	8.7	187	4	US-09-680-175-4	Sequence 4, Appli
266	227.5	9.6	485	3	US-09-390-200-2	Sequence 2, Appli	339	205	8.7	228	3	US-09-219-849-38	Sequence 38, Appl
267	224.5	9.5	748	3	US-09-219-849-10	Sequence 10, Appl	340	205	8.7	1415	4	US-09-252-991A-26438	Sequence 26438, A
268	223	9.4	378	2	US-08-707-237A-104	Sequence 104, App	341	203.5	8.6	1603	4	US-09-949-016-6136	Sequence 6136, Ap
269	223	9.4	378	3	US-08-642-246-26	Sequence 26, Appl	342	203	8.6	688	4	US-09-902-540-10297	Sequence 10297, A
270	223	9.4	378	4	US-09-451-206-26	Sequence 26, Appl	343	201.5	8.5	1259	4	US-09-949-016-10366	Sequence 10366, A
271	223	9.4	378	5	PCT-US96-06229-26	Sequence 26, Appl	344	201.5	8.5	123	4	US-09-072-596-243	Sequence 243, App
272	222.5	9.4	966	3	US-08-642-246-34	Sequence 34, Appl	345	201.5	8.5	123	4	US-09-072-967-248	Sequence 248, App
273	222.5	9.4	966	4	US-09-451-206-34	Sequence 34, Appl	346	201.5	8.5	312	3	US-08-806-029-34	Sequence 34, Appl
274	222.5	9.4	966	5	PCT-US96-06229-34	Sequence 34, Appl	347	201.5	8.5	433	4	US-09-524-101D-20	Sequence 20, Appl
275	222.5	9.4	1343	4	US-09-949-016-10641	Sequence 10641, A	348	201	8.5	684	4	US-09-949-016-8348	Sequence 8348, Ap
276	222	9.4	412	4	US-09-248-796A-26345	Sequence 26345, A	349	200.5	8.5	1712	4	US-09-561-403-9	Sequence 9, Appli
277	222	9.4	637	4	US-09-949-016-8152	Sequence 8152, Ap	350	200.5	8.5	341	2	US-08-538-711A-8	Sequence 8, Appli
278	222	9.4	1694	1	US-08-494-168-2	Sequence 2, Appli	351	200.5	8.5	341	3	US-08-725-027-8	Sequence 8, Appli
279	220.5	9.3	645	4	US-09-919-172-41	Sequence 41, Appl	352	200.5	8.5	341	4	US-09-542-552-8	Sequence 8, Appli
280	219.5	9.3	168	3	US-09-444-791A-52	Sequence 52, Appl	353	200.5	8.5	353	2	US-08-538-711A-7	Sequence 7, Appli
281	219.5	9.3	829	1	US-08-642-255-132	Sequence 132, App	354	200.5	8.5	353	3	US-08-725-027-7	Sequence 7, Appli
282	219.5	9.3	829	1	US-08-397-633A-53	Sequence 53, Appl	355	200.5	8.5	353	4	US-09-542-552-7	Sequence 7, Appli
283	219	9.3	274	4	US-09-976-594-417	Sequence 417, App	356	200.5	8.5	353	4	US-09-538-092-989	Sequence 989, App
284	218.5	9.2	378	4	US-10-164-595-2	Sequence 2, Appli	357	200.5	8.5	410	4	US-09-949-016-10345	Sequence 10345, A
285	217.5	9.2	495	2	US-08-794-795-2	Sequence 2, Appli	358	199	8.4	541	4	US-09-248-796A-26119	Sequence 26119, A
286	217.5	9.2	495	3	US-09-249-200-2	Sequence 2, Appli	359	199	8.4	599	4	US-09-949-016-8890	Sequence 8890, Ap
287	217	9.2	295	4	US-09-248-796A-25715	Sequence 25715, A	360	199	8.4	825	4	US-10-210-428-1	Sequence 1, Appli
288	216.5	9.2	595	4	US-09-370-838-187	Sequence 187, App	361	199	8.4	825	4	US-10-237-551-161	Sequence 161, App
289	216.5	9.2	595	4	US-09-854-133-187	Sequence 187, App	362	199	8.4	826	4	US-09-894-998A-47	Sequence 47, Appl
290	216.5	9.2	684	1	US-08-555-669-12	Sequence 12, Appl	363	199	8.4	826	4	US-10-237-551-47	Sequence 47, Appl
291	216.5	9.2	684	3	US-09-073-663-12	Sequence 12, Appl	364	198.5	8.4	547	1	US-08-494-168-7	Sequence 7, Appli
292	216.5	9.2	2090	4	US-09-538-092-1081	Sequence 1081, App	365	198	8.4	541	4	US-09-538-092-347	Sequence 347, App
293	216.5	9.2	2120	4	US-09-949-016-9768	Sequence 9768, Ap	366	197.5	8.4	464	4	US-09-252-991A-24883	Sequence 24883, A
294	215.5	9.1	520	2	US-08-794-795-6	Sequence 6, Appli	367	197	8.3	1078	4	US-09-949-016-11185	Sequence 11185, A
295	215.5	9.1	520	3	US-09-249-200-6	Sequence 6, Appli	368	197	8.3	1143	4	US-09-949-016-6137	Sequence 6137, Ap
296	215	9.1	390	1	US-08-106-981-4	Sequence 4, Appli	369	195.5	8.3	279	3	US-09-010-999-2	Sequence 2, Appli
297	215	9.1	479	3	US-09-177-349-3	Sequence 3, Appli	370	195	8.3	146	1	US-07-609-716-105	Sequence 105, App
298	215	9.1	479	4	US-09-918-951-3	Sequence 3, Appli	371	195	8.3	146	3	US-08-475-411A-105	Sequence 105, App
299	215	9.1	1218	4	US-09-949-016-7065	Sequence 7065, Ap	372	195	8.3	146	3	US-08-475-411A-105	Sequence 105, App
300	215	9.1	1319	4	US-09-538-092-1291	Sequence 1291, Ap	373	195	8.3	281	1	US-08-397-633A-75	Sequence 75, Appl
301	215	9.1	1690	4	US-09-949-016-5884	Sequence 5884, Ap	374	194.5	8.2	166	4	US-09-841-334A-21	Sequence 21, Appl
302	214	9.1	406	4	US-09-949-016-9243	Sequence 9243, Ap	375	194.5	8.2	166	4	US-09-837-969A-21	Sequence 21, Appl
303	213.5	9.0	310	3	US-09-219-849-47	Sequence 47, Appl	376	194.5	8.2	442	4	US-09-248-796A-21400	Sequence 21400, A
304	213.5	9.0	1670	4	US-09-949-016-5883	Sequence 5883, Ap	377	194.5	8.2	1268	4	US-09-949-016-7487	Sequence 7487, Ap
305	213	9.0	529	4	US-09-381-656-1	Sequence 1, Appli	378	193	8.2	359	4	US-09-270-767-43751	Sequence 43751, A
306	212.5	9.0	347	4	US-09-623-497-1	Sequence 1, Appli	379	192	8.1	623	3	US-09-029-348-3	Sequence 3, Appli
307	212	9.0	100	4	US-09-411-067C-5	Sequence 5, Appli	380	192	8.1	744	4	US-09-949-016-9607	Sequence 9607, Ap
308	211	8.9	371	4	US-09-538-092-884	Sequence 884, App	381	192	8.1	1345	2	US-08-977-767-3	Sequence 3, Appli
309	210.5	8.9	262	1	US-08-397-633A-73	Sequence 73, Appl	382	191.5	8.1	160	3	US-08-542-051-18	Sequence 18, Appl
310	210	8.9	1609	4	US-09-949-016-10910	Sequence 10910, A	383	191.5	8.1	644	4	US-09-919-039-121	Sequence 121, App
311	209.5	8.9	333	2	US-08-687-702-37	Sequence 37, Appl	384	191.5	8.1	847	4	US-09-373-157-4	Sequence 4, Appli
312	209.5	8.9	1034	4	US-09-252-991A-26658	Sequence 26658, A	385	191.5	8.1	875	4	US-09-949-016-8582	Sequence 8582, Ap
313	208.5	8.8	435	4	US-09-902-540-12731	Sequence 12731, A	386	190.5	8.1	637	4	US-09-248-796A-19134	Sequence 19134, A
314	208	8.8	689	4	US-09-949-016-11276	Sequence 11276, A	387	190.5	8.1	2870	4	US-09-479-467A-15	Sequence 15, Appl
315	208	8.8	1064	1	US-08-642-255-62	Sequence 62, Appl	388	190.5	8.1	3178	4	US-09-479-467A-4	Sequence 4, Appli
316	207	8.8	680	4	US-09-949-001-15	Sequence 15, Appl	389	190	8.0	276	3	US-08-506-553C-26	Sequence 26, Appl
317	207	8.8	680	4	US-09-949-001-20	Sequence 20, Appl	390	190	8.0	344	1	US-08-891-254-7	Sequence 7, Appli
318	206.5	8.7	938	4	US-09-949-016-9992	Sequence 9992, Ap	391	190	8.0	344	2	US-08-819-539-7	Sequence 7, Appli
319	206	8.7	417	1	US-08-175-155-69	Sequence 69, Appl	392	190	8.0	344	2	US-09-030-270A-7	Sequence 7, Appli

393	190	8.0	344	3	US-08-984-207-7	Sequence 7, Appli	466	171.5	7.3	1127	3	US-09-150-460B-11	Sequence 11, Appli
394	190	8.0	344	3	US-09-013-587-7	Sequence 7, Appli	467	171.5	7.3	2211	3	US-09-738-884-1	Sequence 1, Appli
395	190	8.0	344	4	US-09-086-118-27	Sequence 27, Appli	468	171.5	7.3	2211	4	US-10-096-961A-1	Sequence 1, Appli
396	190	8.0	344	4	US-09-431-614-15	Sequence 15, Appli	469	171	7.2	641	4	US-09-270-767-41562	Sequence 41562, A
397	190	8.0	344	5	PCT-US96-08819-7	Sequence 7, Appli	470	170.5	7.2	591	4	US-09-949-016-10914	Sequence 10914, A
398	190	8.0	344	6	US-09-029-348-2	Sequence 2, Appli	471	170.5	7.2	591	4	US-09-949-016-10914	Sequence 10914, A
399	189.5	8.0	549	1	US-08-494-168-8	Sequence 8, Appli	472	170	7.2	513	4	US-09-248-796A-25078	Sequence 25078, A
400	189.5	8.0	644	1	US-08-206-176-2	Sequence 2, Appli	473	170	7.2	519	3	US-09-453-702B-265	Sequence 265, App
401	189	8.0	643	2	US-08-551-356-4	Sequence 4, Appli	474	169.5	7.2	415	3	US-09-025-769B-280	Sequence 280, App
402	189	8.0	643	5	PCT-US93-12687-4	Sequence 4, Appli	475	169.5	7.2	415	4	US-09-490-070A-280	Sequence 280, App
403	189	8.0	1336	2	US-08-551-356-6	Sequence 6, Appli	476	169.5	7.2	415	4	US-09-490-153-280	Sequence 280, App
404	189	8.0	1336	5	PCT-US93-12687-6	Sequence 6, Appli	477	169.5	7.2	415	4	US-09-490-324-280	Sequence 280, App
405	188	8.0	287	1	US-08-397-633A-76	Sequence 76, Appli	478	168.5	7.1	208	5	US-08-212-237-9	Sequence 9, Appli
406	187.5	7.9	180	4	US-09-248-796A-22352	Sequence 22352, A	479	168.5	7.1	208	5	PCT-US95-02772-9	Sequence 9, Appli
407	187	7.9	252	1	US-08-642-255-61	Sequence 61, Appli	480	168.5	7.1	755	4	US-09-919-497-57	Sequence 57, Appli
408	186.5	7.9	532	1	US-08-494-168-9	Sequence 9, Appli	481	168	7.1	111	3	US-08-963-168C-15	Sequence 15, Appli
409	186.5	7.9	1566	4	US-09-581-472B-2	Sequence 2, Appli	482	168	7.1	131	3	US-08-963-168C-8	Sequence 8, Appli
410	186	7.9	251	1	US-08-397-633A-74	Sequence 74, Appli	483	168	7.1	136	3	US-08-963-168C-6	Sequence 6, Appli
411	186	7.9	336	4	US-09-270-767-44531	Sequence 44531, A	484	168	7.1	316	4	US-09-248-796A-26455	Sequence 26455, A
412	186	7.9	605	4	US-09-976-594-616	Sequence 616, App	485	168	7.1	345	4	US-09-657-013-112	Sequence 112, App
413	186	7.9	1581	3	US-09-110-517-2	Sequence 2, Appli	486	168	7.1	684	4	US-09-961-403-5	Sequence 5, Appli
414	185.5	7.9	673	4	US-09-107-532A-5134	Sequence 5134, Ap	487	167.5	7.1	357	1	US-07-609-716-66	Sequence 66, Appli
415	185	7.8	546	1	US-08-494-168-10	Sequence 10, Appli	488	167.5	7.1	357	1	US-08-642-255-33	Sequence 33, Appli
416	184.5	7.8	174	4	US-09-270-767-61801	Sequence 61801, A	489	167.5	7.1	357	3	US-08-475-411A-66	Sequence 66, Appli
417	184.5	7.8	216	3	US-08-506-553C-23	Sequence 23, Appli	490	167.5	7.1	357	3	US-08-478-029A-66	Sequence 66, Appli
418	184	7.8	159	1	US-07-609-716-104	Sequence 104, App	491	167.5	7.1	551	4	US-09-489-039A-9083	Sequence 9083, Ap
419	184	7.8	159	3	US-08-475-411A-104	Sequence 104, App	492	167.5	7.1	558	4	US-09-071-035-288	Sequence 288, App
420	184	7.8	159	3	US-08-478-029A-104	Sequence 104, App	493	167.5	7.1	1638	4	US-09-071-035-288	Sequence 288, App
421	182.5	7.7	472	4	US-09-538-092-312	Sequence 312, App	494	167.5	7.1	1638	4	US-09-071-035-262	Sequence 262, App
422	181	7.7	234	4	US-09-995-674A-12	Sequence 1, Appli	495	167.5	7.1	1638	4	US-09-071-035-266	Sequence 266, App
423	180	7.6	730	4	US-09-961-403-8	Sequence 8, Appli	496	167.5	7.1	1747	4	US-09-134-000C-5999	Sequence 5999, Ap
424	180	7.6	731	2	US-08-911-364-1	Sequence 1, Appli	497	166.5	7.0	1088	3	US-09-130-242-2	Sequence 2, Appli
425	180	7.6	733	3	US-08-464-700-2	Sequence 2, Appli	498	166.5	7.0	1088	4	US-09-583-610D-2	Sequence 2, Appli
426	180	7.6	792	2	US-08-678-039A-40	Sequence 40, Appli	499	166.5	7.0	1088	4	US-09-949-016-6935	Sequence 6935, Ap
427	179.5	7.6	960	5	US-09-219-849-5	Sequence 5, Appli	500	166.5	7.0	2504	4	US-09-328-352-5821	Sequence 5821, Ap
428	179	7.6	345	4	US-09-270-767-45883	Sequence 45883, A	501	165.5	7.0	116	3	US-08-963-168C-13	Sequence 13, Appli
429	178.5	7.6	216	4	US-09-248-796A-14221	Sequence 14221, A	502	165.5	7.0	132	3	US-08-963-168C-9	Sequence 9, Appli
430	178	7.5	889	3	US-09-336-447A-15	Sequence 15, Appli	503	165.5	7.0	416	4	US-09-902-540-9752	Sequence 11959, A
431	178	7.5	889	4	US-09-352-267B-15	Sequence 15, Appli	504	165	7.0	715	4	US-09-902-540-9752	Sequence 439, App
432	177.5	7.5	337	4	US-09-270-767-46550	Sequence 46550, A	505	165	7.0	823	4	US-09-538-092-4935	Sequence 16, Appli
433	177	7.5	190	2	US-08-560-398-8	Sequence 8, Appli	506	164.5	7.0	112	3	US-08-963-168C-16	Sequence 16, Appli
434	177	7.5	731	4	US-09-340-736B-1	Sequence 1, Appli	507	164.5	7.0	356	4	US-09-252-991A-18206	Sequence 18206, A
435	177	7.5	731	4	US-09-964-662-1	Sequence 1, Appli	508	164.5	7.0	732	4	US-09-270-767-44652	Sequence 44652, A
436	177	7.5	2732	4	US-09-086-436-30	Sequence 30, Appli	509	163.5	6.9	331	4	US-09-949-016-7015	Sequence 7015, Ap
437	176.5	7.5	571	3	US-09-134-001C-3865	Sequence 3865, Ap	510	163.5	6.9	335	4	US-09-949-016-7995	Sequence 7995, Ap
438	174.5	7.4	385	1	US-08-891-254-3	Sequence 3, Appli	511	163.5	6.9	414	1	US-08-343-682-1	Sequence 1, Appli
439	174.5	7.4	385	2	US-08-819-539-3	Sequence 3, Appli	512	163.5	6.9	414	2	US-08-705-660-26	Sequence 26, Appli
440	174.5	7.4	385	5	PCT-US96-08819-3	Sequence 3, Appli	513	163.5	6.9	414	4	US-08-989-045-26	Sequence 26, Appli
441	174.5	7.4	403	2	US-08-200-724A-2	Sequence 2, Appli	514	163.5	6.9	414	4	US-09-976-594-373	Sequence 373, App
442	174.5	7.4	403	2	US-09-030-270A-2	Sequence 2, Appli	515	163.5	6.9	414	4	US-09-315-355A-26	Sequence 26, Appli
443	174.5	7.4	403	3	US-08-851-376A-2	Sequence 2, Appli	516	163.5	6.9	666	2	US-08-737-716-14	Sequence 14, Appli
444	174.5	7.4	403	3	US-08-984-207-3	Sequence 3, Appli	517	163	6.9	384	4	US-09-949-016-11034	Sequence 11034, A
445	174.5	7.4	403	4	US-09-013-587-3	Sequence 3, Appli	518	163	6.9	535	3	US-09-029-348-1	Sequence 1, Appli
446	174.5	7.4	403	4	US-09-086-118-23	Sequence 23, Appli	519	163	6.9	537	3	US-09-029-348-4	Sequence 4, Appli
447	174.5	7.4	403	4	US-09-431-614-3	Sequence 3, Appli	520	163	6.9	920	4	US-09-538-092-1197	Sequence 1197, Ap
448	174.5	7.4	1261	3	US-09-208-742-4	Sequence 4, Appli	521	163	6.9	1216	4	US-09-134-000C-5130	Sequence 5130, Ap
449	174.5	7.4	1261	3	US-09-332-295-2	Sequence 2, Appli	522	163	6.9	1709	4	US-09-949-016-11345	Sequence 11345, A
450	174.5	7.4	1261	4	US-09-709-979-2	Sequence 2, Appli	523	162.5	6.9	878	4	US-09-540-236-3401	Sequence 3401, Ap
451	174.5	7.4	1261	4	US-10-147-268-2	Sequence 2, Appli	524	162	6.9	683	4	US-09-620-412C-357	Sequence 357, App
452	174	7.4	521	4	US-09-270-767-46291	Sequence 46291, A	525	162	6.9	717	4	US-09-598-419-357	Sequence 357, App
453	173.5	7.3	432	4	US-09-403-089A-1	Sequence 1, Appli	526	162	6.9	319	4	US-09-248-796A-18138	Sequence 18138, A
454	173.5	7.3	432	4	US-09-809-517A-25	Sequence 25, Appli	527	161.5	6.8	424	3	US-09-120-817-2	Sequence 2, Appli
455	173.5	7.3	434	4	US-09-809-517A-23	Sequence 23, Appli	528	161.5	6.8	424	4	US-09-431-614-14	Sequence 14, Appli
456	173.5	7.3	434	4	US-09-809-517A-26	Sequence 26, Appli	529	161.5	6.8	534	3	US-09-029-348-5	Sequence 5, Appli
457	173.5	7.3	482	1	US-08-358-160-5	Sequence 5, Appli	530	161.5	6.8	534	3	US-09-320-095-10	Sequence 10, Appli
458	173.5	7.3	484	1	US-08-358-160-7	Sequence 7, Appli	531	161.5	6.8	557	3	US-09-523-487-10	Sequence 10, Appli
459	173	7.3	656	2	US-08-343-443B-2	Sequence 2, Appli	532	161.5	6.8	557	3	US-09-523-487-10	Sequence 52, Appli
460	173	7.3	656	3	US-09-214-564B-4	Sequence 4, Appli	533	161	6.8	503	3	US-08-845-258-52	Sequence 52, Appli
461	173	7.3	656	4	US-09-538-092-1250	Sequence 1250, Ap	534	161	6.8	503	3	US-08-990-571-52	Sequence 52, Appli
462	172.5	7.3	259	4	US-09-436-434-2	Sequence 2, Appli	535	161	6.8	503	4	US-09-528-784A-52	Sequence 52, Appli
463	172.5	7.3	385	5	PCT-US93-06243-2	Sequence 2, Appli	536	161	6.8	503	4	US-09-569-098A-52	Sequence 52, Appli
464	172	7.3	1268	4	US-09-270-767-45320	Sequence 45320, A	537	161	6.8	666	4	US-09-528-784A-85	Sequence 85, Appli
465	171.5	7.3	361	4	US-09-248-796A-20099	Sequence 20099, A	538	161	6.8	666	4	US-09-569-098A-85	Sequence 85, Appli



539	161	6.8	1091	4	US-09-949-016-8595	Sequence 8595, Ap	612	149	6.3	171	3	US-09-029-156-2	Sequence 2, Appli
540	161	6.8	1132	4	US-09-528-784A-87	Sequence 87, Appl	613	149	6.3	351	3	US-09-011-735-1	Sequence 1, Appli
541	161	6.8	1132	4	US-09-569-098A-87	Sequence 87, Appl	614	149	6.3	351	3	US-09-029-156-1	Sequence 1, Appli
542	161	6.8	1850	4	US-09-620-993A-5	Sequence 5, Appli	615	149	6.3	601	4	US-09-252-991A-217784	Sequence 217784, A
543	160.5	6.8	1850	4	US-09-252-993A-5	Sequence 5, Appli	616	148.5	6.3	266	4	US-09-495-880A-26	Sequence 26, Appl
544	160	6.8	300	3	US-08-765-856-2	Sequence 2, Appli	617	148.5	6.3	326	4	US-09-252-991A-17002	Sequence 17002, A
545	160	6.8	300	3	US-08-935-009A-2	Sequence 2, Appli	618	148.5	6.3	656	4	US-09-252-991A-30630	Sequence 30630, A
546	160	6.8	354	4	US-09-949-016-10178	Sequence 10178, A	619	148	6.3	247	4	US-09-248-796A-14517	Sequence 14517, A
547	160	6.8	396	4	US-09-640-211A-1055	Sequence 1055, Ap	620	148	6.3	447	3	US-09-120-927-2	Sequence 2, Appli
548	160	6.8	671	2	US-08-737-716-13	Sequence 13, Appl	621	148	6.3	447	3	US-09-431-614-6	Sequence 6, Appli
549	160	6.8	720	3	US-09-219-849-4	Sequence 4, Appli	622	147.5	6.2	1584	3	US-09-457-040B-27	Sequence 27, Appl
550	160	6.8	777	1	US-08-642-255-53	Sequence 53, Appl	623	147	6.2	97	1	US-08-175-155-15	Sequence 15, Appl
551	159	6.7	546	4	US-09-252-991A-18637	Sequence 18637, A	624	147	6.2	97	1	US-08-477-509B-50	Sequence 50, Appl
552	158	6.7	106	3	US-08-963-168C-14	Sequence 14, Appl	625	147	6.2	97	3	US-08-482-085B-50	Sequence 50, Appl
553	158	6.7	126	3	US-08-963-168C-7	Sequence 7, Appli	626	147	6.2	97	3	US-09-444-791A-50	Sequence 50, Appl
554	158	6.7	166	4	US-09-297-369-41	Sequence 41, Appl	627	147	6.2	98	2	US-08-707-237A-22	Sequence 22, Appl
555	158	6.7	435	4	US-09-270-767-43092	Sequence 43092, A	628	147	6.2	212	4	US-09-270-767-41907	Sequence 41907, A
556	157.5	6.7	430	2	US-08-945-848-8	Sequence 8, Appli	629	147	6.2	230	4	US-09-248-796A-26509	Sequence 26509, A
557	157.5	6.7	1032	4	US-09-270-767-44433	Sequence 44433, A	630	147	6.2	264	3	US-09-128-450-21	Sequence 21, Appl
558	157	6.6	272	4	US-09-949-016-9966	Sequence 9966, Ap	631	147	6.2	264	3	US-09-823-494-21	Sequence 21, Appl
559	157	6.6	272	4	US-09-949-016-9967	Sequence 9967, Ap	632	147	6.2	264	3	US-08-195-152-2	Sequence 2, Appli
560	157	6.6	461	2	US-08-463-587A-26	Sequence 26, Appl	633	147	6.2	760	1	US-08-754-311B-2	Sequence 2, Appli
561	157	6.6	461	2	US-08-463-587A-4	Sequence 4, Appli	634	147	6.2	908	4	US-08-714-741-44	Sequence 44, Appl
562	157	6.6	461	3	US-08-923-854-26	Sequence 26, Appl	635	146.5	6.2	365	4	US-09-270-767-46506	Sequence 46506, A
563	157	6.6	461	5	PCT-US91-09133-27	Sequence 27, Appl	636	146.5	6.2	388	4	US-09-248-796A-17306	Sequence 17306, A
564	156.5	6.6	471	2	US-08-399-889-24	Sequence 24, Appl	637	146.5	6.2	410	4	US-09-252-991A-25812	Sequence 25812, A
565	156.5	6.6	471	3	US-09-167-364-24	Sequence 24, Appl	638	146.5	6.2	717	3	US-08-910-925-1	Sequence 1, Appli
566	156.5	6.6	471	3	US-09-439-897-2	Sequence 2, Appli	639	146.5	6.2	918	3	US-09-041-886-11	Sequence 11, Appl
567	156	6.6	238	4	US-09-495-880A-42	Sequence 42, Appl	640	146	6.2	84	1	US-08-175-155-17	Sequence 17, Appl
568	156	6.6	694	4	US-09-949-016-7117	Sequence 7117, Ap	641	146	6.2	84	1	US-08-477-509B-52	Sequence 52, Appl
569	155.5	6.6	187	4	US-09-634-238-414	Sequence 414, App	642	146	6.2	84	2	US-08-707-237A-23	Sequence 23, Appl
570	155.5	6.6	746	3	US-09-134-001C-3214	Sequence 3214, Ap	643	146	6.2	84	3	US-08-482-085B-52	Sequence 52, Appl
571	155	6.6	618	4	US-09-252-991A-27666	Sequence 27666, A	644	146	6.2	219	4	US-09-380-015B-2	Sequence 2, Appli
572	154.5	6.5	196	4	US-09-252-991A-23071	Sequence 23071, A	645	146	6.2	415	4	US-09-328-352-6430	Sequence 6430, Ap
573	154.5	6.5	302	3	US-08-765-856-4	Sequence 4, Appli	646	146	6.2	467	4	US-09-949-016-7778	Sequence 7778, Ap
574	154.5	6.5	302	3	US-08-935-009A-4	Sequence 4, Appli	647	146	6.2	467	4	US-09-949-016-7779	Sequence 7779, Ap
575	154	6.5	1461	4	US-10-142-231-86	Sequence 86, Appl	648	145.5	6.2	99	4	US-09-072-596-255	Sequence 255, App
576	153	6.5	561	1	US-08-642-255-52	Sequence 52, Appl	649	145.5	6.2	99	4	US-09-072-967-260	Sequence 260, App
577	152.5	6.5	166	4	US-09-270-767-41190	Sequence 41190, A	650	145.5	6.2	743	3	US-08-910-925-3	Sequence 3, Appli
578	152.5	6.5	166	4	US-09-270-767-56406	Sequence 56406, A	651	145.5	6.2	743	4	US-09-949-016-6261	Sequence 6261, Ap
579	152.5	6.5	195	4	US-09-270-767-44458	Sequence 44458, A	652	145.5	6.2	970	4	US-09-270-767-42741	Sequence 42741, A
580	152.5	6.5	284	4	US-09-431-887-24	Sequence 24, Appl	653	145	6.1	264	4	US-09-431-887-27	Sequence 27, Appl
581	152.5	6.5	326	4	US-09-270-767-43241	Sequence 43241, A	654	145	6.1	328	1	US-08-229-287-4	Sequence 4, Appli
582	152.5	6.5	335	4	US-09-821-687-11	Sequence 11, Appl	655	145	6.1	553	3	US-09-083-351-2	Sequence 2, Appli
583	152.5	6.5	504	3	US-09-219-849-3	Sequence 3, Appli	656	145	6.1	553	3	US-09-083-352-2	Sequence 2, Appli
584	152.5	6.5	790	4	US-09-328-352-4283	Sequence 4283, Ap	657	145	6.1	553	4	US-09-612-809B-2	Sequence 2, Appli
585	152.5	6.5	1395	4	US-09-252-991A-30345	Sequence 30345, A	658	145	6.1	572	4	US-09-489-039A-11826	Sequence 11826, A
586	152	6.4	1010	4	US-09-248-796A-16379	Sequence 16379, A	659	145	6.1	633	4	US-09-976-594-282	Sequence 282, App
587	152	6.4	1417	3	US-08-900-230-3	Sequence 3, Appli	660	145	6.1	633	4	US-09-821-687-10	Sequence 10, Appl
588	151.5	6.4	313	4	US-08-186-222-2	Sequence 2, Appli	661	145	6.1	792	4	US-09-252-991A-25823	Sequence 25823, A
589	151	6.4	461	1	US-09-949-016-9265	Sequence 9265, Ap	662	145	6.1	919	4	US-09-538-092-895	Sequence 895, App
590	150.5	6.4	162	3	US-09-575-574-4	Sequence 4, Appli	663	145	6.1	923	4	US-09-497-822C-19	Sequence 19, Appl
591	150.5	6.4	251	1	US-08-209-747-8	Sequence 8, Appli	664	145	6.1	1186	2	US-08-861-464-8	Sequence 8, Appli
592	150.5	6.4	251	1	US-08-458-298-8	Sequence 8, Appli	665	145	6.1	1186	2	US-08-396-001-8	Sequence 8, Appli
593	150.5	6.4	447	4	US-09-916-109-5	Sequence 5, Appli	666	145	6.1	1186	3	US-09-323-433A-8	Sequence 8, Appli
594	150.5	6.4	447	4	US-10-211-412B-5	Sequence 5, Appli	667	145	6.1	1186	4	US-09-826-752-8	Sequence 8, Appli
595	150.5	6.4	483	4	US-09-916-109-4	Sequence 4, Appli	668	145	6.1	2134	3	US-09-268-347-49	Sequence 49, Appl
596	150.5	6.4	483	4	US-10-211-412B-4	Sequence 4, Appli	669	145	6.1	2763	3	US-08-496-944-2	Sequence 2, Appli
597	150.5	6.4	483	4	US-09-538-092-1162	Sequence 1162, Ap	670	144.5	6.1	258	4	US-09-248-796A-23723	Sequence 23723, A
598	150	6.3	72	4	US-09-513-999C-5563	Sequence 5563, Ap	671	144.5	6.1	302	4	US-09-657-013-49	Sequence 49, Appl
599	150	6.3	72	4	US-09-513-999C-5564	Sequence 5564, Ap	672	144.5	6.1	302	4	US-09-949-016-6893	Sequence 6893, Ap
600	150	6.3	207	4	US-10-029-180-70	Sequence 70, Appl	673	144.5	6.1	411	4	US-09-657-013-57	Sequence 57, Appl
601	150	6.3	423	1	US-08-383-744-2	Sequence 2, Appli	674	144.5	6.1	411	4	US-09-949-016-6439	Sequence 6439, Ap
602	150	6.3	423	2	US-08-959-336-2	Sequence 2, Appli	675	144.5	6.1	477	4	US-09-863-901-5	Sequence 5, Appli
603	150	6.3	423	5	PCT-US96-01427-2	Sequence 2, Appli	676	144.5	6.1	906	4	US-09-863-901-6	Sequence 6, Appli
604	149.5	6.3	121	4	US-09-072-596-253	Sequence 253, App	677	144	6.1	91	4	US-09-270-767-39789	Sequence 39789, A
605	149.5	6.3	121	4	US-09-072-967-258	Sequence 258, App	678	144	6.1	91	4	US-09-270-767-55006	Sequence 55006, A
606	149.5	6.3	445	4	US-09-252-991A-24354	Sequence 24354, A	679	144	6.1	123	1	US-07-609-716-103	Sequence 103, App
607	149.5	6.3	1060	3	US-08-911-393-2	Sequence 2, Appli	680	144	6.1	123	3	US-08-475-411A-103	Sequence 103, App
608	149.5	6.3	1060	4	US-09-955-909-2	Sequence 2, Appli	681	144	6.1	123	3	US-08-478-029A-103	Sequence 103, App
609	149	6.3	60	4	US-09-832-297A-12	Sequence 12, Appl	682	144	6.1	375	4	US-09-600-932-29	Sequence 29, Appl
610	149	6.3	124	4	US-09-540-236-3076	Sequence 3076, Ap	683	144	6.1	391	4	US-09-395-017B-2	Sequence 2, Appli
611	149	6.3	171	3	US-09-011-735-2	Sequence 2, Appli	684	144	6.1	402	4	US-09-252-991A-20683	Sequence 20683, A

685	144	6.1	1475	4	US-09-538-092-1160	Sequence 1160, Ap	758	140	5.9	101	3	US-09-247-806-5	Sequence 5, Appli
686	144	6.1	1712	4	US-08-949-016-9450	Sequence 9450, Ap	759	140	5.9	101	3	US-09-247-806-7	Sequence 7, Appli
687	144	6.1	1833	4	US-08-621-944A-4	Sequence 4, Appli	760	140	5.9	101	4	US-09-863-859-11	Sequence 11, Appli
688	144	6.1	1833	4	US-08-945-567D-4	Sequence 4, Appli	761	140	5.9	148	4	US-09-248-796A-26837	Sequence 26837, A
689	144	6.1	1992	4	US-08-621-944A-3	Sequence 3, Appli	762	140	5.9	234	1	US-08-642-255-51	Sequence 51, Appli
690	144	6.1	1992	4	US-08-945-567D-3	Sequence 3, Appli	763	140	5.9	705	4	US-09-252-991A-30792	Sequence 30792, A
691	144	6.1	2123	3	US-08-968-685A-10	Sequence 10, Appl	764	140	5.9	892	3	US-09-336-447A-5	Sequence 5, Appli
692	143.5	6.1	482	4	US-09-509-031-16	Sequence 16, Appl	765	140	5.9	892	4	US-09-952-267B-5	Sequence 5, Appli
693	143.5	6.1	563	4	US-09-949-016-1053	Sequence 10153, A	766	140	5.9	956	4	US-09-949-016-8159	Sequence 8159, Ap
694	143.5	6.1	2142	4	US-09-540-236-3459	Sequence 3459, Ap	767	139.5	5.9	219	4	US-09-809-517A-24	Sequence 24, Appl
695	143	6.1	165	4	US-09-270-767-59895	Sequence 59895, A	768	139.5	5.9	219	4	US-09-809-517A-27	Sequence 27, Appl
696	143	6.1	263	1	US-08-242-188-3	Sequence 3, Appli	769	139.5	5.9	253	4	US-09-252-991A-20659	Sequence 20659, A
697	143	6.1	263	1	US-08-509-261A-3	Sequence 3, Appli	770	139.5	5.9	449	2	US-08-927-394-2	Sequence 2, Appli
698	143	6.1	263	1	US-08-660-626-9	Sequence 9, Appli	771	139.5	5.9	449	4	US-09-538-092-1372	Sequence 1372, Ap
699	143	6.1	263	1	US-08-592-892-3	Sequence 3, Appli	772	139.5	5.9	449	4	US-09-949-016-6004	Sequence 6604, Ap
700	143	6.1	263	2	US-08-713-939A-3	Sequence 3, Appli	773	139.5	5.9	467	4	US-09-252-991A-31427	Sequence 31427, A
701	143	6.1	263	2	US-08-868-162A-23	Sequence 23, Appl	774	139.5	5.9	489	4	US-09-366-009-8	Sequence 8, Appli
702	143	6.1	263	3	US-09-031-168-9	Sequence 9, Appli	775	139.5	5.9	489	4	US-08-809-156B-8	Sequence 8, Appli
703	143	6.1	263	3	US-09-036-579-3	Sequence 3, Appli	776	139.5	5.9	537	4	US-09-252-991A-27024	Sequence 27024, A
704	143	6.1	263	3	US-09-550-374-3	Sequence 3, Appli	777	139.5	5.9	537	4	US-09-345-473B-50	Sequence 50, Appl
705	143	6.1	263	3	US-09-943-906-3	Sequence 3, Appli	778	139.5	5.9	743	4	US-09-252-991A-28327	Sequence 28327, A
706	143	6.1	263	4	US-09-669-516C-9	Sequence 9, Appli	779	139.5	5.9	2291	4	US-09-252-991A-21854	Sequence 21854, A
707	143	6.1	264	4	US-09-627-218B-11	Sequence 11, Appl	780	139	5.9	393	4	US-09-252-991A-30202	Sequence 30202, A
708	143	6.1	544	4	US-09-538-092-1262	Sequence 12138, Ap	781	139	5.9	481	4	US-09-252-991A-16955	Sequence 16955, A
709	142.5	6.0	3969	4	US-09-370-767-56792	Sequence 56792, A	782	138.5	5.9	421	4	US-09-252-991A-32326	Sequence 32326, A
710	142	6.0	137	4	US-09-538-092-412	Sequence 412, App	783	138.5	5.9	437	4	US-09-921-099A-17	Sequence 17, Appl
711	142	6.0	289	4	US-09-252-991A-16628	Sequence 16628, A	784	138.5	5.9	1261	4	US-09-473-716-2	Sequence 2, Appli
712	142	6.0	367	4	US-09-252-991A-22945	Sequence 22945, A	785	138.5	5.9	1261	4	US-10-175-158-2	Sequence 2, Appli
713	142	6.0	424	4	US-09-294-298A-21	Sequence 21, Appl	786	138.5	5.9	1497	4	US-09-060-854B-2	Sequence 2, Appli
714	142	6.0	1135	4	US-09-294-298A-6	Sequence 6, Appli	787	138	5.8	1497	4	US-09-529-904-3	Sequence 3, Appli
715	142	6.0	1325	4	US-09-394-298A-4	Sequence 4, Appli	788	138	5.8	1497	4	US-09-270-767-42654	Sequence 42654, A
716	142	6.0	1326	4	US-09-394-298A-4	Sequence 4, Appli	789	138	5.8	1815	4	US-09-252-991A-30227	Sequence 30227, A
717	142	6.0	1423	4	US-09-394-298A-2	Sequence 2, Appli	790	138	5.8	2736	4	US-09-252-991A-31863	Sequence 31863, A
718	141.5	6.0	233	2	US-08-458-568A-4	Sequence 4, Appli	791	137.5	5.8	263	4	US-09-252-991A-30926	Sequence 30926, A
719	141.5	6.0	474	4	US-09-702-705-1812	Sequence 1812, Ap	792	137.5	5.8	371	4	US-09-252-991A-31834	Sequence 31834, A
720	141.5	6.0	474	4	US-09-736-457-1812	Sequence 1812, Ap	793	137.5	5.8	425	4	US-09-252-991A-25203	Sequence 25203, A
721	141.5	6.0	474	4	US-09-671-325-1812	Sequence 1812, Ap	794	137.5	5.8	518	4	US-09-252-991A-35203	Sequence 35203, A
722	141.5	6.0	474	4	US-09-538-092-1279	Sequence 1279, Ap	795	137.5	5.8	745	4	US-09-841-334A-38	Sequence 38, Appl
723	141.5	6.0	487	4	US-09-386-962C-14	Sequence 14, Appl	796	137.5	5.8	745	4	US-09-837-969A-38	Sequence 38, Appl
724	141.5	6.0	487	4	US-09-386-959-65	Sequence 65, Appl	797	137.5	5.8	1805	1	US-07-853-913-2	Sequence 2, Appli
725	141	6.0	211	1	US-08-276-852-34	Sequence 34, Appl	798	137	5.8	867	4	US-09-540-236-2676	Sequence 2676, Ap
726	141	6.0	211	1	US-08-133-011-16	Sequence 16, Appl	799	137	5.8	995	4	US-09-252-991A-22297	Sequence 22297, A
727	141	6.0	211	1	US-08-322-730A-16	Sequence 16, Appl	800	136.5	5.8	223	4	US-09-248-796A-27735	Sequence 27735, A
728	141	6.0	211	1	US-08-387-874-16	Sequence 16, Appl	801	136.5	5.8	464	2	US-08-836-854-19	Sequence 19, Appl
729	141	6.0	211	1	US-08-899-575-34	Sequence 34, Appl	802	136.5	5.8	464	4	US-09-366-009-7	Sequence 7, Appli
730	141	6.0	211	1	US-08-899-575-34	Sequence 34, Appl	803	136.5	5.8	464	4	US-08-809-156B-7	Sequence 7, Appli
731	141	6.0	211	3	US-08-383-619-16	Sequence 16, Appl	804	136.5	5.8	703	3	US-08-910-923-4	Sequence 4, Appli
732	141	6.0	211	3	US-08-307-739-16	Sequence 16, Appl	805	136.5	5.8	850	4	US-09-129-603-2	Sequence 2, Appli
733	141	6.0	211	4	US-09-729-597-16	Sequence 16, Appl	806	136.5	5.8	1113	4	US-09-252-991A-24385	Sequence 24385, A
734	141	6.0	211	5	PCT-US93-0836A-16	Sequence 16, Appl	807	136.5	5.8	1290	3	US-09-150-460B-6	Sequence 6, Appli
735	141	6.0	211	5	PCT-US95-08743-34	Sequence 34, Appl	808	136.5	5.8	1376	4	US-09-252-991A-30344	Sequence 30344, A
736	141	6.0	293	3	US-08-438-745-4	Sequence 4, Appli	809	136.5	5.8	1388	4	US-09-463-048A-6	Sequence 6, Appli
737	141	6.0	293	3	US-08-438-745-6	Sequence 6, Appli	810	136	5.8	50	4	US-09-863-901-22	Sequence 22, Appl
738	141	6.0	293	3	US-09-219-019-4	Sequence 4, Appli	811	136	5.8	199	3	US-08-506-553C-8	Sequence 8, Appli
739	141	6.0	293	3	US-09-219-019-6	Sequence 6, Appli	812	136	5.8	247	4	US-09-252-991A-21412	Sequence 21412, A
740	141	6.0	293	5	PCT-US94-05669A-4	Sequence 4, Appli	813	136	5.8	339	4	US-09-252-991A-32096	Sequence 32096, A
741	141	6.0	293	5	PCT-US94-05669A-6	Sequence 6, Appli	814	135.5	5.7	260	4	US-09-431-887-6	Sequence 6, Appli
742	141	6.0	378	4	US-09-395-017B-1	Sequence 1, Appli	815	135.5	5.7	400	3	US-09-086-010-2	Sequence 2, Appli
743	141	6.0	434	4	US-09-270-767-61286	Sequence 61286, A	816	135.5	5.7	590	4	US-09-252-991A-19127	Sequence 19127, A
744	141	6.0	694	4	US-09-823-240A-9	Sequence 9, Appli	817	135	5.7	139	4	US-09-050-739-68	Sequence 68, Appl
745	141	6.0	1059	4	US-09-270-767-45764	Sequence 45764, A	818	135	5.7	302	2	US-08-893-853-3	Sequence 3, Appli
746	141	6.0	2284	4	US-09-252-991A-23547	Sequence 23547, A	819	135	5.7	302	3	US-09-113-921-3	Sequence 3, Appli
747	140.5	5.9	456	4	US-09-438-745-19417	Sequence 19417, A	820	135	5.7	302	3	US-08-845-258-19	Sequence 19, Appl
748	140.5	5.9	462	4	US-09-248-796A-14808	Sequence 14808, A	821	135	5.7	310	3	US-08-990-571-19	Sequence 19, Appl
749	140.5	5.9	484	4	US-09-242-913B-17	Sequence 17, Appl	822	135	5.7	310	3	US-08-723-142A-19	Sequence 19, Appl
750	140.5	5.9	506	4	US-09-949-016-11518	Sequence 11518, A	823	135	5.7	310	3	US-09-528-784A-19	Sequence 19, Appl
751	140.5	5.9	569	4	US-09-252-991A-24513	Sequence 24513, A	824	135	5.7	310	4	US-09-569-098A-19	Sequence 19, Appl
752	140.5	5.9	1776	4	US-09-556-877-179	Sequence 179, App	825	135	5.7	545	4	US-09-252-991A-30910	Sequence 30910, A
753	140.5	5.9	1776	4	US-09-620-412C-179	Sequence 179, App	826	135	5.7	558	3	US-09-199-637A-277	Sequence 277, App
754	140.5	5.9	3969	3	US-09-598-419-179	Sequence 5, Appli	827	135	5.7	2516	3	US-08-374-077C-2	Sequence 2, Appli
755	140.5	5.9	101	3	US-08-061-376-5	Sequence 22, Appl	828	135	5.7	2516	3	US-08-374-077C-2	Sequence 2, Appli
756	140	5.9	101	3	US-08-556-978B-22	Sequence 62, Appl	829	135	5.7	2516	4	US-08-895-590-2	Sequence 2, Appli
757	140	5.9	101	3	US-08-556-978B-62	Sequence 62, Appl	830	135	5.7	2516	4	US-09-539-879A-2	Sequence 2, Appli

831	134.5	5.7	101	3	US-08-556-978B-20	Sequence 20, Appl	904	130.5	5.5	72	3	US-09-444-791A-87	Sequence 87, Appl
832	134.5	5.7	101	3	US-09-247-806-3	Sequence 3, Appl	905	130.5	5.5	128	3	US-08-806-029-13	Sequence 13, Appl
833	134.5	5.7	101	4	US-09-863-859-10	Sequence 10, Appl	906	130.5	5.5	223	3	US-09-248-796A-24067	Sequence 24067, A
834	134.5	5.7	168	3	US-09-512-342-20	Sequence 20, Appl	907	130.5	5.5	301	4	US-09-252-991A-28663	Sequence 28663, A
835	134.5	5.7	339	4	US-09-252-991A-21715	Sequence 21715, A	908	130.5	5.5	362	4	US-09-252-991A-17884	Sequence 17884, A
836	134.5	5.7	634	4	US-09-248-796A-19513	Sequence 19513, A	909	130.5	5.5	365	4	US-09-252-991A-30166	Sequence 30166, A
837	134.5	5.7	984	1	US-08-257-073-3	Sequence 3, Appl	910	130.5	5.5	803	4	US-09-252-991A-23614	Sequence 23614, A
838	134.5	5.7	984	2	US-08-184-009-120	Sequence 120, App	911	130.5	5.5	2508	4	US-09-627-650B-7	Sequence 7, Appl
839	134.5	5.7	984	2	US-08-458-356-120	Sequence 120, App	912	130.5	5.5	2508	4	US-09-436-063C-7	Sequence 7, Appl
840	134.5	5.7	984	2	US-08-460-736-120	Sequence 120, App	913	130.5	5.5	2544	4	US-09-627-650B-3	Sequence 3, Appl
841	134.5	5.7	984	4	US-09-535-370-120	Sequence 120, App	914	130.5	5.5	2544	4	US-09-436-063C-3	Sequence 3, Appl
842	134.5	5.7	984	4	US-09-663-667-120	Sequence 120, App	915	130.5	5.5	2601	4	US-09-627-650B-9	Sequence 9, Appl
843	134.5	5.7	2703	1	US-08-185-432-19	Sequence 19, Appl	916	130.5	5.5	2601	4	US-09-436-063C-9	Sequence 9, Appl
844	134.5	5.7	2703	4	US-08-899-232-4	Sequence 4, Appl	917	130.5	5.5	176	4	US-09-252-991A-28622	Sequence 28622, A
845	134.5	5.7	2703	4	US-09-121-457-4	Sequence 4, Appl	918	130.5	5.5	176	4	US-09-328-352-6964	Sequence 6964, A
846	134	5.7	104	3	US-09-219-849-33	Sequence 33, Appl	919	130.5	5.5	223	3	US-09-206-676C-1	Sequence 1, Appl
847	134	5.7	387	4	US-09-252-991A-23334	Sequence 23334, A	920	130.5	5.5	223	3	US-09-431-887-16	Sequence 16, Appl
848	134	5.7	1043	4	US-08-851-567B-61	Sequence 61, Appl	921	130.5	5.5	223	4	US-09-431-887-18	Sequence 18, Appl
849	134	5.7	1298	4	US-09-252-991A-30579	Sequence 30579, A	922	130.5	5.5	278	3	US-09-260-283-2	Sequence 2, Appl
850	134	5.7	2048	3	US-09-268-347-48	Sequence 48, Appl	923	130.5	5.5	425	4	US-09-252-991A-22321	Sequence 22321, A
851	133.5	5.6	148	1	US-08-207-904-15	Sequence 15, Appl	924	130.5	5.5	441	4	US-09-252-991A-24396	Sequence 24396, A
852	133.5	5.6	378	6	5171843-9	Patent No. 5171843	925	130.5	5.5	510	4	US-09-252-991A-17695	Sequence 17695, A
853	133.5	5.6	378	6	5171843-9	Patent No. 5171843	926	130.5	5.5	514	4	US-09-252-991A-18306	Sequence 18306, A
854	133.5	5.6	442	4	US-09-538-092-1123	Sequence 1123, App	927	130.5	5.5	635	4	US-09-252-991A-33100	Sequence 33100, A
855	133	5.6	141	4	US-09-252-991A-23427	Sequence 23427, A	928	130.5	5.5	941	3	US-09-336-447A-9	Sequence 9, Appl
856	133	5.6	486	4	US-09-710-279-788	Sequence 788, App	929	130.5	5.5	941	3	US-09-952-267B-9	Sequence 9, Appl
857	133	5.6	513	4	US-09-252-991A-18177	Sequence 18177, A	930	130.5	5.5	1618	1	US-07-853-913-4	Sequence 4, Appl
858	133	5.6	855	4	US-09-902-540-14518	Sequence 14518, A	931	130.5	5.5	1618	4	US-09-538-092-1143	Sequence 1143, Ap
859	132.5	5.6	80	4	US-09-248-796A-23892	Sequence 23892, A	932	129.5	5.5	103	1	US-08-209-747-4	Sequence 4, Appl
860	132.5	5.6	182	4	US-09-489-039A-8301	Sequence 8301, App	933	129.5	5.5	103	1	US-08-458-298-4	Sequence 4, Appl
861	132.5	5.6	247	3	US-09-199-637A-363	Sequence 363, App	934	129.5	5.5	119	3	US-08-556-978B-60	Sequence 60, Appl
862	132.5	5.6	301	3	US-08-469-318-142	Sequence 142, App	935	129.5	5.5	119	3	US-09-247-806-9	Sequence 9, Appl
863	132.5	5.6	301	3	US-08-468-609A-142	Sequence 142, App	936	129.5	5.5	368	3	US-08-591-685-13	Sequence 13, Appl
864	132.5	5.6	301	3	US-08-446-872A-142	Sequence 142, App	937	129.5	5.5	423	4	US-09-252-991A-27333	Sequence 27333, A
865	132.5	5.6	301	4	US-08-762-227A-142	Sequence 142, App	938	129.5	5.5	564	4	US-09-949-016-66828	Sequence 6628, Ap
866	132.5	5.6	301	5	FCT-US95-01185-142	Sequence 142, App	939	129.5	5.5	569	4	US-09-949-016-11035	Sequence 11035, A
867	132.5	5.6	466	3	US-09-134-001C-4749	Sequence 4749, App	940	129.5	5.5	577	4	US-09-252-991A-25632	Sequence 25632, A
868	132.5	5.6	468	4	US-09-252-991A-24394	Sequence 24394, A	941	129.5	5.5	865	4	US-09-252-991A-18683	Sequence 18683, A
869	132.5	5.6	706	4	US-09-270-767-40994	Sequence 40994, A	942	129.5	5.5	873	3	US-09-336-447A-13	Sequence 13, Appl
870	132.5	5.6	706	4	US-09-270-767-56210	Sequence 56210, A	943	129.5	5.5	873	3	US-09-952-267B-13	Sequence 13, Appl
871	132	5.6	186	4	US-09-366-009-6	Sequence 6, Appl	944	129.5	5.5	1705	3	US-08-669-785-4	Sequence 4, Appl
872	132	5.6	186	4	US-08-809-156B-6	Sequence 6, Appl	945	129.5	5.5	1705	3	US-08-669-785-4	Patent No. 5183745
873	132	5.6	430	4	US-09-252-991A-22599	Sequence 22599, A	946	129.5	5.5	1794	6	5183745-6	Patent No. 5183745
874	132	5.6	455	4	US-09-270-767-45531	Sequence 45531, A	947	129.5	5.5	45	4	US-09-863-901-25	Sequence 25, Appl
875	132	5.6	580	4	US-09-252-991A-29979	Sequence 29979, A	948	129.5	5.5	122	3	US-08-956-307B-19	Sequence 19, Appl
876	132	5.6	615	4	US-09-252-991A-23203	Sequence 23203, A	949	129.5	5.5	256	3	US-09-128-450-22	Sequence 22, Appl
877	132	5.6	929	4	US-09-252-991A-19203	Sequence 19203, A	950	129.5	5.5	256	3	US-09-823-494-22	Sequence 22, Appl
878	131.5	5.6	136	4	US-09-270-767-46188	Sequence 46188, A	951	129.5	5.5	334	4	US-09-949-016-11006	Sequence 11006, A
879	131.5	5.6	256	4	US-09-431-887-31	Sequence 31, Appl	952	129.5	5.5	456	4	US-09-919-172-31	Sequence 31, Appl
880	131.5	5.6	257	4	US-09-431-887-30	Sequence 30, Appl	953	129.5	5.5	707	4	US-09-919-039-278	Sequence 278, App
881	131.5	5.6	268	3	US-08-961-083-140	Sequence 140, App	954	129.5	5.5	707	4	US-09-538-092-993	Sequence 993, App
882	131.5	5.6	268	4	US-09-536-784-140	Sequence 140, App	955	129.5	5.5	729	4	US-09-949-016-10790	Sequence 10790, A
883	131.5	5.6	268	4	US-09-252-991A-25667	Sequence 25667, A	956	129.5	5.5	729	4	US-09-949-016-10791	Sequence 10791, A
884	131.5	5.6	388	4	US-09-252-991A-30608	Sequence 30608, A	957	128.5	5.4	226	3	US-09-206-676C-2	Sequence 2, Appl
885	131.5	5.6	647	2	US-08-770-761A-8	Sequence 8, Appl	958	128.5	5.4	247	4	US-09-252-991A-29972	Sequence 29972, A
886	131.5	5.6	705	4	US-08-770-761A-7	Sequence 7, Appl	959	128.5	5.4	365	4	US-09-252-991A-32327	Sequence 32327, A
887	131.5	5.6	709	4	US-09-702-705-335	Sequence 335, App	960	128.5	5.4	441	4	US-09-794-422-4	Sequence 4, Appl
888	131.5	5.6	709	4	US-09-736-457-335	Sequence 335, App	961	128.5	5.4	487	4	US-09-270-767-57297	Sequence 57297, A
889	131.5	5.6	709	4	US-09-614-124B-335	Sequence 335, App	962	128.5	5.4	569	4	US-09-349-016-11036	Sequence 11036, A
890	131.5	5.6	709	4	US-09-671-325-335	Sequence 335, App	963	128.5	5.4	975	4	US-09-270-767-42040	Sequence 42040, A
891	131.5	5.6	709	4	US-09-589-184-335	Sequence 335, App	964	128.5	5.4	297	4	US-09-252-991A-27909	Sequence 27909, A
892	131.5	5.6	709	4	US-09-658-824-335	Sequence 335, App	965	128.5	5.4	376	3	US-09-056-556-202	Sequence 202, App
893	131.5	5.6	945	4	US-09-252-991A-30699	Sequence 30699, A	966	128.5	5.4	376	4	US-09-072-596-197	Sequence 197, App
894	131.5	5.6	1706	3	US-08-669-785-2	Sequence 2, Appl	967	128.5	5.4	376	4	US-09-072-967-202	Sequence 202, App
895	131	5.5	302	4	US-09-252-991A-23166	Sequence 23166, A	968	128.5	5.4	499	4	US-09-252-991A-28010	Sequence 28010, A
896	131	5.5	456	4	US-09-495-880A-11	Sequence 11, Appl	969	128.5	5.4	555	4	US-09-252-991A-28734	Sequence 28734, A
897	130.5	5.5	72	1	US-07-609-716-35	Sequence 35, Appl	970	128.5	5.4	1164	4	US-09-902-540-12627	Sequence 12627, A
898	130.5	5.5	72	1	US-08-175-155-52	Sequence 52, Appl	971	128.5	5.4	1970	4	US-09-538-092-1005	Sequence 1005, Ap
899	130.5	5.5	72	1	US-08-477-509B-87	Sequence 87, Appl	972	127.5	5.4	192	4	US-09-902-540-10307	Sequence 10307, A
900	130.5	5.5	72	1	US-08-707-237A-60	Sequence 60, Appl	973	127.5	5.4	324	4	US-09-107-433-4143	Sequence 4143, Ap
901	130.5	5.5	72	3	US-08-482-085B-87	Sequence 87, Appl	974	127.5	5.4	375	4	US-09-252-991A-31128	Sequence 31128, A
902	130.5	5.5	72	3	US-08-475-411A-35	Sequence 35, Appl	975	127.5	5.4	391	4	US-09-538-092-1097	Sequence 1097, Ap
903	130.5	5.5	72	3	US-08-478-029A-35	Sequence 35, Appl	976	127.5	5.4	394	4	US-09-949-016-9912	Sequence 9912, Ap

977	127.5	5.4	406	4	US-09-949-016-8507	Sequence 8507, Ap	1050	125	5.3	254	3	US-09-823-494-26	Sequence 26, Appl
978	127.5	5.4	630	4	US-09-252-991A-19702	Sequence 19702, A	1051	125	5.3	349	3	US-08-469-318-151	Sequence 151, App
979	127.5	5.4	878	3	US-08-653-648A-15	Sequence 15, Appl	1052	125	5.3	349	3	US-08-468-609A-151	Sequence 151, App
980	127.5	5.4	878	4	US-09-564-418-8	Sequence 8, Appl	1053	125	5.3	349	3	US-08-446-872A-151	Sequence 151, App
981	127.5	5.4	253	1	US-08-242-188-2	Sequence 2, Appl	1054	125	5.3	349	4	US-08-762-227A-151	Sequence 151, App
982	127.5	5.4	253	1	US-08-509-261A-2	Sequence 2, Appl	1055	125	5.3	349	5	PCT-US95-01185-151	Sequence 151, App
983	127.5	5.4	253	1	US-08-660-626-8	Sequence 8, Appl	1056	125	5.3	432	4	US-09-248-796A-16450	Sequence 16450, A
984	127.5	5.4	253	1	US-08-692-892-2	Sequence 2, Appl	1057	125	5.3	712	4	US-09-248-796A-16474	Sequence 16474, A
985	127.5	5.4	253	2	US-08-713-939A-2	Sequence 2, Appl	1058	125	5.3	716	4	US-09-107-532A-5208	Sequence 5208, Ap
986	127.5	5.4	253	2	US-08-868-162A-22	Sequence 22, Appl	1059	124.5	5.3	60	3	US-08-469-318-195	Sequence 195, App
987	127.5	5.4	253	3	US-09-031-168-8	Sequence 8, Appl	1060	124.5	5.3	60	3	US-08-468-609A-195	Sequence 195, App
988	127.5	5.4	253	3	US-09-128-450-20	Sequence 20, Appl	1061	124.5	5.3	60	3	US-08-446-872A-195	Sequence 195, App
989	127.5	5.4	253	3	US-09-036-579-2	Sequence 2, Appl	1062	124.5	5.3	60	4	US-08-762-227A-195	Sequence 195, App
990	127.5	5.4	253	3	US-08-923-494-20	Sequence 20, Appl	1063	124.5	5.3	60	5	PCT-US95-01185-195	Sequence 195, App
991	127.5	5.4	253	3	US-09-350-374-2	Sequence 2, Appl	1064	124.5	5.3	184	4	US-09-270-767-5165	Sequence 5165, A
992	127.5	5.4	253	4	US-09-431-887-1	Sequence 1, Appl	1065	124.5	5.3	281	4	US-09-252-991A-18173	Sequence 18173, A
993	127.5	5.4	253	4	US-09-431-887-2	Sequence 2, Appl	1066	124.5	5.3	294	4	US-09-270-767-43772	Sequence 43772, A
994	127.5	5.4	253	4	US-09-431-887-3	Sequence 3, Appl	1067	124.5	5.3	349	3	US-08-469-318-139	Sequence 139, App
995	127.5	5.4	253	4	US-09-431-887-4	Sequence 4, Appl	1068	124.5	5.3	349	3	US-08-468-609A-139	Sequence 139, App
996	127.5	5.4	253	4	US-09-431-887-8	Sequence 8, Appl	1069	124.5	5.3	349	3	US-08-446-872A-139	Sequence 139, App
997	127.5	5.4	253	4	US-09-431-887-19	Sequence 19, Appl	1070	124.5	5.3	349	4	US-08-762-227A-139	Sequence 139, App
998	127.5	5.4	253	4	US-09-943-906-2	Sequence 2, Appl	1071	124.5	5.3	349	5	PCT-US95-01185-139	Sequence 139, App
999	127.5	5.4	253	4	US-09-669-516C-8	Sequence 8, Appl	1072	124.5	5.3	383	4	US-09-252-991A-24223	Sequence 24223, A
1000	127.5	5.4	253	4	US-09-304-987-3	Sequence 3, Appl	1073	124.5	5.3	425	4	US-09-252-991A-19054	Sequence 19054, A
1001	127.5	5.4	253	4	US-09-431-887-29	Sequence 29, Appl	1074	124.5	5.3	510	4	US-09-252-991A-33084	Sequence 33084, A
1002	127.5	5.4	257	4	US-08-122-458B-11	Sequence 11, Appl	1075	124.5	5.3	534	4	US-09-252-991A-20468	Sequence 20468, A
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1004	127.5	5.4	374	4	US-09-248-796A-17283	Sequence 17283, A	1077	124.5	5.3	1261	4	US-09-248-796A-16620	Sequence 16620, A
1005	127.5	5.4	886	4	US-09-252-991A-24378	Sequence 24378, A	1078	124.5	5.3	1665	4	US-09-858-664A-2	Sequence 2, Appl
1006	127.5	5.4	1004	3	US-09-368-347-30	Sequence 30, Appl	1079	124.5	5.3	1665	4	US-10-274-978-2	Sequence 2, Appl
1007	126.5	5.4	217	4	US-09-270-767-31877	Sequence 31877, A	1080	124.5	5.3	1665	4	US-10-697-263-2	Sequence 2, Appl
1008	126.5	5.4	217	4	US-08-270-767-47094	Sequence 47094, A	1081	124	5.2	76	1	US-08-089-863-10	Sequence 10, Appl
1009	126.5	5.4	219	4	US-09-248-796A-23661	Sequence 23661, A	1082	124	5.2	76	1	US-08-587-333-17	Sequence 17, Appl
1010	126.5	5.4	256	4	US-09-431-887-25	Sequence 25, Appl	1083	124	5.2	76	5	PCT-US94-07776-15	Sequence 15, Appl
1011	126.5	5.4	256	4	US-09-431-887-28	Sequence 28, Appl	1084	124	5.2	155	4	US-09-252-991A-27532	Sequence 27532, A
1012	126.5	5.4	351	4	US-09-252-991A-29678	Sequence 29678, A	1085	124	5.2	212	4	US-09-252-991A-24512	Sequence 24512, A
1013	126.5	5.4	405	4	US-09-166-265-1	Sequence 1, Appl	1086	124	5.2	212	4	US-09-252-991A-37887	Sequence 37887, A
1014	126.5	5.4	427	4	US-09-270-767-45426	Sequence 45426, A	1087	124	5.2	469	4	US-09-252-991A-26584	Sequence 26584, A
1015	126.5	5.4	439	4	US-09-252-991A-16736	Sequence 16736, A	1088	124	5.2	482	4	US-09-270-767-43292	Sequence 43292, A
1016	126.5	5.4	451	4	US-09-252-991A-25804	Sequence 25804, A	1089	124	5.2	586	4	US-09-252-991A-24514	Sequence 24514, A
1017	126.5	5.4	476	4	US-09-252-991A-17887	Sequence 17887, A	1090	123.5	5.2	229	4	US-09-248-796A-24831	Sequence 24831, A
1018	126.5	5.4	650	4	US-09-252-991A-23546	Sequence 23546, A	1091	123.5	5.2	325	4	US-09-902-540-13678	Sequence 13678, A
1019	126.5	5.4	834	4	US-09-252-991A-28145	Sequence 28145, A	1092	123.5	5.2	501	4	US-09-252-991A-19191	Sequence 19191, A
1020	126.5	5.4	1011	4	US-09-252-991A-32419	Sequence 32419, A	1093	123.5	5.2	704	4	US-09-270-767-46362	Sequence 46362, A
1021	126.5	5.4	2142	4	US-09-538-092-1142	Sequence 1142, Ap	1094	123.5	5.2	742	4	US-09-949-016-7729	Sequence 7729, Ap
1022	126.5	5.4	2442	3	US-09-514-247A-10	Sequence 10, Appl	1095	123.5	5.2	783	4	US-09-252-991A-18035	Sequence 18035, A
1023	126.5	5.4	2442	3	US-09-538-092-1370	Sequence 1370, Ap	1096	123.5	5.2	1403	2	US-08-387-942C-3	Sequence 3, Appl
1024	126	5.3	97	1	US-07-609-716-99	Sequence 99, Appl	1097	123	5.2	179	4	US-09-270-767-57837	Sequence 57837, A
1025	126	5.3	97	3	US-08-475-411A-99	Sequence 99, Appl	1098	123	5.2	208	4	US-09-252-991A-27661	Sequence 27661, A
1026	126	5.3	97	3	US-08-478-029A-99	Sequence 99, Appl	1099	123	5.2	252	4	US-09-431-887-17	Sequence 17, Appl
1027	126	5.3	208	3	US-09-128-450-18	Sequence 18, Appl	1100	123	5.2	321	3	US-08-485-511A-4	Sequence 4, Appl
1028	126	5.3	208	3	US-09-823-494-18	Sequence 18, Appl	1101	123	5.2	522	4	US-09-538-092-1096	Sequence 1096, Ap
1029	126	5.3	253	4	US-09-919-172-57	Sequence 57, Appl	1102	123	5.2	524	4	US-09-252-991A-23901	Sequence 23901, A
1030	126	5.3	253	4	US-09-976-594-72	Sequence 72, Appl	1103	123	5.2	588	4	US-09-252-991A-18578	Sequence 18578, A
1031	126	5.3	374	4	US-09-949-016-7191	Sequence 7191, Ap	1104	123	5.2	801	1	US-07-906-349A-6	Sequence 6, Appl
1032	126	5.3	383	4	US-09-252-991A-22283	Sequence 22283, A	1105	123	5.2	1620	1	US-08-542-363-2	Sequence 2, Appl
1033	126	5.3	584	4	US-09-252-991A-21071	Sequence 21071, A	1106	123	5.2	1620	3	US-09-100-089-2	Sequence 2, Appl
1034	126	5.3	819	4	US-09-252-991A-19569	Sequence 19569, A	1107	123	5.2	1620	4	US-09-670-827-2	Sequence 2, Appl
1035	126	5.3	891	4	US-09-949-016-7798	Sequence 7798, Ap	1108	123	5.2	1620	4	US-09-827-949-2	Sequence 2, Appl
1036	126	5.3	1394	4	US-09-902-540-16497	Sequence 16497, A	1109	122.5	5.2	155	1	US-08-209-747-15	Sequence 15, Appl
1037	126	5.3	1400	3	US-08-630-915A-37	Sequence 37, Appl	1110	122.5	5.2	155	1	US-08-458-298-15	Sequence 15, Appl
1038	126	5.3	1400	4	US-09-879-957-37	Sequence 37, Appl	1111	122.5	5.2	189	4	US-09-710-279-2692	Sequence 2692, Ap
1039	125.5	5.3	232	6	517843-7	Patent No. 517843	1112	122.5	5.2	203	4	US-09-270-767-35326	Sequence 35326, A
1040	125.5	5.3	232	6	517843-7	Patent No. 517843	1113	122.5	5.2	203	4	US-09-270-767-50543	Sequence 50543, A
1041	125.5	5.3	333	2	US-08-712-948-1	Sequence 1, Appl	1114	122.5	5.2	226	4	US-09-252-991A-23893	Sequence 23893, A
1042	125.5	5.3	344	1	US-07-941-523-24	Sequence 24, Appl	1115	122.5	5.2	528	4	US-09-270-767-42914	Sequence 42914, A
1043	125.5	5.3	556	4	US-09-252-991A-27601	Sequence 27601, A	1116	122.5	5.2	601	4	US-09-252-991A-22594	Sequence 22594, A
1044	125.5	5.3	757	4	US-09-352-991A-25918	Sequence 25918, A	1117	122.5	5.2	606	4	US-09-248-796A-14276	Sequence 14276, A
1045	125.5	5.3	933	3	US-08-293-728-2	Sequence 2, Appl	1118	122.5	5.2	763	4	US-09-252-991A-30146	Sequence 30146, A
1046	125.5	5.3	933	3	US-09-421-868-2	Sequence 2, Appl	1119	122.5	5.2	930	4	US-09-198-452A-470	Sequence 470, App
1047	125.5	5.3	936	4	US-08-956-171B-5249	Sequence 5249, Ap	1120	122.5	5.2	938	4	US-09-438-185A-448	Sequence 448, App
1048	125.5	5.3	936	4	US-08-781-986A-5249	Sequence 5249, Ap	1121	122.5	5.2	1085	4	US-09-841-334A-39	Sequence 39, Appl
1049	125	5.3	254	3	US-09-128-450-26	Sequence 26, Appl	1122	122.5	5.2	1085	4	US-09-837-969A-39	Sequence 39, Appl

1123	122.5	5.2	1633	4	US-09-902-540-12892	Sequence 12892, A	1196	121	5.1	917	4	US-09-252-991A-25101	Sequence 25101, A
1124	122	5.2	253	4	US-09-431-887-7	Sequence 7, Appli	1197	121	5.1	2104	2	US-08-808-793-4	Sequence 4, Appli
1125	122	5.2	253	4	US-09-431-887-9	Sequence 9, Appli	1198	121	5.1	2104	3	US-08-772-512A-4	Sequence 4, Appli
1126	122	5.2	253	4	US-09-431-887-10	Sequence 10, Appl	1199	121	5.1	2104	4	US-09-428-371-4	Sequence 4, Appli
1127	122	5.2	253	4	US-09-431-887-11	Sequence 11, Appl	1200	120.5	5.1	83	1	US-07-609-716-101	Sequence 101, App
1128	122	5.2	253	4	US-09-431-887-12	Sequence 12, Appl	1201	120.5	5.1	83	3	US-08-475-411A-101	Sequence 101, App
1129	122	5.2	253	4	US-09-431-887-13	Sequence 13, Appl	1202	120.5	5.1	83	3	US-08-478-029A-101	Sequence 101, App
1130	122	5.2	256	4	US-09-431-887-14	Sequence 14, Appl	1203	120.5	5.1	88	4	US-09-248-796A-27988	Sequence 27988, A
1131	122	5.2	302	4	US-10-029-180-18	Sequence 18, Appl	1204	120.5	5.1	119	4	US-09-902-540-10158	Sequence 10158, A
1132	122	5.2	304	4	US-09-252-991A-23016	Sequence 23016, A	1205	120.5	5.1	133	4	US-09-270-767-39893	Sequence 39893, A
1133	122	5.2	311	4	US-09-949-016-8142	Sequence 8142, Ap	1206	120.5	5.1	133	4	US-09-270-767-55110	Sequence 55110, A
1134	122	5.2	380	4	US-09-270-767-43626	Sequence 81426, A	1207	120.5	5.1	240	4	US-09-252-991A-21852	Sequence 21852, A
1135	122	5.2	392	4	US-09-949-016-6078	Sequence 6078, Ap	1208	120.5	5.1	252	4	US-09-431-887-32	Sequence 32, Appl
1136	122	5.2	466	3	US-09-215-221-24	Sequence 24, Appl	1209	120.5	5.1	308	4	US-09-252-991A-27249	Sequence 27249, A
1137	122	5.2	471	4	US-09-538-092-837	Sequence 837, App	1210	120.5	5.1	374	4	US-09-252-991A-28527	Sequence 28527, A
1138	122	5.2	476	4	US-09-248-796A-18994	Sequence 18994, A	1211	120.5	5.1	394	4	US-09-252-991A-28148	Sequence 28148, A
1139	122	5.2	551	2	US-09-033-537A-1	Sequence 1, Appli	1212	120.5	5.1	408	4	US-09-543-681A-6442	Sequence 6442, Ap
1140	122	5.2	552	4	US-09-252-991A-25589	Sequence 25589, A	1213	120.5	5.1	434	4	US-09-252-991A-30036	Sequence 30036, A
1141	122	5.2	639	4	US-09-252-991A-28453	Sequence 28453, A	1214	120.5	5.1	474	4	US-09-452-991A-28084	Sequence 28084, A
1142	122	5.2	735	4	US-09-949-016-10120	Sequence 10120, A	1215	120.5	5.1	491	4	US-09-252-991A-22394	Sequence 22394, A
1143	122	5.2	989	3	US-08-213-419B-2	Sequence 2, Appli	1216	120.5	5.1	863	4	US-09-252-991A-26099	Sequence 26099, A
1144	122	5.2	989	3	US-08-213-419B-4	Sequence 4, Appli	1217	120.5	5.1	918	4	US-09-200-650B-1	Sequence 1, Appli
1145	122	5.2	1239	2	US-08-937-931-2	Sequence 2, Appli	1218	120.5	5.1	1591	4	US-09-270-767-45698	Sequence 45698, A
1146	122	5.2	1239	3	US-09-285-502-2	Sequence 2, Appli	1219	120.5	5.1	72	1	US-07-609-716-44	Sequence 44, Appl
1147	122	5.2	1239	3	US-09-709-126-2	Sequence 2, Appli	1220	120.5	5.1	72	3	US-08-475-411A-44	Sequence 44, Appl
1148	122	5.2	1239	3	US-09-871-385A-2	Sequence 2, Appli	1221	120.5	5.1	72	3	US-08-478-029A-44	Sequence 44, Appl
1149	121.5	5.1	75	1	US-07-609-716-39	Sequence 39, Appl	1222	120.5	5.1	171	4	US-09-489-039A-8235	Sequence 8235, Ap
1150	121.5	5.1	75	3	US-08-475-411A-39	Sequence 39, Appl	1223	120.5	5.1	262	4	US-09-949-016-7209	Sequence 7209, Ap
1151	121.5	5.1	75	3	US-08-478-029A-39	Sequence 39, Appl	1224	120.5	5.1	269	4	US-09-134-001C-3461	Sequence 3461, Ap
1152	121.5	5.1	86	1	US-07-609-716-102	Sequence 102, App	1225	120.5	5.1	271	4	US-09-252-991A-17292	Sequence 17292, A
1153	121.5	5.1	86	3	US-08-475-411A-102	Sequence 102, App	1226	120.5	5.1	337	3	US-08-469-318-148	Sequence 148, App
1154	121.5	5.1	86	3	US-08-478-029A-102	Sequence 102, App	1227	120.5	5.1	337	3	US-08-468-609A-148	Sequence 148, App
1155	121.5	5.1	180	4	US-10-029-180-38	Sequence 38, Appl	1228	120.5	5.1	337	3	US-08-446-872A-148	Sequence 148, App
1156	121.5	5.1	207	4	US-09-248-796A-21137	Sequence 21137, A	1229	120.5	5.1	337	4	US-08-762-227A-148	Sequence 148, App
1157	121.5	5.1	236	4	US-09-248-796A-22126	Sequence 22126, A	1230	120.5	5.1	337	5	PCT-US95-01185-148	Sequence 148, App
1158	121.5	5.1	256	4	US-09-252-991A-25670	Sequence 25670, A	1231	120.5	5.1	382	3	US-08-213-419B-19	Sequence 19, Appl
1159	121.5	5.1	330	2	US-08-712-948-2	Sequence 2, Appli	1232	120.5	5.1	468	4	US-09-863-901-4	Sequence 4, Appl
1160	121.5	5.1	330	4	US-09-949-016-6621	Sequence 6621, Ap	1233	120.5	5.1	477	4	US-09-252-991A-19831	Sequence 19831, A
1161	121.5	5.1	334	4	US-09-949-016-7988	Sequence 7988, Ap	1234	120.5	5.1	508	4	US-09-949-016-6316	Sequence 6316, Ap
1162	121.5	5.1	464	4	US-09-270-767-61287	Sequence 61287, A	1235	120.5	5.1	508	4	US-09-902-540-10562	Sequence 10562, A
1163	121.5	5.1	495	3	US-08-828-7A1B-4	Sequence 4, Appli	1236	120.5	5.1	518	4	US-09-949-016-11589	Sequence 11589, A
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1165	121.5	5.1	495	4	US-09-710-299-4	Sequence 4, Appli	1238	120.5	5.1	539	3	US-09-334-775A-4	Sequence 4, Appli
1166	121.5	5.1	495	4	US-09-509-031-4	Sequence 4, Appli	1239	120.5	5.1	539	3	US-08-789-275-6	Sequence 6, Appli
1167	121.5	5.1	514	3	US-08-796-899-25	Sequence 25, Appl	1240	119.5	5.1	213	4	US-09-489-039A-11130	Sequence 11130, A
1168	121.5	5.1	635	4	US-09-252-991A-17122	Sequence 17122, A	1241	119.5	5.1	354	4	US-09-949-016-11550	Sequence 11550, A
1169	121.5	5.1	683	4	US-09-949-016-11117	Sequence 11117, A	1242	119.5	5.1	420	2	US-08-845-998-8	Sequence 8, Appli
1170	121.5	5.1	718	4	US-09-902-540-14365	Sequence 14365, A	1243	119.5	5.1	420	3	US-09-206-537-8	Sequence 8, Appli
1171	121	5.1	191	4	US-09-252-991A-18626	Sequence 18626, A	1244	119.5	5.1	420	3	US-09-430-854-8	Sequence 8, Appli
1172	121	5.1	194	4	US-09-431-887-13	Sequence 13, Appl	1245	119.5	5.1	464	4	US-09-949-016-9828	Sequence 9828, Ap
1173	121	5.1	252	4	US-09-431-887-13	Sequence 13, Appl	1246	119.5	5.1	531	4	US-09-252-991A-31109	Sequence 31109, A
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1175	121	5.1	330	1	US-08-642-255-32	Sequence 32, Appl	1248	119.5	5.1	1427	4	US-09-252-991A-20577	Sequence 20577, A
1176	121	5.1	335	3	US-08-469-318-143	Sequence 143, App	1249	119.5	5.1	1548	4	US-09-252-991A-22301	Sequence 22301, A
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1178	121	5.1	335	3	US-08-446-872A-143	Sequence 143, App	1251	119.5	5.0	163	4	US-09-270-767-55088	Sequence 55088, A
1179	121	5.1	335	4	US-08-762-227A-143	Sequence 143, App	1252	119.5	5.0	213	4	US-09-252-991A-16621	Sequence 16621, A
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1181	121	5.1	337	3	US-09-270-767-45762	Sequence 45762, A	1254	119.5	5.0	255	1	US-08-509-261A-4	Sequence 4, Appli
1182	121	5.1	367	3	US-08-213-419B-15	Sequence 15, Appl	1255	119.5	5.0	255	1	US-08-660-626-10	Sequence 10, Appl
1183	121	5.1	408	1	US-07-609-716-65	Sequence 65, Appl	1256	119.5	5.0	255	1	US-08-692-892-4	Sequence 4, Appli
1184	121	5.1	408	3	US-08-475-411A-65	Sequence 65, Appl	1257	119.5	5.0	255	2	US-08-713-939A-4	Sequence 4, Appli
1185	121	5.1	408	3	US-08-478-029A-65	Sequence 65, Appl	1258	119.5	5.0	255	2	US-08-868-162A-24	Sequence 24, Appl
1186	121	5.1	412	4	US-09-252-991A-26284	Sequence 26284, A	1259	119.5	5.0	255	3	US-09-031-168-10	Sequence 10, Appl
1187	121	5.1	444	4	US-09-252-991A-22448	Sequence 22448, A	1260	119.5	5.0	255	3	US-09-036-579-4	Sequence 4, Appli
1188	121	5.1	461	4	US-09-902-540-10506	Sequence 10506, A	1261	119.5	5.0	255	3	US-09-350-374-4	Sequence 4, Appli
1189	121	5.1	509	4	US-09-252-991A-32576	Sequence 32576, A	1262	119.5	5.0	255	4	US-09-943-906-4	Sequence 4, Appli
1190	121	5.1	546	2	US-09-067-351-1	Sequence 1, Appli	1263	119.5	5.0	255	4	US-09-669-516C-10	Sequence 10, Appl
1191	121	5.1	546	3	US-09-360-490-1	Sequence 1, Appli	1264	119.5	5.0	259	4	US-09-252-991A-21547	Sequence 21547, A
1192	121	5.1	642	4	US-09-252-991A-21889	Sequence 21889, A	1265	119.5	5.0	322	1	US-08-014-943A-2	Sequence 2, Appli
1193	121	5.1	686	4	US-09-252-991A-20509	Sequence 20509, A	1266	119.5	5.0	322	1	US-08-486-421-3	Sequence 3, Appli
1194	121	5.1	859	1	US-08-395-580-2	Sequence 2, Appli	1267	119.5	5.0	322	1	US-08-470-911-3	Sequence 3, Appli
1195	121	5.1	859	5	PCT-US95-02792-2	Sequence 2, Appli	1268	119.5	5.0	322	2	US-08-486-809-3	Sequence 3, Appli

1269	119	5.0	397	4	US-09-252-991A-24025	Sequence 24025, A	1342	117	5.0	691	1	US-08-066-167-4	Sequence 4, Appli
1270	119	5.0	407	4	US-09-252-991A-26060	Sequence 26060, A	1343	117	5.0	691	2	US-08-449-733-2	Sequence 2, Appli
1271	119	5.0	446	2	US-08-636-854-15	Sequence 15, Appl	1344	117	5.0	692	3	US-08-448-194-62	Sequence 62, Appl
1272	119	5.0	541	4	US-09-252-991A-24521	Sequence 24521, A	1345	117	5.0	692	3	US-08-867-921-62	Sequence 62, Appl
1273	119	5.0	616	4	US-09-252-991A-20777	Sequence 20777, A	1346	117	5.0	711	1	US-08-487-890A-98	Sequence 98, Appl
1274	119	5.0	654	4	US-09-620-412C-341	Sequence 341, App	1347	117	5.0	711	1	US-08-478-435-98	Sequence 98, Appl
1275	119	5.0	654	4	US-09-598-419-341	Sequence 341, App	1348	117	5.0	711	2	US-08-337-483-98	Sequence 98, Appl
1276	119	5.0	1007	4	US-09-252-991A-18614	Sequence 18614, A	1349	117	5.0	711	2	US-08-478-373-98	Sequence 98, Appl
1277	119	5.0	1321	2	US-08-317-310A-64	Sequence 64, Appl	1350	117	5.0	711	3	US-08-474-671-98	Sequence 98, Appl
1278	119	5.0	2110	4	US-09-270-767-46347	Sequence 46347, A	1351	117	5.0	711	3	US-08-483-577A-98	Sequence 98, Appl
1279	118.5	5.0	74	1	US-07-609-716-63	Sequence 63, Appl	1352	117	5.0	711	3	US-08-448-194-8	Sequence 8, Appli
1280	118.5	5.0	74	3	US-08-475-011A-63	Sequence 63, Appl	1353	117	5.0	711	3	US-08-867-438-98	Sequence 98, Appl
1281	118.5	5.0	74	3	US-08-478-029A-63	Sequence 63, Appl	1354	117	5.0	711	3	US-08-867-921-8	Sequence 8, Appli
1282	118.5	5.0	309	4	US-09-270-767-44846	Sequence 44846, A	1355	117	5.0	711	3	US-08-637-654-98	Sequence 98, Appl
1283	118.5	5.0	310	4	US-09-248-796A-24630	Sequence 24630, A	1356	117	5.0	711	3	US-08-649-518-98	Sequence 98, Appl
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1285	118.5	5.0	473	4	US-09-252-991A-16904	Sequence 16904, A	1358	117	5.0	785	4	US-09-538-092-872	Sequence 872, App
1286	118.5	5.0	499	4	US-09-252-991A-16940	Sequence 16940, A	1359	117	5.0	1266	4	US-09-949-016-8963	Sequence 8963, Ap
1287	118.5	5.0	508	4	US-09-270-767-43201	Sequence 43201, A	1360	116.5	4.9	258	4	US-09-252-991A-30969	Sequence 30969, A
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1291	118	5.0	139	4	US-09-270-767-51884	Sequence 51884, A	1364	116.5	4.9	404	4	US-09-252-991A-25762	Sequence 25762, A
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1296	118	5.0	460	4	US-09-252-991A-33090	Sequence 33090, A	1369	116.5	4.9	617	1	US-08-137-614A-26	Sequence 26, Appl
1297	118	5.0	478	4	US-09-252-991A-25191	Sequence 25191, A	1370	116.5	4.9	637	3	US-08-072-064-1	Sequence 1, Appli
1298	118	5.0	524	4	US-09-252-991A-19671	Sequence 19671, A	1371	116.5	4.9	637	3	US-08-072-064-4	Sequence 4, Appli
1299	118	5.0	551	4	US-09-252-991A-30116	Sequence 30116, A	1372	116.5	4.9	637	3	US-08-072-064-6	Sequence 6, Appli
1300	118	5.0	656	4	US-09-302-540-12404	Sequence 12404, A	1373	116.5	4.9	637	3	US-08-072-064-8	Sequence 8, Appli
1301	118	5.0	861	4	US-09-252-991A-30624	Sequence 30624, A	1374	116.5	4.9	637	5	PCT-US92-08558-1	Sequence 1, Appli
1302	118	5.0	1749	4	US-09-640-419C-28	Sequence 28, Appl	1375	116.5	4.9	728	4	US-09-252-991A-23613	Sequence 23613, A
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1304	117.5	5.0	142	1	US-07-609-716-100	Sequence 100, App	1377	116.5	4.9	990	4	US-09-252-991A-32469	Sequence 32469, A
1305	117.5	5.0	142	3	US-08-475-411A-100	Sequence 100, App	1378	116.5	4.9	1155	1	US-08-094-948A-29	Sequence 29, Appl
1306	117.5	5.0	142	3	US-08-478-029A-100	Sequence 100, App	1379	116.5	4.9	1155	5	PCT-US96-09319-29	Sequence 29, Appl
1307	117.5	5.0	163	4	US-09-248-796A-18929	Sequence 18929, A	1380	116	4.9	173	4	US-09-270-767-60931	Sequence 60931, A
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1309	117.5	5.0	187	4	US-09-640-211A-1129	Sequence 1129, Ap	1382	116	4.9	314	4	US-09-736-457-1863	Sequence 1863, Ap
1310	117.5	5.0	249	4	US-09-270-767-44857	Sequence 44857, A	1383	116	4.9	326	4	US-09-252-991A-33000	Sequence 33000, A
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1314	117.5	5.0	359	4	US-09-252-991A-18788	Sequence 18788, A	1387	116	4.9	569	4	US-09-252-991A-25582	Sequence 25582, A
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1316	117.5	5.0	428	4	US-09-252-991A-20199	Sequence 20199, A	1389	116	4.9	580	4	US-10-115-415-2	Sequence 2, Appli
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1319	117.5	5.0	444	1	US-08-478-675-3	Sequence 3, Appli	1392	116	4.9	624	3	US-09-336-447A-7	Sequence 7, Appli
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1323	117.5	5.0	718	4	US-09-252-991A-32743	Sequence 32743, A	1396	116	4.9	979	4	US-09-538-092-990	Sequence 990, App
1324	117.5	5.0	1489	6	5183745-2	Patent No. 5183745	1397	116	4.9	997	2	US-08-387-942C-4	Sequence 4, Appli
1325	117.5	5.0	1489	6	5183745-2	Patent No. 5183745	1398	116	4.9	1414	4	US-09-438-185A-446	Sequence 446, App
1326	117	5.0	63	4	US-09-646-691B-10	Sequence 10, Appl	1399	116	4.9	1663	5	PCT-US93-07261-16	Sequence 16, Appl
1327	117	5.0	144	1	US-08-642-255-49	Sequence 49, Appl	1400	116	4.9	206	4	US-09-252-991A-31481	Sequence 31481, A
1328	117	5.0	235	4	US-09-205-258-318	Sequence 318, App	1401	116	4.9	241	1	US-08-194-468-2	Sequence 2, Appli
1329	117	5.0	235	4	US-09-205-258-738	Sequence 738, App	1402	116	4.9	241	3	US-08-961-739-2	Sequence 2, Appli
1330	117	5.0	233	4	US-09-252-991A-32459	Sequence 32459, A	1403	116	4.9	241	3	US-09-514-247A-8	Sequence 8, Appli
1331	117	5.0	234	4	US-09-431-887-20	Sequence 20, Appl	1404	116	4.9	241	4	US-09-686-316-2	Sequence 2, Appli
1332	117	5.0	254	4	US-09-431-887-21	Sequence 21, Appl	1405	115.5	4.9	93	4	US-09-072-596-272	Sequence 272, App
1333	117	5.0	254	4	US-09-431-887-22	Sequence 22, Appl	1406	115.5	4.9	93	4	US-09-072-967-277	Sequence 277, App
1334	117	5.0	259	4	US-09-431-887-33	Sequence 33, Appl	1407	115.5	4.9	206	4	US-09-252-991A-31481	Sequence 31481, A
1335	117	5.0	314	4	US-09-949-016-6437	Sequence 6437, Ap	1408	115.5	4.9	215	4	US-09-252-991A-25666	Sequence 25666, A
1336	117	5.0	321	4	US-09-252-991A-24270	Sequence 24270, A	1409	115.5	4.9	245	4	US-09-949-016-8385	Sequence 8385, Ap
1337	117	5.0	343	4	US-09-252-991A-17876	Sequence 17876, A	1410	115.5	4.9	253	4	US-09-252-991A-29632	Sequence 29632, A
1338	117	5.0	344	4	US-09-949-016-9889	Sequence 9889, Ap	1411	115.5	4.9	271	4	US-10-237-551-74	Sequence 74, Appl
1339	117	5.0	356	4	US-09-252-991A-21526	Sequence 21526, A	1412	115.5	4.9	411	4	US-09-248-796A-14848	Sequence 14848, A
1340	117	5.0	662	4	US-09-252-991A-30943	Sequence 30943, A	1413	115.5	4.9	446	3	US-08-956-254-2	Sequence 2, Appli
1341	117	5.0	691	1	US-08-064-174-2	Sequence 2, Appli	1414	115.5	4.9	446	3	US-09-008-388-1	Sequence 1, Appli

1415	115.5	4.9	448	2	US-09-015-815-1	Sequence 1, Appl	Sequence 1, Appl
1416	115.5	4.9	463	4	US-09-252-991A-29731	Sequence 27331, A	Sequence 27331, A
1417	115.5	4.9	475	2	US-08-861-464-14	Sequence 14, Appl	Sequence 14, Appl
1418	115.5	4.9	475	2	US-08-396-001-14	Sequence 14, Appl	Sequence 14, Appl
1419	115.5	4.9	475	3	US-09-332-433A-14	Sequence 14, Appl	Sequence 14, Appl
1420	115.5	4.9	475	4	US-09-826-752-14	Sequence 14, Appl	Sequence 14, Appl
1421	115.5	4.9	499	2	US-07-952-853-6	Sequence 6, Appl	Sequence 6, Appl
1422	115.5	4.9	499	2	US-09-914-848-6	Sequence 6, Appl	Sequence 6, Appl
1423	115.5	4.9	556	4	US-09-252-991A-17793	Sequence 17793, A	Sequence 17793, A
1424	115.5	4.9	560	4	US-09-248-796A-22980	Sequence 22980, A	Sequence 22980, A
1425	115.5	4.9	592	3	US-09-377-155-17	Sequence 17, Appl	Sequence 17, Appl
1426	115.5	4.9	592	3	US-09-669-974-17	Sequence 17, Appl	Sequence 17, Appl
1427	115.5	4.9	592	4	US-09-797-862-17	Sequence 17, Appl	Sequence 17, Appl
1428	115.5	4.9	718	4	US-09-252-991A-25696	Sequence 25696, A	Sequence 25696, A
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1431	115.5	4.9	817	4	US-09-252-991A-25598	Sequence 25598, A	Sequence 25598, A
1432	115.5	4.9	875	4	US-09-252-991A-30056	Sequence 30056, A	Sequence 30056, A
1433	115.5	4.9	1824	4	US-09-543-681A-5009	Sequence 5009, Ap	Sequence 5009, Ap
1434	115	4.9	187	4	US-09-270-767-33039	Sequence 33039, A	Sequence 33039, A
1435	115	4.9	187	4	US-09-270-767-48256	Sequence 48256, A	Sequence 48256, A
1436	115	4.9	197	4	US-09-252-991A-28165	Sequence 28165, A	Sequence 28165, A
1437	115	4.9	254	4	US-09-431-887-23	Sequence 23, Appl	Sequence 23, Appl
1438	115	4.9	263	4	US-09-248-796A-15305	Sequence 15305, A	Sequence 15305, A
1439	115	4.9	274	4	US-09-270-767-61923	Sequence 61923, A	Sequence 61923, A
1440	115	4.9	299	4	US-09-252-991A-21857	Sequence 21857, A	Sequence 21857, A
1441	115	4.9	336	4	US-09-252-991A-29624	Sequence 29624, A	Sequence 29624, A
1442	115	4.9	394	4	US-09-270-767-46353	Sequence 46353, A	Sequence 46353, A
1443	115	4.9	398	4	US-09-252-991A-30286	Sequence 30286, A	Sequence 30286, A
1444	115	4.9	451	4	US-09-489-039A-13406	Sequence 13406, A	Sequence 13406, A
1445	115	4.9	456	4	US-09-252-991A-17335	Sequence 17335, A	Sequence 17335, A
1446	115	4.9	473	4	US-09-252-991A-21690	Sequence 21690, A	Sequence 21690, A
1447	115	4.9	591	4	US-09-252-991A-28760	Sequence 28760, A	Sequence 28760, A
1448	115	4.9	625	4	US-09-270-767-42376	Sequence 42376, A	Sequence 42376, A
1449	115	4.9	695	4	US-09-252-991A-27647	Sequence 27647, A	Sequence 27647, A
1450	115	4.9	1245	4	US-09-252-991A-30935	Sequence 30935, A	Sequence 30935, A
1451	114.5	4.8	218	4	US-09-270-767-38592	Sequence 38592, A	Sequence 38592, A
1452	114.5	4.8	218	4	US-09-270-767-53809	Sequence 53809, A	Sequence 53809, A
1453	114.5	4.8	324	4	US-09-252-991A-28194	Sequence 28194, A	Sequence 28194, A
1454	114.5	4.8	370	4	US-09-248-796A-14522	Sequence 14522, A	Sequence 14522, A
1455	114.5	4.8	418	2	US-09-026-587-1	Sequence 1, Appl	Sequence 1, Appl
1456	114.5	4.8	418	2	US-09-227-420-1	Sequence 1, Appl	Sequence 1, Appl
1457	114.5	4.8	418	4	US-09-387-811-1	Sequence 1, Appl	Sequence 1, Appl
1458	114.5	4.8	442	4	US-09-252-991A-27308	Sequence 27308, A	Sequence 27308, A
1459	114.5	4.8	457	4	US-09-248-796A-26659	Sequence 26659, A	Sequence 26659, A
1460	114.5	4.8	589	3	US-09-377-155-19	Sequence 19, Appl	Sequence 19, Appl
1461	114.5	4.8	589	3	US-09-669-974-19	Sequence 19, Appl	Sequence 19, Appl
1462	114.5	4.8	589	4	US-09-797-862-19	Sequence 19, Appl	Sequence 19, Appl
1463	114.5	4.8	655	4	US-09-949-016-9577	Sequence 9577, Ap	Sequence 9577, Ap
1464	114.5	4.8	735	4	US-09-252-991A-32172	Sequence 32172, A	Sequence 32172, A
1465	114.5	4.8	767	4	US-09-252-991A-28262	Sequence 28262, A	Sequence 28262, A
1466	114.5	4.8	808	4	US-09-252-991A-32826	Sequence 32826, A	Sequence 32826, A
1467	114.5	4.8	1180	4	US-09-252-991A-32464	Sequence 32464, A	Sequence 32464, A
1468	114.5	4.8	1729	4	US-09-134-000C-5675	Sequence 5675, Ap	Sequence 5675, Ap
1469	114	4.8	138	3	US-08-990-571-74	Sequence 74, Appl	Sequence 74, Appl
1470	114	4.8	138	4	US-09-528-784A-74	Sequence 74, Appl	Sequence 74, Appl
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1472	114	4.8	194	4	US-09-252-991A-32646	Sequence 32646, A	Sequence 32646, A
1473	114	4.8	250	4	US-09-248-796A-22986	Sequence 22986, A	Sequence 22986, A
1474	114	4.8	266	4	US-09-252-991A-229964	Sequence 29964, A	Sequence 29964, A
1475	114	4.8	276	4	US-09-538-092-889	Sequence 889, App	Sequence 889, App
1476	114	4.8	291	4	US-09-252-991A-28572	Sequence 28572, A	Sequence 28572, A
1477	114	4.8	303	3	US-08-818-112-92	Sequence 92, Appl	Sequence 92, Appl
1478	114	4.8	303	3	US-08-818-111-93	Sequence 93, Appl	Sequence 93, Appl
1479	114	4.8	303	3	US-09-056-556-92	Sequence 92, Appl	Sequence 92, Appl
1480	114	4.8	303	4	US-09-072-596-93	Sequence 93, Appl	Sequence 93, Appl
1481	114	4.8	303	4	US-09-072-967-92	Sequence 92, Appl	Sequence 92, Appl
1482	114	4.8	357	4	US-09-252-991A-30141	Sequence 30141, A	Sequence 30141, A
1483	114	4.8	383	4	US-09-252-991A-24300	Sequence 24300, A	Sequence 24300, A
1484	114	4.8	435	4	US-09-949-016-8415	Sequence 8415, Ap	Sequence 8415, Ap
1485	114	4.8	435	4	US-09-949-016-8792	Sequence 8792, Ap	Sequence 8792, Ap
1486	114	4.8	550	4	US-09-242-913B-14	Sequence 14, Appl	Sequence 14, Appl
1487	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1488	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1489	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1490	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1491	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1492	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1493	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1494	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1495	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1496	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1497	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1498	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1499	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl
1500	114	4.8	552	4	US-09-242-913B-19	Sequence 19, Appl	Sequence 19, Appl

## ALIGNMENTS

## RESULT 1

US-09-673-395A-256  
; Sequence 256, Application US/09673395A  
; Patent No. 6620923  
; GENERAL INFORMATION:  
; APPLICANT: SPECHT, THOMAS  
; APPLICANT: HINZMANN, BERND  
; APPLICANT: SCHMITT, ARMIN  
; APPLICANT: PILARSKY, CHRISTIAN  
; APPLICANT: DAHL, EDGAR  
; APPLICANT: ROSENTHAL, ANDRE  
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE  
; FILE REFERENCE: ALBRE-12  
; CURRENT APPLICATION NUMBER: US/09/673,395A  
; CURRENT FILING DATE: 2000-10-17  
; NUMBER OF SEQ ID NOS: 637  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 256  
; LENGTH: 230  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-673-395A-256

Query Match 28.3%; Score 669; DB 4; Length 230;  
Best Local Similarity 98.4%; Pred. No. 1e-39;  
Matches 122; Conservative 0; Indels 0; Gaps 0;

QY 311 GSSTGSSGNHGGGGGNGHKPCERKPGNEARGSGGIGQFRGQGVSSNNRISKEGNR 370

Db 13 GSSTGSSGNHGGGGGNGHKPCERKPGNEARGSGGIGQFRGQGVSSNNRISKEGNR 72

QY 371 LLGGSGDNYRGQSSGSGGDAVGGVNTVNSFTSPGMFNFTFWKNFKSKLGFINWDAI 430

Db 73 LLGGSGDNYRGQSSGSGGDAVGGVNTVNSFTSPGMFNFTFWKNFKSKLGFINWDAI 132

QY 431 NKDQ 434

Db 133 NKNQ 136

## RESULT 2

US-08-806-029-9  
; Sequence 9, Application US/08806029  
; Patent No. 6380154  
; GENERAL INFORMATION:  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Stedronsky, Erwin R.  
; TITLE OF INVENTION: Synthetic Proteins for in vivo Drug  
; TITLE OF INVENTION: Delivery and Tissue Augmentation  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California







APPLICANT: Dorman, Mary A.  
TITLE OF INVENTION: Methods for Preparing Synthetic  
TITLE OF INVENTION: Repetitive DNA  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/175,155  
FILING DATE: 29-DEC-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I.  
REGISTRATION NUMBER: 20015  
REFERENCE/DOCKET NUMBER: A-55186-5/BIR  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1177 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-175-155-29

Query Match 17.0%; Score 402.5; DB 1; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 3e-20;  
Matches 126; Conservative 38; Mismatches 224; Indels 27; Gaps 10;  
QY 17 GSGEAGPLOSGETGTNIGENLGHGLDALSSEGVKAIGKEAGGAGSKVSEALGQCTR 76  
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DB 831 AGSGAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 890  
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QY 194 GQG-GNGGPPNFTNTQGAVAOPGYSVRASNQEGCTNPPPSGSGGS-----SNSGGG 247  
DB 944 GSGAGAGSAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1003  
QY 248 SGSGSGS---SGSGSNDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSG 304  
DB 1004 SGAGAGSAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 1063  
QY 305 GSSESSWSSSTGSSGNHG---GSGGGNGHKPGCEKPGNEARGSGE-SGIQGFPGQGVSSN 360  
DB 1064 GAGAGSAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 1123  
QY 361 MREISKEGNLLGSGDNYRGQSSWSGCGDVGGVNTVNSSETSPGMFDFTW 415  
DB 1124 AGAGSGAG----AGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 1174

RESULT 5  
US-08-477-509B-64  
; Sequence 64, Application US/08477509B  
; Patent No. 5770697

GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A  
APPLICANT: Cappello, Joseph  
APPLICANT: Criesman, John W  
APPLICANT: Dorman, Mary A  
TITLE OF INVENTION: No. 570697el Peptides Comprising Repetitive  
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,509B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1177 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-509B-64

Query Match 17.0%; Score 402.5; DB 1; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 3e-20;  
Matches 126; Conservative 38; Mismatches 224; Indels 27; Gaps 10;  
QY 17 GSGEAGPLOSGETGTNIGENLGHGLDALSSEGVKAIGKEAGGAGSKVSEALGQCTR 76  
DB 771 GAGSGAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 830  
QY 77 EAVGTGVQR-VPGFGAADALGNRVGEAAHALGNTGHEIGRQAEVDVIRHGADAVRGSWQV 135  
DB 831 AGSGAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 890  
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DB 891 GSGAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 943  
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DB 944 GSGAGAGSAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1003  
QY 248 SGSGSGS---SGSGSNDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSG 304

[illegible]

RESULT 6  
US-08-707-237A-35  
; Sequence 35, Application US/08707237A  
; Patent No. 5830713  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; APPLICANT: Capello, Joseph  
; APPLICANT: Cressman, John W.  
; APPLICANT: Dorman, Mary A.  
; TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC  
; TITLE OF INVENTION: REPETITIVE DNA  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08707,237A  
; FILING DATE: 03-SEP-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,155  
; FILING DATE: 29-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/609,716  
; FILING DATE: 06-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/269,429  
; FILING DATE: 09-NOV-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/114,618  
; FILING DATE: 29-OCT-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/927,258  
; FILING DATE: 04-NOV-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-10/WHO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1177 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein

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US-08-707-237A-35
Query Match 17.0%; Score 402.5; DB 2; Length 1177;
Best Local Similarity 30.4%; Pred. No. 3e-20;
Matches 126; Conservative 38; Mismatches 224; Indels 27; Caps 10;

QY 17 GSGEAGPLOSRESSTCTNIGALHGLDGLDSEGVGKAIGKEAGGAGKGVSEALQGTR 76
Db 771 GAGSGAGAGSAGAGYAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 830
QY 77 EAVGTGTVRQ-VPFGAADALGNRVGEAAHALGNTGHEIGRQAEDEVIRHGADAVRGSWQGV 135
Db 831 AGSGAGAGSAGAGYAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
QY 136 PGHSGAWETSGGHHI-FGSQGLG-QGQGNPGGLTGMVHGYPGNSAGSFGMNPQGPW 193
Db 891 GSGAGAGSAGAGYAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 943
QY 194 GQG-GNGGPPNFTGTQGAOPGYGVSVPASQNECTNPPPSGSGGS-----SNSGGG 247
Db 944 GSGAGAGAGAGSAGAGYAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1003
QY 248 SSGSGS-----SGSGSNGDNNNGSSSGSGSSSGSGSGSGSGSGSGSGSGSGSGSG 304
Db 1004 SGAGAGAGAGAGSAGAGYAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1063
QY 305 GSSEWSGSTSGSSNGHG---GSGGNGHKGPKGCEKPGNEARGSGE-SG1QGFRGQGVSSN 360
Db 1064 GAGAGAGAGAGSAGAGYAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1123
QY 361 MREISKBNRLIGSGDNTVRGSGSSWGSGGDAVGVTGVTNSETSPGMFNFTTFW 415
Db 1124 AGAGSAG-----AGSAGAGYAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1174

RESULT 7
US-08-482-085B-64
; Sequence 64, Application US/08482085B
; Patent No. 6018030
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Richardson, Charles
; APPLICANT: Chambers, James
; APPLICANT: Causey, Stuart
; APPLICANT: Pollock, Thomas J.
; APPLICANT: Cappello, Joseph
; APPLICANT: Crisman, John W.
; TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,085B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-6/RPT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-482-085B-64

Query Match 17.0%; Score 402.5; DB 3; Length 1177;
Best Local Similarity 30.4%; Pred. No. 3e-20;
Matches 126; Conservative 38; Mismatches 224; Indels 27; Gaps 10;

QY 17 GSCEAGPLQSGEESTGTNIGELGHLGDLALSGVGKAIKGEAGGAAGSKVSEALGQTR 76
D 177 GAGSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 830
QY 77 EAVGTGVQK-VPGFGADALGNRVGEAAHALGNTGHEIGRQAEVIRHGADAVRGSQGV 135
D 831 AGSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 890
QY 136 PGHSAGWETSGHGI-FGSGGGLG-GGCGNPGGLGTPVHGYPGNSAGSFGHNPQCAPW 193
D 891 GSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 943
QY 194 GQG-GNGGPPNFGTNTQGAQVAPQGYGSRASNQNEGCTNPPPSGGGGS-----SNSGGG 247
D 944 GSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1003
QY 248 SGSSQSGS---SGSSGNDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSG 304
D 1004 SGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1063
QY 305 GSSESWSSSTGSSSGNHG---GSGCGNGHKPGCEKPGNEARSGE-SGIQGFQGVSSN 360
D 1064 GAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 1123
QY 361 MREISKEGNRLGSGDNYRGQSSWSSGGGDAVGGVNTVNSSTSPGMFNFDFW 415
D 1124 AGAGSGAG---AGSGAAGYAGAGSGAGAGSGAGAGAGMDPGRYQLSAGRYHYQLVW 1174

RESULT 8
US-08-475-411A-31
; Sequence 31, Application US/08475411A
; Patent No. 6140072
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: Functional Recombinantly Prepared
; TITLE OF INVENTION: Synthetic Protein Polymer
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,411A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 06-NOV-1990
; APPLICATION NUMBER: US 07/609,716
; PRIOR APPLICATION DATA:
; FILING DATE: 09-NOV-1988
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-9/RPT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-411A-31

Query Match 17.0%; Score 402.5; DB 3; Length 1177;
Best Local Similarity 30.4%; Pred. No. 3e-20;
Matches 126; Conservative 38; Mismatches 224; Indels 27; Gaps 10;

QY 17 GSCEAGPLQSGEESTGTNIGELGHLGDLALSGVGKAIKGEAGGAAGSKVSEALGQTR 76
D 771 GAGSGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 830
QY 77 EAVGTGVQK-VPGFGADALGNRVGEAAHALGNTGHEIGRQAEVIRHGADAVRGSQGV 135
D 831 AGSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 890
QY 136 PGHSAGWETSGHGI-FGSGGGLG-GGCGNPGGLGTPVHGYPGNSAGSFGHNPQCAPW 193
D 891 GSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 943
QY 194 GQG-GNGGPPNFGTNTQGAQVAPQGYGSRASNQNEGCTNPPPSGGGGS-----SNSGGG 247
D 944 GSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1003
QY 248 SGSSQSGS---SGSSGNDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSG 304
D 1004 SGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1063
QY 305 GSSESWSSSTGSSSGNHG---GSGCGNGHKPGCEKPGNEARSGE-SGIQGFQGVSSN 360
D 1064 GAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 1123
QY 361 MREISKEGNRLGSGDNYRGQSSWSSGGGDAVGGVNTVNSSTSPGMFNFDFW 415
D 1124 AGAGSGAG---AGSGAAGYAGAGSGAGAGSGAGAGAGMDPGRYQLSAGRYHYQLVW 1174

RESULT 9
US-08-478-029A-31
; Sequence 31, Application US/08478029A
; Patent No. 6184348
; GENERAL INFORMATION:
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; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-10/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-707-237A-54

Query Match 16.9%; Score 399; DB 2; Length 1059;
Best Local Similarity 30.4%; Pred. No. 4.7e-20;
Matches 123; Conservative 43; Mismatches 220; Indels 18; Gaps 9;

QY 17 GSGEAGPLOSREESTGTNIGELGHLGDALSGVGKAIKKEAGGAGSKVSEALQGQTR 76
DB 666 GSG-AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 724
QY 77 EAVGTGVROPVPGGAADALGNRVGEAAHALGNTGHEIGRQABDVIRHGADAVRGSWQV 136
DB 725 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 784
QY 137 GHSAGWETSGHGIFGSGGLG-GQGQNPGLGTPVWHYPCNSAGSGFQMNPGAPWQ 195
DB 836 AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 895
QY 255 -SGSGGNDNNNGSSG-GSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGS 312
DB 896 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 955
QY 313 STGSSGNHGGSGGNGHKPGCEKPGNEARSGE-SGIQGFQGVSSNMREISKEGNRL 371
DB 956 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 1015
QY 372 LGSGDNYRQGSWSGCGDAVGGVNTVNSSETSPGMFNFTFW 415
DB 1016 GAGAGS---GAGAGSGAGAGSGAGAGMDPGRYQLSAGRYHYQLVW 1056

RESULT 13
US-08-806-029-10
; Sequence 10, Application US/0806029
; Patent No. 6380154
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; APPLICANT: Stedronsky, Erwin R.
; TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
; TITLE OF INVENTION: Delivery and Tissue Augmentation
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/806,029
; FILING DATE: 24-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,237
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-806-029-10

Query Match 16.9%; Score 399; DB 3; Length 1059;
Best Local Similarity 30.4%; Pred. No. 4.7e-20;
Matches 123; Conservative 43; Mismatches 220; Indels 18; Gaps 9;

QY 17 GSGEAGPLOSREESTGTNIGELGHLGDALSGVGKAIKKEAGGAGSKVSEALQGQTR 76
DB 666 GSG-AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 724
QY 77 EAVGTGVROPVPGGAADALGNRVGEAAHALGNTGHEIGRQABDVIRHGADAVRGSWQV 136
DB 725 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 784
QY 137 GHSAGWETSGHGIFGSGGLG-GQGQNPGLGTPVWHYPCNSAGSGFQMNPGAPWQ 195
DB 785 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 835
QY 196 CGNGGPPNFTGTQGAQVAPGYGVSRAVNQNGECTNPPPSGSGSGS-SNSGGSGSGS 254
DB 836 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 895
QY 255 -SGSGGNDNNNGSSG-GSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGS 312
DB 896 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 955
QY 313 STGSSGNHGGSGGNGHKPGCEKPGNEARSGE-SGIQGFQGVSSNMREISKEGNRL 371
DB 956 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 1015
QY 372 LGSGDNYRQGSWSGCGDAVGGVNTVNSSETSPGMFNFTFW 415
DB 1016 GAGAGS---GAGAGSGAGAGSGAGAGMDPGRYQLSAGRYHYQLVW 1056

RESULT 14
US-08-477-509B-83
; Sequence 83, Application US/08477509B
; Patent No. 5770697
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A
; APPLICANT: Cappello, Joseph
; APPLICANT: Crisman, John W
; APPLICANT: Dorman, Mary A
; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/477,509B

FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155

FILING DATE: 29-DEC-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049

FILING DATE: 22-APR-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258

Db 1058 GAGAGS---GAGAGSGAGAGSGAGAMPDPRYQLSAGRYHYQLVM 1098

RESULT 15

US-08-482-085B-83  
Sequence 83, Application US/08482085B  
Patent No. 6018030  
GENERAL INFORMATION:

APPLICANT: Ferrari, Franco A.  
APPLICANT: Richardson, Charles  
APPLICANT: Chambers, James

APPLICANT: Causey, Stuart  
APPLICANT: Pollock, Thomas J.  
APPLICANT: Cappello, Joseph

APPLICANT: Crissman, John W.  
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive  
UNITS OF AMINO ACIDS AND DNA SEQUENCES ENCODING THE SAME

NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California

COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,085B

FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
PRIORITY APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801

REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 83:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1101 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-085B-83

Query Match 16.9%; Score 399; DB 3; Length 1101;

Best Local Similarity 30.4%; Pred. No. 4.9e-20;

Matches 123; Conservative 43; Mismatches 220; Indels 18; Gaps 9;

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Db 708 GSG-AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 766

QY 77 EAVGTGVRQVPGFGAADALGNRVEAAHALGNTGHEIGRQAEADVIRHGADAVRGSHQGV 136

Db 767 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 826

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QY	196	GGNGGPFNFGTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGSGGGS-SNSGGGSGSQSGS	254
Db	878	GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS	937
QY	255	-SGSGSNGDNNNGSSG-GSSSGSSSGSSSGSGSSGSGSSGSGSRDSDGSGESSWGS	312
Db	938	GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS	997
QY	313	STGSSSGNHGSGGNGHKPCCKPNEARGSGE-SGIQGFRQGVSSNNWREISKGNRL	371
Db	998	GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS	1057
QY	372	LGGSGDNYRGSGSSWGSGGDAVGGYNTVNSETSPGMFNFTFW	415
Db	1058	GAGAGS---GAGAGSGAGAGSGAGMDPGRYQLSAGRYHYQLYW	1098

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 7, 2005, 00:10:21 ; Search time 144 Seconds  
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1014.436 Million cell updates/sec

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Scoring table: BLOSUM62  
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Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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516	2363	100.0	440	14	US-10-223-085-150	Sequence 150, App
522	2363	100.0	440	14	US-10-219-065-156	Sequence 156, App
565	2363	100.0	440	14	US-10-223-084-150	Sequence 150, App
566	2363	100.0	440	14	US-10-223-088-150	Sequence 150, App
567	2363	100.0	440	14	US-10-223-090-150	Sequence 150, App
573	2363	100.0	440	14	US-10-223-087-150	Sequence 150, App
586	2363	100.0	440	14	US-10-223-083-150	Sequence 150, App
592	2363	100.0	440	14	US-10-223-085-150	Sequence 150, App
618	2363	100.0	440	14	US-10-174-587-202	Sequence 202, App
688	2363	100.0	440	14	US-10-063-742-52	Sequence 52, App
764	2363	100.0	440	14	US-10-013-909A-52	Sequence 52, App
769	2363	100.0	440	14	US-10-223-081-150	Sequence 150, App
807	2363	100.0	440	14	US-10-223-082-150	Sequence 150, App

839	2363	100.0	440	15	US-10-305-654-150	Sequence 150, App
848	2363	100.0	440	15	US-10-081-056-150	Sequence 150, App
859	2363	100.0	440	17	US-10-972-317-52	Sequence 52, App
860	2030	85.9	386	14	US-10-050-704-100	Sequence 100, App
861	2030	85.9	386	16	US-10-798-512-100	Sequence 100, App
862	450.5	19.1	1079	10	US-09-820-843A-20	Sequence 20, App
863	439.5	18.6	1306	15	US-10-282-122A-64405	Sequence 64405, A
864	415.5	17.6	1381	15	US-10-282-122A-64895	Sequence 64895, A
865	412.5	17.5	484	10	US-09-820-843A-19	Sequence 19, App
866	412.5	17.5	484	15	US-10-282-122A-64867	Sequence 64867, A
867	406.5	17.2	357	9	US-09-864-761-35807	Sequence 35807, A
868	404.5	17.1	532	15	US-10-282-122A-64658	Sequence 64658, A
869	402.5	17.0	1136	8	US-08-806-029-9	Sequence 9, App
870	402.5	17.0	1177	14	US-10-096-986-64	Sequence 64, App
871	399	16.9	1059	8	US-08-806-029-10	Sequence 10, App
872	399	16.9	1101	14	US-10-096-986-83	Sequence 83, App
873	392.5	16.6	923	15	US-10-282-122A-64474	Sequence 64474, A
874	386	16.3	778	15	US-10-282-122A-64751	Sequence 64751, A
875	383	16.2	641	14	US-10-138-098-52	Sequence 52, App
876	383	16.2	641	14	US-10-294-804-4	Sequence 4, App
877	383	16.2	641	15	US-10-225-838B-22	Sequence 22, App
878	383	16.2	641	16	US-10-732-694-11	Sequence 11, App
879	383	16.2	641	17	US-10-476-615-52	Sequence 52, App
880	380.5	16.1	837	15	US-10-282-122A-64362	Sequence 64362, A
881	378	16.0	588	15	US-10-282-122A-64869	Sequence 64869, A
882	378	16.0	646	16	US-10-406-832-27	Sequence 27, App
883	378	16.0	646	17	US-10-893-588-27	Sequence 27, App
884	375	15.9	914	15	US-10-282-122A-64606	Sequence 64606, A
885	373.5	15.8	584	15	US-10-282-122A-64903	Sequence 64903, A
886	373.5	15.8	667	15	US-10-282-122A-64494	Sequence 64494, A
887	372	15.7	615	15	US-10-282-122A-64726	Sequence 64726, A
888	371	15.7	694	15	US-10-282-122A-64786	Sequence 64786, A
889	371	15.7	651	9	US-09-861-597-1	Sequence 1, App
890	371	15.7	651	14	US-10-414-760-1	Sequence 1, App
891	371	15.7	651	17	US-10-887-100-1	Sequence 1, App
892	370.5	15.7	420	15	US-10-282-122A-64558	Sequence 64558, A
893	368	15.6	431	16	US-10-437-963-201378	Sequence 201378, A
894	367	15.5	1011	17	US-10-096-986-94	Sequence 94, App
895	366	15.5	691	17	US-10-488-056-48	Sequence 48, App
896	366	15.5	766	14	US-10-096-986-88	Sequence 88, App
897	366	15.5	799	14	US-10-096-986-89	Sequence 89, App
898	365	15.4	576	15	US-10-282-122A-64547	Sequence 64547, A
899	365	15.4	591	15	US-10-282-122A-64363	Sequence 64363, A
900	364.5	15.4	2018	14	US-10-096-986-80	Sequence 80, App
901	364	15.4	606	15	US-10-282-122A-64464	Sequence 64464, A
902	363	15.4	639	15	US-10-282-122A-64609	Sequence 64609, A
903	360	15.2	562	15	US-10-282-122A-64514	Sequence 64514, A
904	359.5	15.2	1011	15	US-10-282-122A-64589	Sequence 64589, A
905	359	15.2	525	17	US-10-488-056-54	Sequence 54, App
906	359	15.2	854	17	US-10-488-056-47	Sequence 47, App
907	358.5	15.2	486	16	US-10-437-963-117435	Sequence 117435, A
908	358.5	15.2	2055	14	US-10-096-986-81	Sequence 81, App
909	358	15.2	606	9	US-09-861-597-4	Sequence 4, App
910	358	15.2	606	9	US-09-861-597-6	Sequence 6, App
911	358	15.2	606	9	US-09-861-597-8	Sequence 8, App
912	358	15.2	606	17	US-10-887-100-4	Sequence 4, App
913	358	15.2	606	17	US-10-887-100-6	Sequence 6, App
914	358	15.2	606	17	US-10-887-100-8	Sequence 8, App
915	358	15.2	809	14	US-10-414-760-13	Sequence 13, App
916	358	15.2	818	14	US-10-414-760-22	Sequence 22, App
917	358	15.2	1617	14	US-10-414-760-14	Sequence 14, App
918	358	15.2	1626	14	US-10-414-760-24	Sequence 24, App
919	353	14.9	505	15	US-10-282-122A-62341	Sequence 62341, A
920	352	14.9	603	15	US-10-282-122A-64537	Sequence 64537, A
921	351.5	14.9	1056	8	US-08-806-029-29	Sequence 29, App
922	351	14.9	957	15	US-10-282-122A-64361	Sequence 64361, A
923	350.5	14.8	461	15	US-10-282-122A-64750	Sequence 64750, A
924	350.5	14.8	2257	14	US-10-096-986-82	Sequence 82, App
925	349	14.6	618	15	US-10-282-122A-64608	Sequence 64608, A
926	346	14.6	648	17	US-10-488-056-30	Sequence 30, App
927	344	14.6	283	9	US-09-864-761-36720	Sequence 36720, A
928	344	14.6	525	15	US-10-282-122A-64763	Sequence 64763, A
929	344	14.6	651	17	US-10-488-056-45	Sequence 45, App

930	342.5	14.5	629	16	US-10-406-832-29	Sequence 29, Appl	1027	302	12.8	714	17	US-10-887-100-10	Sequence 10, Appl
931	342.5	14.5	629	17	US-10-893-588-29	Sequence 29, Appl	1028	301.5	12.8	285	16	US-10-437-963-187773	Sequence 187773
932	342.5	14.5	629	18	US-10-282-122A-64613	Sequence 29, Appl	1029	300.5	12.7	768	16	US-08-806-023-35	Sequence 35, Appl
933	339.5	14.4	515	15	US-10-282-122A-64347	Sequence 64347, A	1030	300.5	12.7	768	14	US-10-117-931-15	Sequence 15, Appl
934	337	14.3	1002	17	US-10-488-056-46	Sequence 46, Appl	1031	299	12.7	884	14	US-10-488-056-40	Sequence 40, Appl
935	336	14.2	1169	8	US-08-806-029-33	Sequence 33, Appl	1032	297.5	12.6	373	17	US-10-437-963-122263	Sequence 122263
936	334	14.1	498	15	US-10-225-838B-21	Sequence 21, Appl	1033	296.5	12.5	1024	8	US-08-806-029-31	Sequence 31, Appl
937	334	14.1	498	15	US-10-282-122A-64610	Sequence 64610, A	1034	294.5	12.5	832	8	US-08-806-029-27	Sequence 27, Appl
938	330	14.0	447	17	US-10-488-056-29	Sequence 29, Appl	1035	294	12.4	529	9	US-09-865-597-2	Sequence 2, Appl
939	329	13.9	780	15	US-10-441-965-19	Sequence 19, Appl	1036	294	12.4	529	17	US-10-887-100-2	Sequence 2, Appl
940	329	13.9	780	16	US-10-800-179-19	Sequence 19, Appl	1037	294	12.4	821	15	US-10-292-798-1370	Sequence 1370, Ap
941	327.5	13.9	334	14	US-10-259-678-728	Sequence 728, App	1038	293.5	12.4	611	14	US-10-086-510-4	Sequence 4, Appl
942	326	13.8	422	16	US-10-437-963-121579	Sequence 121579, A	1039	293	12.4	256	10	US-09-820-843A-18	Sequence 18, Appl
943	325.5	13.8	439	15	US-10-282-122A-64905	Sequence 64905, A	1040	292	12.4	912	17	US-10-488-056-50	Sequence 50, Appl
944	324	13.7	1038	16	US-10-800-179-30	Sequence 30, Appl	1041	290.5	12.3	406	14	US-10-156-761-14828	Sequence 14828, A
945	322.5	13.6	972	8	US-08-806-029-30	Sequence 30, Appl	1042	290.5	12.3	805	14	US-10-029-386-34042	Sequence 34042, A
946	320.5	13.6	263	15	US-10-425-114-49960	Sequence 49960, A	1043	289	12.2	295	11	US-09-855-604-902	Sequence 902, App
947	320	13.5	594	15	US-10-282-122A-64397	Sequence 64397, A	1044	289	12.2	627	16	US-10-406-832-28	Sequence 28, Appl
948	320	13.5	1953	17	US-10-488-056-42	Sequence 42, Appl	1045	289	12.2	627	17	US-10-893-588-28	Sequence 28, Appl
949	319.5	13.5	318	14	US-10-259-678-727	Sequence 727, App	1046	288.5	12.2	953	8	US-08-806-029-14	Sequence 14, Appl
950	318	13.5	884	16	US-10-800-179-25	Sequence 25, Appl	1047	286	12.1	454	16	US-10-767-701-45105	Sequence 45105, A
951	317.5	13.4	988	8	US-08-806-029-28	Sequence 28, Appl	1048	286	12.1	563	17	US-10-488-056-43	Sequence 43, Appl
952	315.5	13.4	965	16	US-10-800-179-31	Sequence 31, Appl	1049	285.5	12.1	234	16	US-10-767-701-45603	Sequence 45603, A
953	314.5	13.3	1968	14	US-10-123-155-163	Sequence 163, App	1050	283.5	12.0	401	15	US-10-342-331-34	Sequence 34, Appl
954	314	13.3	116	10	US-09-764-891-2877	Sequence 2877, App	1051	283	12.0	764	15	US-10-424-599-143917	Sequence 143917, A
955	312	13.2	242	15	US-10-425-114-61520	Sequence 61520, A	1052	281.5	11.9	185	16	US-10-437-963-126075	Sequence 126075, A
956	309.5	13.1	200	9	US-09-798-584-18	Sequence 18, Appl	1053	281	11.8	223	15	US-10-424-599-244310	Sequence 244310, A
957	309.5	13.1	200	9	US-09-967-624-19	Sequence 19, Appl	1054	280	11.8	444	17	US-10-488-056-37	Sequence 37, Appl
958	309.5	13.1	200	9	US-09-998-667-18	Sequence 18, Appl	1055	280	11.8	1466	14	US-09-918-715-226	Sequence 226, App
959	309.5	13.1	200	10	US-09-921-159-34	Sequence 34, Appl	1056	280	11.8	1466	14	US-10-177-293-68	Sequence 68, Appl
960	309.5	13.1	200	10	US-09-990-940-21	Sequence 21, Appl	1057	280	11.8	1466	14	US-10-301-822-33	Sequence 33, Appl
961	309.5	13.1	200	10	US-09-989-981A-13	Sequence 13, Appl	1058	280	11.8	1466	15	US-10-257-021-72	Sequence 72, Appl
962	309.5	13.1	200	10	US-09-850-948-29	Sequence 29, Appl	1059	280	11.8	1466	16	US-10-357-851-3	Sequence 3, Appl
963	309.5	13.1	200	14	US-10-160-354-4	Sequence 4, Appl	1060	280	11.8	1466	16	US-10-358-024-3	Sequence 3, Appl
964	309.5	13.1	200	14	US-10-026-021-8	Sequence 8, Appl	1061	280	11.8	1466	16	US-10-734-564-103	Sequence 103, App
965	309.5	13.1	200	14	US-10-161-165-3	Sequence 3, Appl	1062	279	11.7	1036	17	US-10-741-849-7179	Sequence 7179, Ap
966	309.5	13.1	200	14	US-10-160-663-3	Sequence 3, Appl	1063	277.5	11.7	332	15	US-10-437-963-122258	Sequence 122258, A
967	309.5	13.1	200	14	US-10-071-838-15	Sequence 15, Appl	1064	277.5	11.7	332	15	US-10-437-963-137540	Sequence 137540, A
968	309.5	13.1	200	14	US-10-094-417-25	Sequence 25, Appl	1065	276	11.7	1040	15	US-10-282-122A-68044	Sequence 68044, A
969	309.5	13.1	200	14	US-10-188-405-13	Sequence 13, Appl	1066	276	11.7	1040	15	US-10-104-889-30	Sequence 30, Appl
970	309.5	13.1	200	14	US-10-273-575-29	Sequence 29, Appl	1067	276	11.7	1040	15	US-10-104-889-32	Sequence 32, Appl
971	309.5	13.1	200	14	US-10-233-098-5	Sequence 5, Appl	1068	276	11.7	1078	14	US-10-058-124-21	Sequence 21, Appl
972	309.5	13.1	200	14	US-10-245-850-3	Sequence 3, Appl	1069	276	11.7	1366	10	US-09-918-715-214	Sequence 214, App
973	309.5	13.1	200	14	US-10-293-582-27	Sequence 27, Appl	1070	276	11.7	1366	10	US-09-918-715-234	Sequence 234, App
974	309.5	13.1	200	14	US-10-100-818-14	Sequence 14, Appl	1071	276	11.7	1366	14	US-10-171-311-38	Sequence 38, Appl
975	309.5	13.1	200	14	US-10-237-467-18	Sequence 18, Appl	1072	276	11.7	1366	14	US-10-301-822-31	Sequence 31, Appl
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977	309.5	13.1	200	14	US-10-179-766-12	Sequence 12, Appl	1074	275	11.6	208	14	US-10-029-386-33055	Sequence 33055, A
978	309.5	13.1	200	14	US-10-123-568-4	Sequence 4, Appl	1075	275	11.6	525	15	US-10-755-889-650	Sequence 650, App
979	309.5	13.1	200	14	US-10-123-731-10	Sequence 10, Appl	1076	275	11.6	593	15	US-10-435-696-50	Sequence 50, Appl
980	309.5	13.1	200	15	US-10-308-393-53	Sequence 53, Appl	1077	274	11.6	593	15	US-10-435-696-50	Sequence 50, Appl
981	309.5	13.1	200	15	US-10-352-724-5	Sequence 5, Appl	1078	272.5	11.5	696	15	US-10-441-965-21	Sequence 21, Appl
982	309.5	13.1	200	15	US-10-352-724-5	Sequence 5, Appl	1079	272	11.5	696	8	US-08-806-029-36	Sequence 36, Appl
983	309.5	13.1	200	15	US-10-452-015-3	Sequence 3, Appl	1080	272	11.5	696	15	US-10-441-965-23	Sequence 23, Appl
984	309.5	13.1	200	15	US-10-364-861-94	Sequence 94, Appl	1081	272	11.5	750	8	US-08-806-029-25	Sequence 25, Appl
985	309.5	13.1	200	15	US-10-231-956A-521	Sequence 521, App	1082	271.5	11.5	370	15	US-10-282-122A-64566	Sequence 64566, A
986	309.5	13.1	200	15	US-10-255-775-3	Sequence 3, Appl	1083	271.5	11.5	2338	14	US-10-029-386-31982	Sequence 31982, A
987	309.5	13.1	200	15	US-10-459-190-24	Sequence 24, Appl	1084	270.5	11.4	1368	16	US-10-437-963-108730	Sequence 2, Appl
988	309.5	13.1	200	15	US-10-339-744-4	Sequence 4, Appl	1085	270.5	11.4	1366	16	US-10-357-851-2	Sequence 2, Appl
989	309.5	13.1	200	16	US-10-649-400-7	Sequence 7, Appl	1086	270.5	11.4	1366	16	US-10-358-024-2	Sequence 2, Appl
990	309.5	13.1	200	16	US-10-620-052A-78	Sequence 78, Appl	1087	270.5	11.4	1366	16	US-10-788-792-153	Sequence 153, App
991	309.5	13.1	200	17	US-10-616-403-7	Sequence 40, Appl	1088	270	11.4	920	15	US-10-292-798-1514	Sequence 1514, Ap
992	309.5	13.1	200	9	US-09-818-094-40	Sequence 40, Appl	1089	270	11.4	1466	15	US-10-402-089-12	Sequence 12, Appl
993	309.5	13.1	201	9	US-09-848-990-22	Sequence 22, Appl	1090	269.5	11.4	1466	15	US-10-402-072A-12	Sequence 12, Appl
994	309.5	13.1	201	9	US-09-760-364-14	Sequence 14, Appl	1091	269.5	11.4	360	17	US-10-488-056-31	Sequence 31, Appl
995	309.5	13.1	201	11	US-09-754-947-5	Sequence 5, Appl	1092	268.5	11.4	278	15	US-10-425-114-54522	Sequence 54522, A
996	309.5	13.1	201	15	US-10-339-744-5	Sequence 5, Appl	1093	268.5	11.4	287	16	US-10-437-963-161543	Sequence 161543, A
997	309.5	13.1	1670	14	US-10-123-155-325	Sequence 325, App	1094	268.5	11.3	1027	15	US-10-360-101-221	Sequence 221, App
998	307.5	12.9	242	16	US-10-471-587A-1	Sequence 1, Appl	1095	267.5	11.3	1366	14	US-10-058-124-19	Sequence 19, Appl
999	304.5	12.9	889	15	US-08-806-029-19	Sequence 19, Appl	1096	266	11.3	1366	15	US-10-257-021-76	Sequence 76, Appl
1000	302	12.8	592	15	US-10-369-493-17534	Sequence 17534, A	1097	265.5	11.2	1088	16	US-10-437-963-158455	Sequence 158455, A
1001	302	12.8	714	9	US-09-861-597-10	Sequence 10, Appl	1098	265.5	11.2	265	16	US-10-437-963-154907	Sequence 154907, A
1002	302	12.8					1099	265.5	11.2	568	14	US-10-086-510-5	Sequence 5, Appl

1100	265.5	11.2	1366	15	US-10-402-089-10	Sequence 10, Appl	1185	244	10.3	492	16	US-10-639-286-12	Sequence 12, Appl
1101	265.5	11.2	1366	15	US-10-402-072A-10	Sequence 10, Appl	1186	244	10.3	591	14	US-10-233-553-23	Sequence 23, Appl
1102	265	11.2	343	14	US-10-148-306-21	Sequence 21, Appl	1187	243.5	10.3	1046	14	US-10-156-761-10088	Sequence 10088, A
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1104	264.5	11.2	1008	15	US-10-342-331-8	Sequence 8, Appl	1191	243	10.3	714	14	US-10-233-885-44	Sequence 44, Appl
1105	264.5	11.2	1008	15	US-10-441-965-22	Sequence 22, Appl	1191	243	10.3	714	14	US-10-233-885-44	Sequence 44, Appl
1106	264.5	11.2	1063	16	US-10-800-179-29	Sequence 29, Appl	1192	243	10.3	714	14	US-10-231-581-44	Sequence 10, Appl
1107	264.5	11.2	1065	14	US-10-117-931-16	Sequence 16, Appl	1193	243	10.3	714	15	US-10-326-508A-15	Sequence 15, Appl
1108	263.5	11.2	920	14	US-10-017-161-1858	Sequence 1858, Ap	1194	243	10.3	1017	16	US-10-639-286-10	Sequence 10, Appl
1109	262.5	11.1	1466	15	US-10-402-089-4	Sequence 4, Appl	1195	242.5	10.3	345	15	US-10-425-114-42660	Sequence 42660, A
1110	262.5	11.1	1466	15	US-10-402-089-6	Sequence 6, Appl	1196	242.5	10.3	940	15	US-10-291-172-363	Sequence 363, App
1111	262.5	11.1	1466	15	US-10-402-072A-4	Sequence 4, Appl	1197	242.5	10.3	940	15	US-10-221-278-363	Sequence 363, App
1112	262.5	11.1	1466	15	US-10-402-072A-6	Sequence 6, Appl	1198	242.5	10.3	1014	17	US-10-901-816A-9	Sequence 9, Appl
1113	260.5	11.0	2498	14	US-10-123-155-483	Sequence 483, App	1199	242.5	10.3	1014	17	US-10-901-816A-11	Sequence 11, Appl
1116	259.5	11.0	399	17	US-10-488-056-41	Sequence 41, Appl	1200	242.5	10.3	1496	14	US-10-177-293-70	Sequence 70, Appl
1127	258.5	10.9	478	15	US-10-425-114-58912	Sequence 58912, A	1201	242.5	10.3	1496	14	US-10-301-822-35	Sequence 35, Appl
1128	258.5	10.9	480	15	US-10-425-114-61022	Sequence 61022, A	1202	242.5	10.3	1496	15	US-10-236-031B-74	Sequence 74, Appl
1129	257	10.9	974	15	US-10-282-122A-44999	Sequence 44999, A	1203	242.5	10.3	1496	16	US-10-468-091-22	Sequence 22, Appl
1130	254	10.7	1040	8	US-08-806-029-32	Sequence 32, Appl	1204	242.5	10.3	1496	16	US-10-788-792-248	Sequence 248, App
1131	254	10.7	1745	10	US-09-795-061-4	Sequence 4, Appl	1205	242	10.2	319	16	US-10-437-963-148500	Sequence 148500,
1132	253	10.7	780	15	US-10-441-965-25	Sequence 25, Appl	1206	242	10.2	319	15	US-10-282-122A-62423	Sequence 62423, A
1133	253	10.7	1014	14	US-10-194-441A-1	Sequence 1, Appl	1207	242	10.2	3721	14	US-10-123-155-543	Sequence 543, App
1134	253	10.7	1217	14	US-10-311-406-2	Sequence 2, Appl	1220	241.5	10.2	185	16	US-10-437-963-182893	Sequence 182893,
1135	253	10.7	1418	14	US-10-058-124-20	Sequence 20, Appl	1221	241.5	10.2	968	15	US-10-291-172-739	Sequence 739, App
1136	253	10.7	1418	14	US-10-468-091-5	Sequence 5, Appl	1222	241.5	10.2	968	15	US-10-221-278-739	Sequence 739, App
1137	252.5	10.7	455	15	US-10-425-114-65134	Sequence 65134, A	1226	241	10.2	342	17	US-10-488-056-39	Sequence 39, Appl
1138	252.5	10.7	529	15	US-10-425-114-49406	Sequence 49406, A	1227	241	10.2	1744	14	US-10-369-493-5832	Sequence 5832, Ap
1139	252.5	10.7	1014	17	US-10-901-816A-12	Sequence 12, Appl	1228	240.5	10.2	943	15	US-10-193-002-139	Sequence 199, App
1140	252	10.7	1497	16	US-10-468-091-23	Sequence 23, Appl	1229	240.5	10.2	943	14	US-10-084-843-204	Sequence 204, App
1141	251.5	10.6	462	10	US-09-919-039-324	Sequence 324, App	1230	240.5	10.2	1159	15	US-10-104-889-6	Sequence 6, Appl
1142	250.5	10.6	284	10	US-09-804-014A-24	Sequence 24, Appl	1231	240.5	10.2	1637	16	US-10-437-963-180397	Sequence 180397,
1143	250.5	10.6	585	9	US-09-738-626-6032	Sequence 6032, Ap	1232	240	10.2	678	15	US-10-282-122A-64573	Sequence 64573, A
1144	250	10.6	597	9	US-09-793-306-146	Sequence 146, App	1233	240	10.2	1212	15	US-10-331-496A-26	Sequence 26, Appl
1145	249.5	10.6	669	15	US-10-282-122A-53462	Sequence 53462, A	1236	239.5	10.1	264	16	US-10-437-963-135092	Sequence 135092,
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1147	247.5	10.5	943	10	US-09-997-182-131	Sequence 131, App	1238	239.5	10.1	663	14	US-10-156-761-9799	Sequence 9799, Ap
1148	247.5	10.5	943	10	US-09-997-181-131	Sequence 131, App	1239	239.5	10.1	1057	15	US-10-104-889-16	Sequence 16, Appl
1149	247.5	10.5	1739	10	US-09-795-061-2	Sequence 2, Appl	1240	239.5	10.1	1464	15	US-09-918-715-261	Sequence 161, App
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1151	246.5	10.4	595	15	US-10-342-331-48	Sequence 48, Appl	1242	239.5	10.1	1464	14	US-10-171-311-36	Sequence 36, Appl
1152	246.5	10.4	595	15	US-10-342-331-50	Sequence 50, Appl	1243	239.5	10.1	1464	14	US-10-149-352-2	Sequence 2, Appl
1153	246.5	10.4	822	15	US-10-342-331-49	Sequence 49, Appl	1244	239.5	10.1	1464	14	US-10-177-293-65	Sequence 65, Appl
1154	246.5	10.4	1341	14	US-10-058-124-18	Sequence 18, Appl	1245	239.5	10.1	1464	14	US-10-301-822-28	Sequence 28, Appl
1155	246.5	10.4	1453	16	US-10-468-091-26	Sequence 26, Appl	1246	239.5	10.1	1464	16	US-10-734-564-79	Sequence 79, Appl
1156	245.5	10.4	135	16	US-10-437-963-122260	Sequence 122260,	1247	239	10.1	584	15	US-10-282-122A-50604	Sequence 50604, A
1157	245.5	10.4	354	14	US-09-820-843A-21	Sequence 21, Appl	1248	239	10.1	662	14	US-10-233-175-33	Sequence 33, Appl
1158	245.5	10.4	1014	14	US-10-194-441A-48	Sequence 48, Appl	1249	239	10.1	960	15	US-10-342-331-6	Sequence 6, Appl
1159	245.5	10.4	1449	15	US-10-402-089-8	Sequence 8, Appl	1250	239	10.1	1463	15	US-10-402-089-2	Sequence 2, Appl
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1163	245	10.4	1684	16	US-10-408-765A-811	Sequence 811, App	1254	238.5	10.1	1471	14	US-10-123-155-281	Sequence 281, App
1164	244.5	10.3	492	16	US-10-639-286-11	Sequence 11, Appl	1267	238	10.1	498	17	US-10-901-816A-1	Sequence 1, Appl
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1166	244.5	10.3	660	17	US-10-901-816A-4	Sequence 4, Appl	1269	238	10.1	2380	16	US-10-239-399A-19	Sequence 19, Appl
1167	244.5	10.3	1002	14	US-10-117-931-25	Sequence 25, Appl	1270	237.5	10.1	185	16	US-10-437-963-121283	Sequence 121283,
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1169	244.5	10.3	1014	17	US-10-901-816A-6	Sequence 6, Appl	1272	237	10.0	628	16	US-10-437-963-158059	Sequence 158059,
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1171	244.5	10.3	1014	17	US-10-901-816A-8	Sequence 8, Appl	1274	236.5	10.0	1465	14	US-10-096-986-74	Sequence 74, Appl
1172	244.5	10.3	1014	17	US-10-901-816A-9	Sequence 9, Appl	1275	236	10.0	552	15	US-10-342-331-7	Sequence 7, Appl
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1176	244.5	10.3	1171	15	US-10-104-889-8	Sequence 8, Appl	1279	234.5	9.9	510	14	US-10-232-175-26	Sequence 26, Appl
1177	244.5	10.3	1388	15	US-10-104-889-10	Sequence 10, Appl	1280	234.5	9.9	936	17	US-08-806-029-26	Sequence 26, Appl
1178	244.5	10.3	1461	16	US-10-468-091-25	Sequence 25, Appl	1281	234.5	9.9	2944	17	US-10-741-600-1629	Sequence 1629, Ap
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1183	244.5	10.3	1464	16	US-10-788-792-150	Sequence 150, App	1286	232.5	9.8	416	14	US-10-234-175-25	Sequence 25, Appl
1184	244	10.3	266	14	US-10-148-306-20	Sequence 20, Appl	1289	232	9.8	391	15	US-10-425-114-56680	Sequence 56680, A
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1302	230.5	9.8	936	14	US-10-117-931-30	Sequence 30, Appl
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1306	228.5	9.7	430	16	US-10-451-467A-314	Sequence 314, App
1307	228.5	9.7	733	15	US-10-138-588-40	Sequence 40, Appl
1308	228	9.6	189	16	US-10-437-963-170736	Sequence 170736,
1309	227.5	9.6	166	16	US-10-437-963-112933	Sequence 112933,
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1314	227	9.6	703	14	US-10-219-449-4	Sequence 4, Appli
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1316	227	9.6	1621	14	US-10-185-990-10	Sequence 10, Appl
1317	227	9.6	1626	14	US-10-185-990-11	Sequence 11, Appl
1318	227	9.6	1759	15	US-10-369-493-7032	Sequence 7032, Ap
1319	227	9.6	2502	17	US-10-741-600-1627	Sequence 1627, Ap
1320	226.5	9.6	448	15	US-10-244-596-14	Sequence 14, Appl
1321	226	9.6	189	16	US-10-437-963-125315	Sequence 125315,
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1323	226	9.6	1669	15	US-10-372-683-8	Sequence 8, Appli
1324	225.5	9.5	308	15	US-10-424-599-247149	Sequence 247149,
1325	225	9.5	2368	14	US-10-123-155-423	Sequence 423, App
1326	224.5	9.5	197	15	US-10-425-114-67750	Sequence 67750, A
1327	224.5	9.5	748	15	US-10-342-331-10	Sequence 10, Appl
1328	224	9.5	1497	14	US-10-157-031-128	Sequence 128, App
1329	223	9.4	378	14	US-10-117-931-26	Sequence 26, Appl
1330	222.5	9.4	966	14	US-10-117-931-34	Sequence 34, Appl
1331	221.5	9.4	326	16	US-10-437-963-201447	Sequence 201447,
1332	221.5	9.4	979	15	US-10-282-122A-47372	Sequence 47372, A
1333	221	9.4	214	6	US-10-437-963-119143	Sequence 119143,
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1335	220.5	9.3	192	16	US-10-437-963-143943	Sequence 143943,
1336	220	9.3	1838	14	US-10-123-155-289	Sequence 289, App
1337	219.5	9.3	168	14	US-10-096-986-52	Sequence 52, Appl
1338	219.5	9.3	1019	15	US-10-236-031B-72	Sequence 72, Appl
1339	219.5	9.3	2276	14	US-10-123-155-9	Sequence 9, Appli
1340	219	9.3	716	14	US-10-156-761-15050	Sequence 15050, A
1341	219	9.3	775	14	US-10-156-761-12824	Sequence 12824, A
1342	218.5	9.2	684	14	US-10-157-031-62	Sequence 62, Appl
1343	218	9.2	202	16	US-10-437-963-133505	Sequence 133505,
1344	218	9.2	215	15	US-10-425-114-68305	Sequence 68305, A
1345	218	9.2	284	17	US-10-488-056-34	Sequence 34, Appl
1346	218	9.2	360	16	US-10-437-963-118547	Sequence 118547,
1347	216.5	9.2	595	9	US-09-738-973-187	Sequence 187, App
1348	216.5	9.2	595	9	US-09-854-133-187	Sequence 187, App
1349	216.5	9.2	595	14	US-10-144-649A-187	Sequence 187, App
1350	216.5	9.2	828	16	US-10-789-378-24	Sequence 24, Appl
1351	216.5	9.2	863	15	US-10-112-944-366	Sequence 366, App
1352	216.5	9.2	999	17	US-10-486-678-14	Sequence 14, Appl
1353	216.5	9.2	1019	17	US-10-486-678-13	Sequence 13, Appl
1354	216.5	9.2	2956	14	US-10-123-155-15	Sequence 15, Appl
1355	216	9.1	195	16	US-10-437-963-157867	Sequence 157867,
1356	216	9.1	446	16	US-10-437-963-142366	Sequence 142366,
1357	216	9.1	638	13	US-10-001-887-108	Sequence 108, App
1358	216	9.1	638	17	US-10-958-863-108	Sequence 108, App
1359	215.5	9.1	494	9	US-09-925-302-690	Sequence 690, App
1360	215.5	9.1	494	10	US-09-925-302-690	Sequence 690, App

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OM protein - protein search, using sw model

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920.334 Million cell updates/sec

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Searched: 283416 seqs, 96216763 residues

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Listing first 1500 summaries

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3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	450.5	19.1	1079	2 B70807	hypothetical glyci
2	439.5	18.6	1306	2 A70934	hypothetical glyci
3	423	17.9	396	2 T49109	glycine-rich prote
4	415.5	17.6	1381	2 F70806	hypothetical glyci
5	412.5	17.5	484	2 F70846	hypothetical glyci
6	406	17.2	1901	2 F70806	hypothetical glyci
7	404.5	17.1	532	2 F70580	hypothetical glyci
8	403	17.1	1489	2 D70807	hypothetical glyci
9	400.5	16.9	1538	2 H70846	hypothetical glyci
10	399.5	16.9	853	2 A70896	hypothetical glyci
11	395	16.7	714	2 A70807	hypothetical glyci
12	395	16.7	1660	2 A70869	hypothetical glyci
13	392.5	16.6	923	2 E70820	hypothetical glyci
14	392	16.6	731	2 C70974	hypothetical glyci
15	392	16.6	1329	2 E70917	hypothetical glyci
16	386	16.3	778	2 F70963	hypothetical glyci
17	383.5	16.2	767	2 F70895	hypothetical glyci
18	383	16.2	641	1 Q0B31	nuclear antigen EB
19	381.5	16.1	741	2 G70917	hypothetical glyci
20	380.5	16.1	837	2 E70835	hypothetical glyci
21	379	16.0	465	1 S01820	glycine-rich cell
22	378	16.0	588	2 F70971	hypothetical glyci
23	376.5	15.9	749	2 A70812	hypothetical glyci
24	375	15.9	914	2 H70987	hypothetical glyci
25	373.5	15.8	584	2 G70804	hypothetical glyci
26	373.5	15.8	667	2 A70893	hypothetical glyci
27	372	15.7	694	2 F70868	hypothetical glyci
28	371	15.7	615	2 H70589	hypothetical glyci
29	371	15.7	718	2 A36068	major ampullate fi

30	370.5	15.7	491	2 D70916	hypothetical glyci
31	369.5	15.6	1428	2 T08852	lustrin A - Califo
32	366	15.5	408	2 S57483	glycin-rich protei
33	365.5	15.5	496	2 H70839	hypothetical glyci
34	365	15.4	576	2 A70900	hypothetical glyci
35	365	15.4	591	2 B70523	hypothetical glyci
36	364.5	15.4	801	2 F70824	hypothetical glyci
37	364	15.4	606	2 H70816	hypothetical glyci
38	363	15.4	481	2 A35628	hypothetical glyci
39	363	15.4	639	2 D70931	hypothetical glyci
40	360	15.2	562	2 B70953	hypothetical glyci
41	359.5	15.2	1011	2 F70820	hypothetical glyci
42	359	15.2	463	2 B70893	hypothetical glyci
43	358.5	15.2	338	1 K0MU	glycine-rich cell
44	355	15.0	291	1 S31415	glycine-rich prote
45	352.5	14.9	384	1 A26099	hypothetical glyci
46	352	14.9	274	2 T25404	hypothetical glyci
47	352	14.9	603	2 A70770	hypothetical glyci
48	351	14.9	957	2 D70835	hypothetical glyci
49	350.5	14.8	461	2 F70571	hypothetical glyci
50	350	14.8	316	1 A38743	hypothetical glyci
51	349	14.8	618	2 A70989	hypothetical glyci
52	349	14.8	882	2 B70812	hypothetical glyci
53	345	14.6	713	1 UMMS	period clock prote
54	345	14.6	966	2 A33626	fibrinogen alpha c
55	344	14.6	525	2 D70878	hypothetical glyci
56	344	14.6	783	2 E70824	hypothetical glyci
57	342	14.5	515	2 H70663	hypothetical glyci
58	339.5	14.4	487	2 E70983	hypothetical glyci
59	339	14.3	937	2 S58135	hypally regulated
60	335	14.2	434	2 E70768	hypothetical glyci
61	334	14.1	255	2 B84777	hypothetical prote
62	334	14.1	498	2 C70720	hypothetical glyci
63	329	13.9	549	2 T20720	hypothetical prote
64	325.5	13.8	439	2 D70954	hypothetical glyci
65	322	13.6	1207	2 T23754	hypothetical prote
66	320	13.5	594	2 G70545	hypothetical glyci
67	315	13.3	302	2 C84470	hypothetical glyci
68	314.5	13.3	543	2 F70726	hypothetical glyci
69	312.5	13.2	252	1 S01821	glycine-rich prote
70	308.5	13.1	2639	2 T31328	fibroin - Chinese
71	308	13.0	271	2 S34666	glycine-rich prote
72	306.5	13.0	419	1 OZZQAM	circumsporozoite p
73	306	12.9	284	2 T23158	hypothetical prote
74	302	12.8	592	2 E82759	endo-1,4-beta-gluc
75	301	12.7	485	2 A60610	circumsporozoite p
76	300.5	12.7	622	2 I37984	keratin 9, type I
77	299.5	12.7	3198	2 A43426	collagen alpha 2 f
78	298.5	12.6	210	2 JQ1060	glycine-rich prote
79	298.5	12.6	2174	2 E95965	hypothetical glyci
80	296.5	12.5	1585	2 T31611	hypothetical prote
81	296	12.5	627	2 A4112	spidroin 2, dragli
82	293.5	12.4	794	2 T10519	pre-pro-legumin -
83	293	12.4	256	2 A70514	hypothetical glyci
84	290.5	12.3	749	2 I38488	trophinin - human
85	290	12.3	543	2 S19933	glycine-rich prote
86	290	12.3	751	2 S64741	cuticle collagen -
87	289	12.2	1414	1 S23809	collagen alpha 2(I
88	288.5	12.2	528	2 G02127	fus-like protein -
89	287	12.1	13288	2 T03099	mucin, submaxillar
90	286	12.1	286	2 C61615	sericin MG-2 - gre
91	283	12.0	1051	2 A35763	collagen alpha 2 c
92	282	11.9	543	2 T49892	glycine-rich prote
93	280	11.8	1466	1 CGHU7L	collagen alpha 1(I
94	278.5	11.8	526	1 S33799	RNA-binding protei
95	278	11.8	220	2 T14441	glycine-rich prote
96	278	11.8	270	2 A60830	keratin, 70k type
97	277	11.7	256	2 T03371	glycine-rich prote
98	276.5	11.7	682	2 T28899	hypothetical prote
99	275	11.6	1172	2 T32759	hypothetical prote
100	274	11.6	593	1 KRHU0	keratin 10, type I
101	274	11.6	730	2 F96559	hypothetical prote
102	274	11.6	3016	2 S77300	hypothetical prote

103	273.5	11.6	183	2	PN0109	keratin-like prote	176	240	10.2	170	2	JC2213	hypothetical 14.7K
104	272.5	11.5	1373	1	A43291	collagen alpha 2(I	177	240	10.2	678	2	S31521	probable PPE prote
105	272.5	11.5	1492	2	A00333	collagen alpha 1(I	178	239.5	10.1	812	2	S31521	collagen COLF1 - f
106	272	11.5	375	2	JS0427	S-antigen precursor	179	239.5	10.1	1669	1	CGMS4B	collagen alpha 1(I
107	272	11.5	1156	2	T43326	germline RNA helic	180	239	10.1	1806	1	CGHU1E	eggshell protein 1(X
108	271.5	11.5	370	2	G70872	hypothetical glyci	181	238.5	10.1	212	2	A44994	eggshell protein 1
109	271	11.5	681	2	AB2155	hypothetical prote	182	238.5	10.1	387	2	C41156	circumsporozoite p
110	270.5	11.4	1027	2	S28774	collagen alpha cha	183	238.5	10.1	387	2	D41156	circumsporozoite p
111	270	11.4	1844	2	T51890	related to Nup98-N	184	237	10.0	570	2	S07330	keratin, epidermal
112	269	11.4	361	2	G70682	hypothetical glyci	185	236.5	10.0	220	2	A44805	eggshell protein p
113	269	11.4	1366	1	CGHU2S	collagen alpha 2(I	186	236.5	10.0	1733	1	B45344	probable nuclear a
114	268.5	11.4	259	2	T15126	hypothetical prote	187	236	10.0	888	2	S28791	collagen alpha 1(X
115	268	11.3	183	1	KNR2G2	glycine-rich cell	188	235	9.9	839	2	F75518	hypothetical prote
116	266	11.3	683	2	A82704	1,4-beta-cellobios	189	234.5	9.9	207	2	B44994	eggshell protein 2
117	265.5	11.2	568	2	JC7210	molluscan shell ma	190	234.5	9.9	419	2	T14448	oleosin homolog pc
118	265.5	11.2	615	2	F70663	probable PPE prote	191	234.5	9.9	438	2	S53787	collagen alpha cha
119	263	11.1	435	2	T15143	hypothetical prote	192	234.5	9.9	2109	1	I50421	aggreccan precursor
120	263	11.1	1752	2	A45407	collagen alpha 3(I	193	234.5	9.9	2944	2	A54849	collagen alpha 1(V
121	262.5	11.1	645	2	F70825	probable PPE prote	194	234.5	9.9	3507	2	T34513	hypothetical prote
122	262.5	11.1	1049	1	CGH078	collagen alpha 1(I	195	234	9.9	227	2	B41342	circumsporozoite p
123	262.5	11.1	2038	2	A43742	female sterile hom	196	234	9.9	1655	2	T13998	gene mastermind pr
124	262	11.1	1549	2	I48103	type VII collagen	197	233.5	9.9	165	1	KNR2G1	glycine-rich cell
125	260	11.0	730	2	A36226	collagen alpha 1 c	198	233.5	9.9	171	2	H84709	probable glycine-r
126	260	11.0	1486	1	B40333	collagen alpha 1(I	199	233.5	9.9	180	2	T28938	hypothetical prote
127	258.5	10.9	462	4	S33798	FUS/CHOP mutant fu	200	233	9.9	783	2	T35389	probable serine-th
128	257.5	10.9	386	1	S22315	snRNP-associated p	201	233	9.9	864	1	EART	elastin precursor
129	257.5	10.9	581	1	KRMS2	keratin, type II c	202	232.5	9.8	290	2	T23416	hypothetical prote
130	257.5	10.9	1464	2	S59856	collagen alpha 1(I	203	232.5	9.8	643	1	KRHU2	keratin I, type II
131	255.5	10.8	589	2	S71954	RNA/ssDNA-binding	204	231.5	9.8	244	2	T49893	glycine-rich prote
132	255	10.8	632	2	S42731	collagen alpha 1 c	205	231	9.8	221	2	T04592	glycine-rich cell
133	254	10.7	1747	2	A54121	collagen alpha-4 c	206	231	9.8	413	2	E70661	probable PE protei
134	253.5	10.7	401	1	OZZQAC	circumsporozoite p	207	231	9.8	1758	2	T29350	hypothetical prote
135	253.5	10.7	539	2	T28770	hypothetical prote	208	230.5	9.8	1300	2	T03166	probable PPE prote
136	253	10.7	1217	2	S52714	sericinB - silkwo	209	230.5	9.8	3157	2	D61615	probable PPE prote
137	253	10.7	1487	1	CGHU6C	collagen alpha 1(I	210	230	9.7	115	2	D61615	sericin MG-1 - gre
138	252.5	10.7	404	2	F54729	RNA-binding protei	211	230	9.7	1778	2	T50074	probable nucleopor
139	252	10.7	582	2	F70675	probable PPE prote	212	229.5	9.7	569	1	KRMSE1	keratin, 59K type
140	252	10.7	149607	2	I49607	procollagen type V	213	229	9.7	162	2	C85356	glycine-rich prote
141	251.5	10.6	490	2	T05444	hypothetical prote	214	229	9.7	391	2	T08224	COR39 protein - wh
142	251.5	10.6	860	1	EMAS	elastin precursor	215	228.5	9.7	190	2	B48571	circumsporozoite p
143	251	10.6	429	2	A45504	circumsporozoite p	216	228.5	9.7	430	1	HHBYD8	heat shock protein
144	251	10.6	671	1	CGRT1S	collagen alpha 1(I	217	228.5	9.7	555	2	S70791	vsaB protein - Myc
145	249.5	10.6	395	2	A41156	circumsporozoite p	218	228.5	9.7	561	2	A31994	keratin 10, type I
146	249.5	10.6	940	2	JB0291	circumsporozoite p	219	228	9.6	373	2	A40777	heterogeneous ribo
147	249	10.5	590	2	F70946	probable PPE prote	220	228	9.6	920	2	B34493	collagen alpha 1(I
148	248.5	10.5	1032	2	G89427	protein T08D2.3 [i	221	227.5	9.6	180	2	T49530	related to glycine
149	248	10.5	343	2	T05221	hypothetical prote	222	227	9.6	371	2	E88633	protein F56B3.1 [i
150	248	10.5	385	2	S40778	ribonucleoprotein	223	227	9.6	402	1	CGBO2S	collagen alpha 2(I
151	247.5	10.5	1418	2	T45467	collagen alpha 1(I	224	227	9.6	1210	2	A25547	ice nucleation pro
152	247.5	10.5	3300	2	D70575	probable PPE prote	225	227	9.6	1759	2	T29351	collagen alpha 2(I
153	246.5	10.4	1453	2	S21626	collagen alpha 1(I	226	226.5	9.6	326	2	A41732	heterogeneous ribo
154	246.5	10.4	1464	1	CGHU1S	collagen alpha 1(I	227	226.5	9.6	469	2	T06987	dehydrin homolog W
155	246.5	10.4	1958	2	B40505	hypothetical prote	228	226.5	9.6	641	2	T30076	hypothetical prote
156	245.5	10.4	354	2	B70663	probable PPE prote	229	226.5	9.6	918	2	S23377	collagen alpha 2(V
157	245.5	10.4	636	2	S41067	collagen alpha 1(I	230	226.5	9.6	1022	2	S04111	collagen alpha 2(V
158	245.5	10.4	1419	2	A41182	collagen alpha 1(I	231	226	9.6	1669	1	CGHU4B	collagen alpha 1(I
159	245.5	10.4	1487	2	B41182	collagen alpha 1(I	232	225.5	9.5	1113	2	S28925	nuclear pore compl
160	245	10.4	886	2	F50694	collagen alpha 1(I	233	224	9.5	167	2	S21359	keratin, type I, c
161	245	10.4	1684	2	T02367	hypothetical prote	234	224	9.5	404	2	B84745	probable RNA-bind
162	243	10.3	424	2	T08093	oleosin homolog ST	235	224	9.5	447	2	T42987	hypothetical prote
163	243	10.3	1226	2	T04045	hypothetical prote	236	224	9.5	1532	2	A61262	collagen alpha 1(X
164	242.5	10.3	1205	2	T07959	probable cell wall	237	223.5	9.5	572	2	T08509	trbl protein - Ent
165	242.5	10.3	1496	1	CGHU2V	collagen alpha 2(I	238	223	9.4	545	2	T15667	hypothetical prote
166	242.5	10.3	1775	2	A31893	collagen alpha 1(I	239	223	9.4	1200	1	SNFSO	ice nucleation pro
167	242	10.2	385	2	T20410	hypothetical prote	240	222.5	9.4	1063	2	D86731	hypothetical prote
168	242	10.2	779	1	CGBO1S	collagen alpha 1(I	241	222.5	9.4	1761	2	T13990	collagen type IV a
169	241.5	10.2	608	2	T05442	glycine-rich prote	242	222.5	9.4	2523	2	F70846	probable PPE prote
170	241.5	10.2	1042	1	CGCH1S	collagen alpha 1(I	243	222	9.4	365	2	A34840	heterogeneous ribo
171	241	10.2	380	2	A48295	collagen 1 - marin	244	222	9.4	552	2	T06064	probable PPE prote
172	241	10.2	964	1	CGCH2S	collagen alpha 2(I	245	222	9.4	1691	1	CGHU6B	collagen alpha 6(I
173	241	10.2	1546	1	CGHU2E	collagen alpha 2(X	246	221.5	9.4	173	2	JQ1064	glycine-rich prote
174	241	10.2	1744	2	S40991	collagen alpha 1(I	247	221	9.4	310	2	I50696	collagen alpha 1(I
175	240.5	10.2	673	1	CGBO6C	collagen alpha 1(I	248	221	9.4	575	2	T52420	dehydrin 5 [import

249	221	9.4	575	2	S35327	protein kinase egg	322	204.5	8.7	770	2	S59623	tropoelastin - she
250	220.5	9.3	316	2	T20497	hypothetical prote	323	204.5	8.7	1019	1	A32856	collagen alpha 1(V
251	220.5	9.3	618	2	H70552	probable ppg prote	324	204	8.6	177	2	A31204	eggshell protein p
252	220.5	9.3	645	2	A44861	keratin, 67K type	325	204	8.6	228	2	S19932	glycine-rich prote
253	220	9.3	917	2	S09646	collagen alpha 2(V	326	204	8.6	547	2	A36046	collagen alpha cha
254	220	9.3	1018	1	CGHU2A	collagen alpha 2(V	327	204	8.6	1146	2	A38587	collagen, cornea-s
255	219.5	9.3	207	2	T07381	glycine-rich prote	328	203	8.6	223	2	B96506	hypothetical prote
256	219.5	9.3	2248	2	A35938	profilaggrin - hum	329	203	8.6	680	2	T08080	probable myrosinas
257	218	9.2	287	2	A60643	antigen 5401 - Bim	330	203	8.6	825	2	JC4163	DNA-binding protei
258	217.5	9.2	1880	2	T18531	tractin - medicina	331	203	8.6	1034	2	JC2143	ice nucleation act
259	217	9.2	575	2	S27761	dehydrin Dhn5 - ba	332	203	8.6	2327	2	T42630	aggreacan - bovine
260	216.5	9.2	674	2	S13301	collagen alpha 1(X	333	202.5	8.6	351	2	B34840	heterogeneous ribo
261	216.5	9.2	2090	2	S26058	probable transform	334	202.5	8.6	677	2	S23296	collagen alpha 2(I
262	216	9.1	409	2	T20847	hypothetical prote	335	202.5	8.6	1028	1	CGHU1A	collagen alpha 1(V
263	215.5	9.1	2132	1	A55182	aggreacan precursor	336	202.5	8.6	3176	2	CGHU3A	collagen alpha 3(V
264	215	9.1	200	2	S10334	glycine-rich prote	337	202	8.5	430	2	S52700	NUP42 protein - Ye
265	215	9.1	479	2	F70573	hypothetical prote	338	201.5	8.5	393	2	T20268	hypothetical prote
266	215	9.1	1029	1	S21369	collagen alpha 2(V	339	201	8.5	1712	1	CGHU2B	collagen alpha 2(I
267	215	9.1	1567	2	S11672	ice nucleation pro	340	200.5	8.5	312	2	T25048	hypothetical prote
268	215	9.1	1690	1	CGHU1B	collagen alpha 4(I	341	200.5	8.5	353	2	B34504	heterogeneous nucl
269	215	9.1	1838	1	CGHU1V	collagen alpha 1(V	342	200.5	8.5	623	1	S33167	gene pointed prote
270	215	9.1	1843	2	S18803	collagen alpha 1(V	343	200.5	8.5	675	2	S20819	collagen alpha 3(I
271	214.5	9.1	290	2	A32249	collagen - sea urc	344	200.5	8.5	2232	2	T34434	hypothetical prote
272	214.5	9.1	388	2	T29173	hypothetical prote	345	200	8.5	1096	2	H86237	protein F14N23.29
273	214.5	9.1	465	2	F75524	hypothetical prote	346	200	8.5	1258	2	JQ0188	ice nucleation pro
274	214.5	9.1	1018	2	H83135	probable adhesin P	347	200	8.5	3716	2	E70969	probable PPE prote
275	214	9.1	1024	2	S18251	collagen alpha 1(X	348	199.5	8.4	214	1	KNNT2S	glycine-rich prote
276	214	9.1	1275	2	T33369	hypothetical prote	349	199.5	8.4	670	2	T49510	fibroin-3 related
277	213.5	9.0	245	2	F70787	hypothetical glyci	350	199.5	8.4	707	2	A48686	probable RNA helic
278	213.5	9.0	695	2	T24950	hypothetical prote	351	199.5	8.4	1022	2	T44663	hypothetical prote
279	213.5	9.0	959	2	B44402	nuclear pore compl	352	199	8.4	825	1	EDBEXD	immediate-early pr
280	213.5	9.0	1670	1	CGHU3B	collagen alpha 3(I	353	198.5	8.4	191	2	A42844	abecisic acid-and
281	213.5	9.0	2415	1	A39086	aggreacan precursor	354	198.5	8.4	320	2	T14447	oleosin homolog pc
282	212.5	9.0	1804	2	H96597	hypothetical prote	355	198.5	8.4	921	2	S40495	collagen alpha 1(I
283	212.5	9.0	2551	2	B98047	hypothetical prote	356	198.5	8.4	1433	2	A46053	bullous pemphigoid
284	212	9.0	390	2	S27766	WCS120 protein - w	357	198.5	8.4	1691	1	S22917	collagen alpha 5(I
285	212	9.0	635	2	A57131	collagen alpha 2(V	358	198	8.4	346	2	S40775	ribonucleoprotein
286	212	9.0	907	2	A45560	sporozoite surface	359	198	8.4	541	2	S51799	nucleoporin NUP57
287	211.5	9.0	488	2	A27353	collagen alpha 1(I	360	198	8.4	1213	2	S16356	ovo protein - frui
288	211	8.9	967	2	S66852	hypothetical prote	361	197.5	8.4	744	2	S15435	oleosin homolog gb
289	210.5	8.9	471	2	T33997	hypothetical prote	362	197	8.3	361	2	T14460	collagen alpha 1(X
290	210.5	8.9	3190	2	T13828	CREB-binding prote	363	197	8.3	1142	2	JX0369	collagen alpha 1(X
291	209.5	8.9	688	2	A53340	collagen alpha 2(I	364	196.5	8.3	571	1	UMFF	period clock prote
292	209.5	8.9	920	2	A45748	collagen alpha 1(V	365	196.5	8.3	754	2	A55267	collagen alpha 5(I
293	209	8.8	680	2	S31216	collagen alpha 1(X	366	196	8.3	136	2	T29282	hypothetical prote
294	209	8.8	1707	2	A33526	collagen alpha 2(I	367	196	8.3	1147	1	MWAXIB	myosin heavy chain
295	209	8.8	3137	2	A37797	collagen alpha 3(V	368	195.5	8.3	314	2	T08675	hypothetical prote
296	208.5	8.8	377	2	T08095	oleosin homolog ST	369	195.5	8.3	633	2	B40983	collagen alpha 1(X
297	208	8.8	201	2	T00799	hypothetical prote	370	195.5	8.3	698	2	JH0163	No-on-transient A
298	208	8.8	307	2	T27609	hypothetical prote	371	195.5	8.3	700	2	JH0162	No-on-transient A
299	208	8.8	457	2	H70820	hypothetical glyci	372	195.5	8.3	921	2	S42617	collagen alpha 1(I
300	208	8.8	618	2	S32436	collagen alpha 2(I	373	195.5	8.3	1560	2	T02885	lipoprotein vsai l
301	207.5	8.8	365	2	A26459	helix-destabilizin	374	195	8.3	358	2	S40776	probable outer mem
302	207	8.8	208	2	T46896	merozoite surface	375	195	8.3	469	2	A24450	ribonucleoprotein
303	207	8.8	313	2	T04776	hypothetical prote	376	195	8.3	1748	2	S42136	collagen alpha 2(V
304	207	8.8	405	2	T29167	hypothetical prote	377	194.5	8.2	383	2	A53053	cnjB protein - Tet
305	207	8.8	645	2	D90782	probable tail fibe	378	194.5	8.2	839	2	H90577	dentin sialoprotei
306	207	8.8	645	2	H85642	probable tail fibe	379	194.5	8.2	959	2	S32605	collagen alpha 3(V
307	207	8.8	680	1	CGHUID	collagen alpha 1(X	380	194	8.2	1028	2	T03516	probable outer mem
308	207	8.8	2124	2	A28452	proteoglycan core	381	194	8.2	1400	2	T31555	hypothetical prote
309	206.5	8.7	190	2	A24713	agrecin - silkworm	382	194	8.2	1436	2	B70520	probable PPE prote
310	206.5	8.7	342	2	S14532	heterogeneous ribo	383	193.5	8.2	931	2	S13580	collagen alpha 1(I
311	206.5	8.7	615	2	A05269	collagen alpha 1(I	384	193.5	8.2	1096	2	T08619	probable metallopr
312	206.5	8.7	1025	2	S34839	collagen alpha 1(V	385	192	8.1	526	1	KRBOVI	keratin, 54K type
313	206	8.7	447	2	G84687	probable disease r	386	191.5	8.1	644	1	FGHUA	fibrinogen alpha c
314	206	8.7	1322	2	S07053	ice nucleation pro	387	191.5	8.1	866	2	D44234	fibrinogen alpha c
315	205.5	8.7	506	2	G71404	probable ribonucle	388	191.5	8.1	1315	2	A56101	collagen alpha 1(X
316	205.5	8.7	518	2	A55840	macrophage bacteri	389	191.5	8.1	1774	2	B56101	collagen alpha 1(X
317	205	8.7	502	2	A48679	differentiated ker	390	191	8.1	323	2	T19142	hypothetical prote
318	205	8.7	775	2	A61228	collagen alpha 2(I	391	190.5	8.1	743	1	S23779	collagen alpha 1(V
319	205	8.7	1417	2	A83080	hypothetical prote	392	190.5	8.1	796	2	S57844	lethal(3)malignant
320	205	8.7	1603	2	S23810	collagen alpha 1(X	393	190.5	8.1	2329	2	T28125	hypothetical prote
321	204.5	8.7	382	2	S23815	collagen alpha 3(V	394	190	8.0	344	2	S41707	PopAI protein - Ps

395	190	8.0	963	2	B70524	probable PPG prote	468	178.5	7.6	335	2	T14449	oleosin homolog pc
396	189.5	8.0	289	2	F96770	protein RNA-bindin	469	178	7.5	300	2	T19929	hypothetical prote
397	189	8.0	301	2	B31219	collagen 2 - Caeno	470	178	7.5	393	2	S5499	cellulase egli - s
398	189	8.0	848	2	S02262	glutenin high mole	471	178	7.5	539	2	T50579	probable membrane
399	189	8.0	1176	2	C26427	period clock prote	472	178	7.5	688	2	T48796	probable ATP-depen
400	189	8.0	1218	2	A26588	period clock prote	473	177.5	7.5	314	2	T34269	hypothetical prote
401	189	8.0	1218	2	A26427	period clock prote	474	177.5	7.5	327	2	T34203	hypothetical prote
402	188.5	8.0	203	1	JQ1061	glycine-rich prote	475	177	7.5	176	2	S30147	glycine-rich RNA b
403	188.5	8.0	363	2	T51341	RNA helicase RH9 [	476	177	7.5	255	2	AF1857	hypothetical prote
404	188.5	8.0	423	2	A41207	collagen 13, nonfi	477	177	7.5	304	2	T26185	hypothetical prote
405	188.5	8.0	632	2	T02627	hypothetical prote	478	177	7.5	304	2	T26184	hypothetical prote
406	188	8.0	487	2	C70830	probable PPG prote	479	177	7.5	495	2	B71360	hypothetical prote
407	188	8.0	1596	2	A33106	neurogenic locus m	480	177	7.5	908	2	A33280	sarcalumenin precu
408	187.5	7.9	752	2	T34355	hypothetical prote	481	177	7.5	1199	2	A40670	nuclear envelope p
409	187.5	7.9	956	2	T08144	myrosinase-binding	482	177	7.5	3759	2	A35085	trithorax protein
410	187.5	7.9	1076	2	C96620	protein T30E16.23	483	176.5	7.5	137	2	T04930	glycine-rich cell
411	187.5	7.9	1718	2	T14603	hypothetical prote	484	176.5	7.5	367	2	A32068	circumsporozoite p
412	187	7.9	596	2	T26667	hypothetical prote	485	176.5	7.5	638	2	I53169	cytokeatin 2 - hu
413	186.5	7.9	252	2	A55047	collagen alpha 1(V	486	176.5	7.5	798	2	T21369	hypothetical prote
414	186.5	7.9	356	2	S16907	collagen alpha 1(I	487	176.5	7.5	1241	2	S01827	period clock prote
415	186.5	7.9	378	1	OZZQAB	circumsporozoite p	488	176.5	7.5	2554	2	AB3528	extracellular seri
416	186.5	7.9	398	1	OZZQAS	homeotic protein o	489	176	7.4	325	2	T18594	hypothetical prote
417	186	7.9	671	2	A35912	circumsporozoite p	490	176	7.4	747	1	EABO	elastin precursor,
418	186	7.9	1763	2	S16366	collagen alpha 2(I	491	175.5	7.4	316	2	S08169	collagen col-12 pr
419	185.5	7.9	346	1	S35500	heterogeneous ribo	492	175.5	7.4	316	2	S08170	collagen col-13 pr
420	185.5	7.9	753	2	JC2099	glutenin, high mol	493	175.5	7.4	403	2	T08471	harpin - Erwinia a
421	185.5	7.9	789	2	A30843	glutenin high mole	494	175.5	7.4	775	1	EDBE11	immediate-early pr
422	185.5	7.9	791	2	JN0690	glutenin, high-mol	495	175	7.4	201	2	F84596	glycine-rich prote
423	185	7.8	704	2	T34034	hypothetical prote	496	175	7.4	352	2	T24279	hypothetical prote
424	185	7.8	867	2	S57795	probable deoxyribo	497	175	7.4	358	2	T26281	hypothetical prote
425	185	7.8	1004	2	C82672	surface-exposed ou	498	175	7.4	363	2	T16831	hypothetical prote
426	184.5	7.8	330	2	T26004	hypothetical prote	499	175	7.4	464	2	S59513	collagen II Al pro
427	184.5	7.8	388	2	JC6164	circumsporozoite p	500	175	7.4	528	2	D46449	hypothetical prote
428	184.5	7.8	798	2	T33022	hypothetical prote	501	175	7.4	598	2	T38403	probable nucleopor
429	184.5	7.8	1063	2	A40523	acidic nuclear pro	502	174.5	7.4	340	2	T20807	hypothetical prote
430	184	7.8	333	2	T23618	hypothetical prote	503	174.5	7.4	406	2	S38170	SRP40 protein - ye
431	184	7.8	625	2	A34615	profilaggrin - rat	504	174.5	7.4	460	2	T33110	hypothetical prote
432	184	7.8	813	2	S70795	vsaa protein precu	505	174.5	7.4	629	2	A29666	keratin, 65K type
433	184	7.8	1102	2	A32247	virG protein - Shi	506	174.5	7.4	672	2	I40333	tracheal colonizat
434	183.5	7.8	445	2	A27263	50K spicule matrix	507	174	7.4	239	2	S49193	GCR 101 protein -
435	183.5	7.8	541	2	T15299	hypothetical prote	508	174	7.4	314	2	T32247	hypothetical prote
436	182.5	7.7	174	2	S18654	variant surface an	509	174	7.4	330	2	S46657	collagen alpha 1(X
437	182.5	7.7	306	2	S33538	embryogenic cell p	510	174	7.4	344	2	T40167	hypothetical calci
438	182.5	7.7	443	2	C70780	probable PPG prote	511	174	7.4	387	2	E95995	hypothetical prote
439	182.5	7.7	472	2	S28026	nuclear pore compl	512	174	7.4	448	2	T15188	hypothetical prote
440	182.5	7.7	1293	2	B40025	maleless protein,	513	174	7.4	475	2	T03170	gene pointed prote
441	182.5	7.7	2204	2	A70524	probable PPG prote	514	174	7.4	718	1	S33168	hypothetical prote
442	182	7.7	287	2	B39615	merozoite 45K surf	515	174	7.4	782	2	T32155	protein corA, cold
443	182	7.7	305	2	T20906	hypothetical prote	516	173.5	7.3	204	2	T09592	coat protein A pre
444	182	7.7	1053	2	B70987	probable PPG prote	517	173.5	7.3	424	1	Z3BPF1	coat protein A pre
445	181.5	7.7	154	2	B84468	probable glycine-r	518	173.5	7.3	424	1	Z3BPF1	coat protein A pre
446	181.5	7.7	1287	2	T146032	nuclear DNA helica	519	173.5	7.3	424	1	Z3BPF3	hypothetical prote
447	181	7.7	256	2	T11669	protein CPRD22, dr	520	173.5	7.3	542	2	T29707	hypothetical glyci
448	181	7.7	356	2	T22827	hypothetical prote	521	173.5	7.3	558	2	E70756	cell surface glyco
449	181	7.7	416	2	A32947	filaggrin precursor	522	173.5	7.3	779	2	A35006	vitellogenin I pre
450	181	7.7	569	2	S42886	collagen - silkwor	523	173.5	7.3	1912	2	T29088	drought-induced pr
451	181	7.7	614	2	T33149	hypothetical prote	524	173	7.3	258	2	S71561	lipoprotein vsaa [
452	181	7.7	1388	2	A53317	collagen alpha 1(X	525	173	7.3	281	2	C90577	merozoite 45K surf
453	181	7.7	1533	2	A46221	abdominal segment	526	173	7.3	347	2	B39112	merozoite 45K surf
454	180.5	7.6	196	2	S49194	GCR 17 protein - f	527	173	7.3	656	1	A49358	RNA-binding protei
455	180.5	7.6	605	2	T33913	hypothetical prote	528	173	7.3	1032	2	T34433	hypothetical prote
456	180.5	7.6	744	1	A34246	collagen alpha 1(V	529	173	7.3	1043	2	T13733	FTZ-F1 protein - f
457	180.5	7.6	744	1	S23298	collagen alpha 1(V	530	172.5	7.3	864	2	A48266	protein-tyrosine k
458	180	7.6	268	2	T61615	fibroin heavy chai	531	172	7.3	446	2	T45525	MSC4 homolog [mpo
459	180	7.6	434	1	Z3BPTK	coat protein A - p	532	172	7.3	1052	2	AF2959	conserved hypochet
460	180	7.6	674	2	T32397	collagen alpha 1(X	533	172	7.3	1341	2	H98323	hypothetical prote
461	180	7.6	792	1	EAHU	elastin precursor,	534	171.5	7.3	655	1	A55726	RNA-binding protei
462	179.5	7.6	784	2	A26601	elastin precursor,	535	171.5	7.3	1127	2	A25018	circadian rhythm p
463	179.5	7.6	838	1	SEWTHW	glutenin, high mol	536	171	7.2	337	2	T23794	hypothetical prote
464	179	7.6	310	2	T29731	hypothetical prote	537	171	7.2	1176	2	T18042	ice nucleation pro
465	179	7.6	314	2	T32985	hypothetical prote	538	170.5	7.2	108	1	S01844	fibroin - silkworm
466	179	7.6	995	2	T22942	hypothetical prote	539	170.5	7.2	367	2	JC4831	adsorption protein
467	178.5	7.6	313	2	T22828	hypothetical prote	540	170.5	7.2	396	2	T29773	hypothetical prote



541	170.5	7.2	1589	2	T42233	submaxillary mucin	614	163	6.9	418	2	T15142	hypothetical prote
542	170.5	7.2	4936	2	AH2515	hypothetical prote	615	163	6.9	490	2	T09084	phosphatidylinosit
543	170	7.2	334	2	S08091	gene III protein -	616	163	6.9	633	2	F84564	probable protein k
544	170	7.2	20839	2	T20839	hypothetical prote	617	162.5	6.9	262	1	TLBPM1	tail fiber protein
545	170	7.2	1208	2	S12786	period clock prote	618	162.5	6.9	289	2	T20177	hypothetical prote
546	170	7.2	3498	2	T22330	hypothetical prote	619	162.5	6.9	658	2	T41309	hypothetical threo
547	169.5	7.2	183	2	S57773	early nodulin GRP3	620	162.5	6.9	925	2	T20333	G protein-coupled
548	169.5	7.2	661	1	S59633	endo-1,4-beta-xyla	621	162.5	6.9	1168	1	MXAXIC	myosin heavy chain
549	169.5	7.2	849	2	A96592	hypothetical prote	622	162	6.9	166	1	KRBO2B	keratin, 68K type
550	169.5	7.2	924	2	F87103	initiation factor	623	162	6.9	198	2	I49558	collagen alpha 1(I
551	169.5	7.2	988	2	T08102	myrosinase-binding	624	162	6.9	323	2	T24582	hypothetical prote
552	169.5	7.2	1504	2	T49896	glycine/proline-ri	625	162	6.9	1087	2	S35423	protein kinase egg
553	169	7.2	290	2	T42986	hypothetical prote	626	162	6.9	1888	2	S78476	collagen alpha 1(X
554	169	7.2	304	2	T22482	hypothetical prote	627	161.5	6.8	316	2	T19288	hypothetical prote
555	169	7.2	308	2	T37286	collagen 40 - Caen	628	161.5	6.8	500	2	T20961	hypothetical prote
556	169	7.2	380	2	T28888	cuticle collagen d	629	161.5	6.8	707	2	S52390	D-hordein precursor
557	168.5	7.1	640	2	A54502	S antigen precursor	630	161.5	6.8	800	2	I51653	deRNA-binding prot
558	168	7.1	234	2	G95989	hypothetical glyci	631	161.5	6.8	978	2	D81411	probable lipoprote
559	168	7.1	252	2	T03160	capsid protein - a	632	161.5	6.8	1441	2	B86807	hypothetical prote
560	168	7.1	633	2	A25473	chorion E2 protein	633	161	6.8	284	2	T29528	hypothetical prote
561	168	7.1	673	2	T00328	hypothetical prote	634	161	6.8	290	2	T24590	hypothetical prote
562	168	7.1	684	2	A53019	collagen alpha 1(X	635	161	6.8	591	2	A45135	profilaggrin - hum
563	167.5	7.1	183	2	S57772	early nodulin GRP3	636	161	6.8	650	2	G87572	calcium-binding pr
564	167.5	7.1	276	2	T33252	hypothetical prote	637	161	6.8	805	2	T25795	hypothetical prote
565	167.5	7.1	286	2	B45632	merozoite surface	638	161	6.8	925	2	T19361	hypothetical prote
566	167.5	7.1	629	2	S42629	keratin K3 - rabbi	639	161	6.8	1701	2	T43213	ENBPI protein - ba
567	167.5	7.1	786	2	T16509	hypothetical prote	640	161	6.8	1852	1	VJCH2	vitellogenin II pr
568	167.5	7.1	1075	2	T48805	hypothetical prote	641	160.5	6.8	212	2	B86179	hypothetical prote
569	167.5	7.1	1366	2	T35985	probable large pro	642	160.5	6.8	281	2	C88638	protein P58P6.1 li
570	167.5	7.1	1747	2	A45974	collagen alpha 1(X	643	160.5	6.8	323	2	T27450	hypothetical prote
571	167.5	7.1	1857	2	S31212	collagen alpha 1(X	644	160.5	6.8	327	2	S25421	hypothetical prote
572	167	7.1	106	2	F84797	hypothetical prote	645	160.5	6.8	1516	2	T01055	ABC-type transport
573	167	7.1	166	2	T10463	glycine-rich prote	646	160.5	6.8	2020	2	C48399	glycine-rich prote
574	167	7.1	303	2	T19289	hypothetical prote	647	160	6.8	169	2	T10465	tail fiber protein
575	167	7.1	325	2	T32248	hypothetical prote	648	160	6.8	262	2	S00275	hypothetical prote
576	167	7.1	369	2	F96788	protein T4012.22 l	649	160	6.8	286	2	T22706	hypothetical prote
577	167	7.1	407	2	T21956	hypothetical prote	650	160	6.8	299	2	T22705	hypothetical prote
578	167	7.1	1221	2	T13283	probable transcrip	651	160	6.8	320	1	DDRT	helix-detabilizin
579	167	7.1	1237	2	D71850	probable outer mem	652	160	6.8	320	1	A44485	heterogeneous ribo
580	167	7.1	1772	2	T36105	probable large gly	653	160	6.8	320	2	S04617	heterogeneous ribo
581	166.5	7.0	313	2	A28444	filaggrin precursor	654	160	6.8	320	2	S02061	circumsporozoite p
582	166.5	7.0	416	2	T32458	hypothetical prote	655	160	6.8	378	1	OZ2QAL	transcription fact
583	166.5	7.0	522	2	T36501	probable serine/th	656	160	6.8	582	2	S10099	autolysin - Entero
584	166.5	7.0	556	2	AH1981	hypothetical prote	657	160	6.8	671	2	A38109	probable PPG prote
585	166.5	7.0	634	2	T08145	myrosinase-binding	658	160	6.8	987	2	E70808	collar protein iso
586	166.5	7.0	738	2	B87627	hypothetical prote	659	160	6.8	1296	2	T13936	hypothetical prote
587	166.5	7.0	1120	2	H88449	protein P54P8.1 li	660	160	6.8	1325	2	T13386	hypothetical prote
588	166	7.0	291	2	T26576	hypothetical prote	661	160	6.8	1649	2	C86822	hypothetical prote
589	166	7.0	617	2	T49444	lustrin A related	662	159.5	6.7	186	2	S28021	rab18 protein - Ar
590	166	7.0	1122	2	B26427	period clock prote	663	159.5	6.7	260	2	S00276	tail fiber protein
591	166	7.0	1519	2	S41525	major ring-forming	664	159.5	6.7	301	2	B84533	hypothetical prote
592	165.5	7.0	220	2	AD2990	conserved hypotet	665	159.5	6.7	336	2	T20348	hypothetical prote
593	165.5	7.0	220	2	E98293	hypothetical prote	666	159.5	6.7	654	2	A34734	transcription fact
594	165.5	7.0	389	2	D26995	homeotic protein U	667	159.5	6.7	742	4	C34734	transcription fact
595	165	7.0	291	2	T20083	hypothetical prote	668	159.5	6.7	825	4	B34734	transcription fact
596	165	7.0	319	2	T22500	hypothetical prote	669	159.5	6.7	1534	2	A56734	ribosome receptor,
597	165	7.0	433	2	S20963	homeotic protein H	670	159	6.7	299	2	T19564	hypothetical prote
598	165	7.0	823	2	S14055	meoskeletal-lik	671	159	6.7	302	2	T32872	hypothetical prote
599	164.5	7.0	200	2	B86181	hypothetical prote	672	159	6.7	494	2	T15502	hypothetical prote
600	164.5	7.0	600	2	T07638	spore coat protein	673	159	6.7	516	2	C44479	collagen alpha 1(X
601	164.5	7.0	819	2	T08745	probable RNA helic	674	159	6.7	1711	1	A47392	chromodomain-helic
602	164.5	7.0	1446	1	A45344	immediate-early pr	675	158.5	6.7	307	2	T16842	hypothetical prote
603	164	6.9	237	2	A88640	protein C34H4.4 li	676	158.5	6.7	461	2	JN0097	secreted 45K prote
604	164	6.9	368	2	H96990	probable membrane	677	158	6.7	231	2	S17367	rab15B protein - w
605	164	6.9	561	2	T16148	hypothetical prote	678	158	6.7	299	2	T25407	hypothetical prote
606	163.5	6.9	299	2	T00837	glycine-rich prote	679	158	6.7	306	2	T21938	hypothetical prote
607	163.5	6.9	414	1	I38977	TAR DNA-binding pr	680	158	6.7	1460	2	S48457	nucleoporin RAP7 -
608	163.5	6.9	623	2	A45137	collagen alpha 4(I	681	158	6.7	3124	2	A40020	collagen alpha 1(X
609	163.5	6.9	666	2	A42296	lysosome 2 (EC 3.2	682	157.5	6.7	317	2	T19143	hypothetical prote
610	163.5	6.9	668	2	C71868	hypothetical prote	683	157.5	6.7	830	2	T15720	glutenin high mole
611	163.5	6.9	729	2	S35332	hnRNA-binding prot	684	157	6.6	145	2	T08435	la costa protein -
612	163.5	6.9	628	2	C81265	probable lipoprote	685	157	6.6	225	2	S05546	dehydrin 18 - barl
613	163	6.9	254	2	A31488	filaggrin - mouse	686	157	6.6	249	2	B33144	homeotic protein U

687	157	6.6	239	2	T24833	hypothetical prote	760	151.5	6.4	486	1	KRXL	keratin 3, type I,
688	157	6.6	363	1	OZZQAK	circumsporozoite p	761	151.5	6.4	797	2	A36811	hypothetical prote
689	157	6.6	386	2	S11449	collagen short cha	762	151.5	6.4	901	2	JC5093	dead ringer nuclea
690	157	6.6	623	2	A45571	surface antigen 2,	763	151.5	6.4	1076	1	A35622	nuclear pore prote
691	157	6.6	624	2	A55576	collagen alpha 2(X	764	151	6.4	161	2	S71453	glycine-rich RNA-b
692	157	6.6	806	2	T13690	hypothetical prote	765	151	6.4	333	2	E48423	homeotic protein e
693	157	6.6	1829	2	E81086	iron-regulated pro	766	151	6.4	339	2	T22607	hypothetical prote
694	157	6.6	1910	2	AF0394	probable adhesin h	767	151	6.4	387	2	T34507	cutical collagen 6
695	156.5	6.6	173	2	S53050	RNA binding protei	768	151	6.4	405	2	S19355	hypothetical prote
696	156.5	6.6	273	2	T40618	probable cell wall	769	151	6.4	537	2	E33485	spore coat protein
697	156.5	6.6	387	2	H86445	probable G-Box bin	770	150.5	6.4	387	2	E95933	probable calcium-b
698	156.5	6.6	471	2	A39024	collagen alpha 3(I	771	150.5	6.4	461	2	T51044	related to spore c
699	156.5	6.6	758	2	T48815	mixed-linked gluc	772	150.5	6.4	524	2	A82580	polyvinylalcohol d
700	156.5	6.6	1217	2	T25894	hypothetical prote	773	150	6.3	234	2	T49448	dehydrin 2 - garde
701	156.5	6.6	1777	2	T34369	hypothetical prote	774	150	6.3	255	2	T08811	hypothetical prote
702	156.5	6.6	3295	2	AB0074	probable adhesin Y	775	150	6.3	283	2	T19732	hypothetical prote
703	156	6.6	169	2	S30148	glycine-rich prote	776	150	6.3	327	2	T29031	hypothetical prote
704	156	6.6	259	1	S46286	RNA-binding protei	777	150	6.3	359	2	T22774	hypothetical prote
705	156	6.6	291	2	T34494	hypothetical prote	778	150	6.3	423	2	A55797	collagen precursor
706	156	6.6	330	2	S30192	heterogeneous ribo	779	150	6.3	1072	2	G95851	probable hemolysin
707	156	6.6	431	1	WJ02ZG	homeotic protein H	780	150	6.3	1390	2	T18883	hypothetical prote
708	156	6.6	571	2	T43456	hypothetical prote	781	149.5	6.3	148	2	T05527	glycine-rich prote
709	156	6.6	1665	2	T29008	hypothetical prote	782	149.5	6.3	287	2	T22637	hypothetical prote
710	155.5	6.6	163	2	T23076	hypothetical prote	783	149.5	6.3	317	2	T29960	hypothetical prote
711	155.5	6.6	169	1	S38331	glycine-rich RNA-b	784	149.5	6.3	325	2	S02170	collagen alpha 1(I
712	155.5	6.6	238	2	T23271	hypothetical prote	785	149.5	6.3	385	2	D41732	heterogeneous nucl
713	155	6.6	419	1	KRXLB2	keratin, 64K type	786	149.5	6.3	419	2	T04886	DAG protein homolo
714	155	6.6	1487	1	EDBEE1	immediate-early pr	787	149.5	6.3	473	2	I50629	collagen - chicken
715	154.5	6.5	270	2	A36034	fibrinogen alpha c	788	149.5	6.3	573	2	C86266	F3F19.21 protein -
716	154.5	6.5	304	2	T22602	hypothetical prote	789	149.5	6.3	1028	2	A50038	DNA-binding protei
717	154.5	6.5	343	2	T29547	hypothetical prote	790	149	6.3	264	2	S37137	prion protein - gr
718	154.5	6.5	433	1	QGBV2	UL44 protein - hum	791	149	6.3	318	2	S27977	cuticle collagen d
719	154.5	6.5	705	2	S18733	glutenin high mole	792	149	6.3	329	2	JS0167	collagen col-6 - C
720	154.5	6.5	3436	2	S55659	tegument protein 6	793	149	6.3	345	1	B41732	heterogeneous nucl
721	154	6.5	205	2	T05713	dehydrin - barley	794	149	6.3	371	1	JN0450	conglutinin precur
722	154	6.5	297	2	T30525	hypothetical prote	795	149	6.3	896	2	T51891	conglutinin - bovi
723	154	6.5	2715	2	T13049	eyelid - fruit fly	796	149	6.3	933	2	T48707	related to regulat
724	153.5	6.5	115	2	T01322	aluminum-induced p	797	149	6.3	1112	2	H95964	probable outer mem
725	153.5	6.5	157	2	S18651	variant surface an	798	149	6.3	107	2	B85356	glycine-rich prote
726	153.5	6.5	178	2	E88637	protein W09G12.6 [	799	148.5	6.3	283	2	T29980	hypothetical prote
727	153.5	6.5	289	2	T34241	hypothetical prote	800	148.5	6.3	302	2	T21257	hypothetical prote
728	153.5	6.5	304	2	T23801	hypothetical prote	801	148.5	6.3	364	2	S43574	C05B5.3 protein (c
729	153.5	6.5	309	2	T19389	hypothetical prote	802	148.5	6.3	454	2	T35380	probable membrane
730	153.5	6.5	311	2	S08110	salivary protein 1	803	148.5	6.3	456	2	E86903	hypothetical prote
731	153.5	6.5	333	2	T20436	hypothetical prote	804	148.5	6.3	660	2	A24266	glutenin high mole
732	153.5	6.5	401	2	C88571	protein C05B5.3 [1	805	148.5	6.3	289	2	T27708	hypothetical prote
733	153.5	6.5	437	2	S15144	hypothetical prote	806	148	6.3	298	2	E95286	hypothetical prote
734	153.5	6.5	1791	2	T02345	hypothetical prote	807	148	6.3	299	2	T20605	hypothetical prote
735	153.5	6.5	1829	2	S35027	cytotoxin RTX homo	808	148	6.3	306	2	T21939	hypothetical prote
736	153	6.5	112	2	S14977	glycine-rich prote	809	148	6.3	447	2	T18447	HrpW protein - Erw
737	153	6.5	164	2	S11846	rab16B protein - r	810	148	6.3	549	2	B86264	hypothetical prote
738	153	6.5	232	2	S18139	dehydrin DHN3 - ga	811	148	6.3	661	2	A58768	Arp-dependent RNA
739	153	6.5	285	2	T29982	hypothetical prote	812	148	6.3	892	2	T27005	hypothetical prote
740	153	6.5	349	2	A41349	histone-specific t	813	148	6.3	1305	2	T00670	probable inositol
741	153	6.5	349	2	S77570	transcription fact	814	148	6.3	235	2	G01226	leukophysin - huma
742	153	6.5	483	1	TVR7KA	protein kinase (EC	815	147.5	6.2	235	2	G01226	hypothetical prote
743	153	6.5	629	2	T37426	probable dehydroge	816	147.5	6.2	300	2	T24482	collagen alpha 1(X
744	153	6.5	1487	1	EDBEF3	155K transcription	817	147.5	6.2	482	2	B31795	hypothetical prote
745	152.5	6.5	257	2	C84533	hypothetical prote	818	147.5	6.2	589	2	T29299	hypothetical prote
746	152.5	6.5	279	2	T26125	hypothetical prote	819	147.5	6.2	1329	2	T29074	protein-tyrosine k
747	152.5	6.5	299	2	T29956	hypothetical prote	820	147.5	6.2	1584	2	T18276	maturation-associa
748	152.5	6.5	316	2	T19291	hypothetical prote	821	147	6.2	226	2	S27759	major prion protei
749	152.5	6.5	420	2	D83556	probable coat prot	822	147	6.2	264	2	A54330	collagen col-8 - C
750	152.5	6.5	584	2	E70825	hypothetical glyci	823	147	6.2	282	2	JS0168	hypothetical prote
751	152.5	6.5	1198	2	T49726	hypothetical prote	824	147	6.2	283	2	T19731	surfactant protein
752	152	6.4	258	2	A29259	Ubq protein - frui	825	147	6.2	374	1	A42046	PSP2 protein - yea
753	152	6.4	474	2	A26421	shufflon A - Bache	826	147	6.2	578	2	S55102	probable integral
754	152	6.4	735	2	T35778	probable fusidic a	827	147	6.2	684	2	T36771	eye cell developme
755	152	6.4	828	2	C30843	glutenin high mole	828	147	6.2	760	2	A45174	siolglycoprotein
756	152	6.4	828	2	C88402	protein H05C05.1 [	829	147	6.2	762	2	S08207	nuclear pore compl
757	151.5	6.4	182	2	A36686	ultra-high-sulfur	830	147	6.2	1317	2	A54831	hemolysin A - Edwa
758	151.5	6.4	294	2	T21668	hypothetical prote	831	147	6.2	1594	2	T43072	hypothetical prote
759	151.5	6.4	367	2	JC6087	helix-loop-helix t	832	146.5	6.2	166	2	T18691	

833	146.5	6.2	294	2	T22639	hypotheical prote	906	142	6.0	449	1	S30205	transcription fact
834	146.5	6.2	310	2	T22641	hypotheical prote	907	142	6.0	475	2	C86863	N-acetylmutamoyl-L
835	146.5	6.2	368	2	G84769	hypotheical prote	908	142	6.0	1166	2	T13958	synGAP-b1 protein
836	146.5	6.2	377	2	A47380	RING finger-contai	909	142	6.0	1249	2	T14270	Ras-GTPase activat
837	146.5	6.2	593	2	A48459	S antigen, heat st	910	142	6.0	1286	2	S28634	adhesin AIDA-I pre
838	146.5	6.2	704	2	S21911	Bscore-NS-Z3 prote	911	142	6.0	1293	2	T14259	ras GTPase-activat
839	146	6.2	258	2	T13591	tail fiber adhesin	912	142	6.0	1588	2	A86036	probable adhesin Z
840	146	6.2	281	2	T32765	hypotheical prote	913	142	6.0	1588	2	H91188	probable hemolysin
841	146	6.2	283	2	JS01770	collagen col-19 -	914	142	6.0	2535	2	AC0304	probable hemolysin
842	146	6.2	295	2	T22833	hypotheical prote	915	141.5	6.0	255	2	AC35026	filaggrin A - mous
843	146	6.2	412	2	A84455	hypotheical prote	916	141.5	6.0	474	2	I38240	transcription fact
844	146	6.2	467	2	I50476	keratin type I - 9	917	141.5	6.0	788	2	JS0747	regulatory protein
845	146	6.2	712	2	A45638	immunodominant mic	918	141.5	6.0	1398	2	T13741	hypotheical prote
846	146	6.2	1215	2	T32734	myosin-1A - Acanth	919	141.5	6.0	3535	2	E83641	probable hemagglut
847	146	6.2	1340	2	A39808	proteoglycan core	920	141.5	6.0	3968	2	A44265	trithorax homolog
848	145.5	6.2	215	2	T17207	hypotheical prote	921	141	6.0	191	2	I46412	keratin KAP5.4 - s
849	145.5	6.2	313	2	T26465	hypotheical prote	922	141	6.0	253	2	AC31144	homeotic protein U
850	145.5	6.2	461	2	A43782	keratin, type II -	923	141	6.0	511	2	S10527	endoglycanase B pr
851	145.5	6.2	561	1	CDECP3	cloacin DF13 prote	924	141	6.0	684	2	A56154	hypotheical prote
852	145.5	6.2	643	2	T03518	hypotheical prote	925	140.5	5.9	148	2	B71419	hypotheical prote
853	145.5	6.2	658	2	AH0110	probable surface p	926	140.5	5.9	309	2	T28708	probable lysophosp
854	145.5	6.2	815	2	JN0689	glutinin, high-mol	927	140.5	5.9	317	2	T39869	probable lysophosp
855	145.5	6.2	1467	2	A75564	conserved hypotet	928	140.5	5.9	431	2	S09824	hypotheical prote
856	145	6.1	150	2	C86224	hypotheical prote	929	140.5	5.9	484	2	S66713	hypotheical prote
857	145	6.1	154	2	S34637	glycine-rich prote	930	140.5	5.9	561	2	T22917	probable ATP-depen
858	145	6.1	170	2	T03018	glycine-rich prote	931	140.5	5.9	579	2	T37248	probable matrix me
859	145	6.1	375	1	A45225	pulmonary surfacta	932	140.5	5.9	1690	2	T35694	ATP dependent DNA
860	145	6.1	380	1	GNVSM8	genome polyprotein	933	140	5.9	111	2	T29295	hypotheical prote
861	145	6.1	451	1	A40168	transcription fact	934	140	5.9	296	2	T29295	hypotheical prote
862	145	6.1	539	2	G95405	hypotheical prote	935	140	5.9	327	2	S38342	hypotheical prote
863	145	6.1	633	2	T02673	serine/threonine p	936	140	5.9	360	2	T37285	fibrillarin - mous
864	145	6.1	633	2	T02673	heterogeneous nucl	937	140	5.9	425	1	KRX12A	collagen dpv-2 - C
865	145	6.1	919	2	A39248	androgen receptor	938	140	5.9	669	2	AC7443	hypotheical prote
866	145	6.1	3345	2	T13423	hypotheical prote	939	140	5.9	669	2	AC2661	hypotheical prote
867	144.5	6.1	156	2	S52246	transposable retro	940	140	5.9	710	2	S28014	outD protein - Erw
868	144.5	6.1	453	2	A41640	vestigial protein	941	140	5.9	888	2	I58378	tyrosine kinase -
869	144.5	6.1	512	2	S70644	annexin VII - Afri	942	140	5.9	1788	2	T31095	vitellogenin precu
870	144.5	6.1	937	2	A56517	nucleoporin Nup98	943	140	5.9	5627	2	C83339	hypotheical prote
871	144.5	6.1	2761	2	T21064	hypotheical prote	944	139.5	5.9	104	2	JC4190	holotricin 3 precu
872	144	6.1	208	2	T21689	hypotheical prote	945	139.5	5.9	543	2	A32693	steroid receptor p
873	144	6.1	283	2	T29837	hypotheical prote	946	139.5	5.9	576	2	S69214	deformed epidermal
874	144	6.1	284	2	T29839	hypotheical prote	947	139.5	5.9	591	2	AC3528	extracellular seri
875	144	6.1	381	2	T27806	hypotheical prote	948	139.5	5.9	653	2	T34356	hypotheical prote
876	144	6.1	492	2	A87471	hypotheical prote	949	139.5	5.9	746	2	B32693	steroid receptor p
877	144	6.1	1475	1	S42718	nuclear pore compl	950	139.5	5.9	845	2	D96799	hypotheical prote
878	143.5	6.1	168	1	S12312	glycine-rich RNA-b	951	139.5	5.9	900	2	B70694	probable infB - My
879	143.5	6.1	228	2	A44982	collagen UCOL1 - p	952	139.5	5.9	914	2	T08081	probable myrosinas
880	143.5	6.1	341	2	B75774	conserved hypotet	953	139	5.9	282	2	T16036	cuticle collagen c
881	143.5	6.1	527	2	B70700	hypotheical prote	954	139	5.9	294	2	T35892	hypotheical prote
882	143.5	6.1	608	2	T32923	hypotheical prote	955	139	5.9	298	2	T27644	hypotheical prote
883	143.5	6.1	660	1	Q0883	BHLFI protein - hu	956	139	5.9	328	2	G88499	protein K04G7.10 l
884	143.5	6.1	709	2	T28712	hypotheical prote	957	139	5.9	524	2	T27043	hypotheical prote
885	143.5	6.1	720	1	A55160	Tf9 protein - frui	958	139	5.9	860	2	S43846	xylanase B - rumen
886	143.5	6.1	1268	2	B99789	hemagglutinin/hemo	959	139	5.9	1209	2	T13153	brama associated
887	143.5	6.1	1270	2	B85649	hypotheical prote	960	139	5.9	1279	2	A47363	RNA helicase A - h
888	143.5	6.1	1666	2	T43169	hypotheical prote	961	139	5.9	1839	2	S77626	mannuronan C-5-epi
889	143	6.1	182	2	A02947	keratin, 60K type	962	138.5	5.9	152	2	G96010	hypotheical expor
890	143	6.1	294	2	T29838	hypotheical prote	963	138.5	5.9	299	2	T05494	glycine-rich prote
891	143	6.1	556	2	T42100	serine/threonine p	964	138.5	5.9	469	2	T326097	probable ATP-bindi
892	142.5	6.0	197	2	T46413	keratin KAP5.5 - s	965	138.5	5.9	576	1	S24453	colicin E7 (EC 3.1
893	142.5	6.0	329	2	T32783	hypotheical prote	966	138.5	5.9	735	2	T45059	hypotheical prote
894	142.5	6.0	590	2	A26638	homeotic protein D	967	138.5	5.9	859	2	D96502	hypotheical prote
895	142.5	6.0	648	2	S04832	glutinin high mole	968	138.5	5.9	949	2	D90803	Aida-I adhesin-lik
896	142.5	6.0	693	2	T33251	hypotheical prote	969	138.5	5.9	1005	2	H85611	probable adhesin Z
897	142	6.0	159	2	C49773	ecdysone-dependent	970	138.5	5.9	1111	2	T29070	hypotheical prote
898	142	6.0	164	2	S11847	rab16c protein - f	971	138.5	5.9	1411	2	T48529	hypotheical prote
899	142	6.0	167	2	T71779	glycine-rich RNA-b	972	138.5	5.9	2441	2	D71623	erythrocyte membra
900	142	6.0	266	1	TLBP2X	tail fiber protein	973	138	5.8	283	2	T19141	hypotheical prote
901	142	6.0	269	2	S48444	probable temperatu	974	138	5.8	532	2	T35119	probable aminotran
902	142	6.0	272	2	C75548	hypotheical prote	975	138	5.8	640	2	T08179	LRG5 protein - Chl
903	142	6.0	324	2	T28032	hypotheical prote	976	138	5.8	1087	2	T30844	serine-repeat anti
904	142	6.0	351	1	OZZQRU	circumsporozoite p	977	137.5	5.8	165	2	T03583	glycine-rich RNA-b
905	142	6.0	387	2	S00867	colicin N - Escher	978	137.5	5.8	448	1	A56018	transcription fact

979	137.5	5.8	598	2	T32166	hypothetical prote	1052	134.5	5.7	297	2	T18638	hypothetical prote
980	137.5	5.8	676	2	S41022	hypothetical prote	1053	134.5	5.7	326	2	T29810	hypothetical prote
981	137.5	5.8	1192	2	T18611	probable serine/th	1054	134.5	5.7	326	2	JS0169	collagen col-14 -
982	137.5	5.8	1219	2	T14578	nucleoporin Nup153	1055	134.5	5.7	380	2	T24786	hypothetical prote
983	137.5	5.8	1468	2	A44345	nucleoporin - rat	1056	134.5	5.7	398	2	T34947	hypothetical prote
984	137.5	5.8	1608	2	A28182	hemolysin A - Serr	1057	134.5	5.7	767	2	A35645	major surface prot
985	137.5	5.8	1770	2	A71517	hypothetical prote	1058	134.5	5.7	1199	2	S20969	Na+/Ca2+,K+-exchan
986	137.5	5.8	1805	2	A34736	nestin - rat	1059	134.5	5.7	1938	2	A37361	probable integral
987	137	5.8	179	1	GZRT0	secretory granule	1060	134	5.7	142	2	SL2311	glycine-rich RNA-b
988	137	5.8	197	2	S25088	dehydrin DHN1 - ga	1061	134	5.7	162	2	T10479	glycine-rich RNA-b
989	137	5.8	232	2	S18138	dehydrin DHN2 - ga	1062	134	5.7	210	2	B44984	collagen - nematod
990	137	5.8	383	2	T46707	proteophosphoglyca	1063	134	5.7	235	2	T33380	hypothetical prote
991	137	5.8	691	2	F91251	probable tape meas	1064	134	5.7	278	2	S44796	F09C8.6 protein -
992	137	5.8	858	2	JG0183	myosin Myok - Dict	1065	134	5.7	492	2	D70870	probable PG protei
993	137	5.8	1005	2	T71513	hypothetical prote	1066	134	5.7	627	2	T35608	polyketide hydroxy
994	136.5	5.8	127	2	D84469	hypothetical prote	1067	134	5.7	632	2	T00084	hypothetical prote
995	136.5	5.8	159	2	S18345	probable glycine-r	1068	134	5.7	803	2	C83561	probable type II s
996	136.5	5.8	222	2	A88102	environmental stre	1069	134	5.7	1065	2	T13230	probable isoform
997	136.5	5.8	228	2	D86416	protein W09G10.1 (	1070	134	5.7	1072	2	T13232	dachshund protein
998	136.5	5.8	301	2	T23441	probable beta-1,3	1071	134	5.7	1074	2	T13229	dachshund protein
999	136.5	5.8	407	2	T14909	hypothetical prote	1072	134	5.7	1081	2	T13231	dachshund protein
1000	136.5	5.8	488	2	S86911	bZIP DNA-binding p	1073	134	5.7	1174	2	A40853	potassium channel
1001	136.5	5.8	1264	2	F46103	conserved hypotet	1074	133.5	5.6	175	2	S54255	probable glycine r
1002	136.5	5.8	1290	2	T00018	type V adenylyl cy	1075	133.5	5.6	349	2	T41394	hypothetical serin
1003	136.5	5.8	1365	2	S14871	period protein hom	1076	133.5	5.6	618	2	T42664	hypothetical prote
1004	136	5.8	440	2	T61183	suppressor two of	1077	133.5	5.6	694	2	S71786	wingless receptor
1005	136	5.8	441	2	T49265	transcription fact	1078	133.5	5.6	743	2	T34853	probable fusidic a
1006	136	5.8	524	2	T08931	hypothetical prote	1079	133.5	5.6	1367	2	T33819	hypothetical prote
1007	136	5.8	635	2	T00011	hypothetical prote	1080	133	5.6	127	2	S49195	GCR 20 protein - f
1008	136	5.8	643	1	FOLJLK	ccal protein - rat	1081	133	5.6	133	2	T09608	environmental stre
1009	136	5.8	647	2	S06450	gene M-twist prote	1082	133	5.6	135	2	C82998	hypothetical prote
1010	136	5.8	924	2	B41359	steroid hormone re	1083	133	5.6	154	2	T01983	tumor related prot
1011	136	5.8	924	2	S12746	potassium channel	1084	133	5.6	155	2	C81983	glycine-rich prote
1012	136	5.8	963	2	T19140	hypothetical prote	1085	133	5.6	195	2	S32123	probable single-st
1013	136	5.8	1823	2	S28974	vitellogenin precu	1086	133	5.6	370	2	T22510	hypothetical prote
1014	135.5	5.7	206	2	J53066	gene M-twist prote	1087	133	5.6	510	2	A32380	nuclear protein fk
1015	135.5	5.7	257	2	T01900	major prion protei	1088	133	5.6	538	2	H86335	T20H2.2 protein -
1016	135.5	5.7	260	2	S53629	major prion protei	1089	133	5.6	611	1	S06047	endo-1,4-beta-xyla
1017	135.5	5.7	298	2	JC1448	collagen col-34 -	1090	133	5.6	622	2	G96762	hypothetical prote
1018	135.5	5.7	342	2	T45886	RNA-binding protei	1091	133	5.6	663	2	S21912	BRCore-Q1-Z1 prote
1019	135.5	5.7	536	2	T37544	hypothetical serin	1092	133	5.6	1077	2	A44067	serine-rich protei
1020	135.5	5.7	610	2	S05807	SAN1 protein - yea	1093	133	5.6	3828	2	T13857	trichorax protein
1021	135.5	5.7	650	2	T22002	hypothetical prote	1094	132.5	5.6	243	2	S27758	maturation-associa
1022	135.5	5.7	716	2	D69855	conserved hypotet	1095	132.5	5.6	308	2	T19846	hypothetical prote
1023	135.5	5.7	1212	2	T13804	shs protein - frui	1096	132.5	5.6	325	2	T38308	hypothetical prote
1024	135.5	5.7	1290	2	S76853	hypothetical prote	1097	132.5	5.6	333	2	C48423	homeotic protein e
1025	135.5	5.7	1576	2	S65774	hypothetical prote	1098	132.5	5.6	547	2	F71287	probable treponema
1026	135	5.7	98	2	S08137	homeotic protein H	1099	132.5	5.6	839	2	E84824	hypothetical prote
1027	135	5.7	129	2	T03861	gene 2C protein -	1100	132.5	5.6	1520	1	TVFFA	protein-tyrosine k
1028	135	5.7	139	2	T33868	hypothetical prote	1101	132.5	5.6	1629	2	T06461	hypothetical prote
1029	135	5.7	162	2	S56703	glycine-rich cell	1102	132.5	5.6	1629	2	F90073	DNA-binding protei
1030	135	5.7	174	2	S00273	period clock prote	1103	132	5.6	2271	2	T04346	hypothetical prote
1031	135	5.7	188	2	S49192	GCR 1 protein - fr	1104	132	5.6	165	2	S59529	glycine-rich RNA-b
1032	135	5.7	241	2	T27929	hypothetical prote	1105	132	5.6	165	2	S41773	glycine-rich RNA-b
1033	135	5.7	302	2	A39615	merozoite 45K surf	1106	132	5.6	300	2	A39112	merozoite 45K surf
1034	135	5.7	369	2	S33603	surfactant protein	1107	132	5.6	302	2	A31921	collagen dpy-13 pr
1035	135	5.7	414	2	JN0866	nucleolar protein	1108	132	5.6	305	2	T30165	hypothetical prote
1036	135	5.7	464	2	E82865	conjugal transfer	1109	132	5.6	348	2	A34705	collagen - Caenorh
1037	135	5.7	467	2	S30839	UTR2 protein - yea	1110	132	5.6	427	2	T20800	hypothetical prote
1038	135	5.7	573	2	A33533	cell surface glyco	1111	132	5.6	428	2	T24769	hypothetical prote
1039	135	5.7	595	2	B86212	protein F2489'20 (	1112	132	5.6	517	2	T10927	3C3.18c protein -
1040	135	5.7	888	2	T46726	secreted acid phos	1113	132	5.6	647	2	SL8737	gag polyprotein -
1041	135	5.7	1302	2	C81182	iron-regulated pro	1114	132	5.6	700	2	IS1235	DEAD box protein -
1042	135	5.7	1804	2	T34518	nestin - golden ha	1115	132	5.6	705	2	S32644	nucleolin - Africa
1043	135	5.7	1904	2	T13256	tail-host specific	1116	132	5.6	782	2	A10062	conserved hypotet
1044	135	5.7	2468	2	A83412	hypothetical prote	1117	132	5.6	1525	2	T14961	hypothetical prote
1045	134.5	5.7	158	2	T08957	hypothetical prote	1118	131.5	5.6	252	2	T10697	immature seed prot
1046	134.5	5.7	197	2	T03442	glycine-rich prote	1119	131.5	5.6	322	2	G95244	hypothetical prote
1047	134.5	5.7	209	2	A41342	Glycine-rich prote	1120	131.5	5.6	355	2	C39725	hypothetical prote
1048	134.5	5.7	278	2	S39310	circumsporozoite p	1121	131.5	5.6	386	2	A48571	circumsporozoite p
1049	134.5	5.7	289	2	S74632	merozoite surface	1122	131.5	5.6	461	2	T10265	arabinogalactan-p
1050	134.5	5.7	291	2	T20942	hypothetical prote	1123	131.5	5.6	463	2	T10015	hypothetical prote
1051	134.5	5.7	297	2	T18637	hypothetical prote	1124	131.5	5.6	471	2	S15035	acetylcholinestera

1125	131.5	5.6	479	2	A38307	metallopeptidase	1198	129	5.5	551	1	NRECE3	colicin E3 (EC 3.1
1126	131.5	5.6	520	2	T37541	probable glycolipase	1199	129	5.5	581	1	NDECE2	colicin E2 (EC 3.1
1127	131.5	5.6	520	2	AB1183	ATP-dependent RNA	1200	129	5.5	626	2	T01485	probable polygalac
1128	131.5	5.6	525	2	A35596	nuclear pore glyco	1201	129	5.5	632	2	T07587	probable polygalac
1129	131.5	5.6	589	2	A22623	hypothetical prote	1202	129	5.5	670	2	F84540	hypothetical prote
1130	131.5	5.6	713	2	UC2534	RVG protein - rat	1203	129	5.5	707	2	A46302	PrB-associated epl
1131	131.5	5.6	940	2	D89723	protein F398.1b [	1204	129	5.5	895	2	AD0541	outer membrane fim
1132	131.5	5.6	945	2	T21998	hypothetical prote	1205	129	5.5	1442	2	T42607	transcription acti
1133	131.5	5.6	962	2	S03818	carboxymethylcellu	1206	129	5.5	1741	2	S74910	hemolysin - Synch
1134	131.5	5.6	1039	2	T35878	hypothetical prote	1207	128.5	5.4	157	1	S14857	glycine-rich prote
1135	131.5	5.6	1130	2	T30251	repetin - mouse	1208	128.5	5.4	271	2	A47156	hexamer-binding pr
1136	131.5	5.6	1704	2	T43141	vitellogenin 1 - m	1209	128.5	5.4	401	2	A48423	engrailed homeodom
1137	131.5	5.6	1732	2	T43026	probable DNA-dirce	1210	128.5	5.4	427	2	A32372	female-specific do
1138	131	5.5	180	2	JC7876	prion protein homo	1211	128.5	5.4	549	2	B32372	male-specific doub
1139	131	5.5	184	1	CGRT58	collagen alpha 2(I	1212	128.5	5.4	564	1	KRHUEB	keratin 6b, type I
1140	131	5.5	304	2	T16107	hypothetical prote	1213	128.5	5.4	564	2	161771	keratin 6f, type I
1141	131	5.5	307	2	T37287	collagen 36 - Caen	1214	128.5	5.4	634	2	A54495	knob protein prote
1142	131	5.5	355	2	F71435	probable nuclear a	1215	128.5	5.4	710	2	T31502	hypothetical prote
1143	131	5.5	440	2	S71795	transcription fact	1216	128.5	5.4	1275	2	T49362	hypothetical prote
1144	131	5.5	485	2	B40552	bindin fertilizati	1217	128.5	5.4	1367	2	T13703	tama protein - fru
1145	131	5.5	642	2	S27806	homeotic protein B	1218	128.5	5.4	1621	2	JC4085	protein-tyrosine k
1146	131	5.5	653	1	S44749	C06G4.2 protein -	1219	128	5.4	185	2	JC4085	glycine-rich cutic
1147	131	5.5	724	2	A48569	antigen Em100 - Ei	1220	128	5.4	321	2	A38712	fibrillarlin [valid
1148	131	5.5	728	2	S21913	BRCore-TN1-Q1-Z1	1221	128	5.4	339	2	S20880	homeotic protein H
1149	131	5.5	753	2	A27041	tyrosine kinase-re	1222	128	5.4	514	2	S21914	BRCore-2 protein -
1150	131	5.5	1053	2	T07965	reverse transcript	1223	128	5.4	547	2	H85699	partial probable a
1151	131	5.5	1148	2	A71446	hypothetical prote	1224	128	5.4	547	2	C90842	partial probable a
1152	131	5.5	1332	2	T15670	hypothetical prote	1225	128	5.4	598	2	A84616	hypothetical prote
1153	131	5.5	2703	1	A24420	notch protein - fr	1226	128	5.4	606	2	S13367	Om(1D) protein - f
1154	130.5	5.5	163	2	JC6571	cold-inducible RNA	1227	128	5.4	640	2	A41726	homeotic protein B
1155	130.5	5.5	251	2	D96010	hypothetical expor	1228	128	5.4	733	2	S10932	probable protein k
1156	130.5	5.5	286	2	S34665	collagen, cuticula	1229	128	5.4	918	2	A88188	protein C18H9.3 [i
1157	130.5	5.5	369	2	S11980	variable major pro	1230	128	5.4	1870	2	S37671	MHC class III hist
1158	130.5	5.5	381	2	A54415	transcription fact	1231	128	5.4	1970	1	S21054	DNA-directed RNA p
1159	130.5	5.5	473	2	F70031	cell wall-binding	1232	128	5.4	2248	1	D42088	adenylate cyclase
1160	130.5	5.5	643	2	I50539	intermediate filam	1233	127.5	5.4	290	2	B88638	protein F58F6.2 [i
1161	130.5	5.5	748	2	T04011	hypothetical prote	1234	127.5	5.4	321	2	F60110	repetitive protein
1162	130.5	5.5	1036	1	A34755	nitrogen regulator	1235	127.5	5.4	325	2	T16324	hypothetical prote
1163	130.5	5.5	2154	2	F83068	hypothetical prote	1236	127.5	5.4	373	2	S43455	hypothetical prote
1164	130.5	5.5	2440	2	S39162	transcription coac	1237	127.5	5.4	550	1	FGRTA	fibrinogen alpha c
1165	130	5.5	123	2	C39777	hypothetical prote	1238	127.5	5.4	693	2	JC7925	nucleolin - common
1166	130	5.5	182	1	KRB02A	keratin, 68K type	1239	127.5	5.4	817	2	T22442	hypothetical prote
1167	130	5.5	250	2	B35026	filaggrin B - mous	1240	127.5	5.4	827	2	JC4900	transferred entry
1168	130	5.5	253	2	S53618	major prion protei	1241	127.5	5.4	1641	2	T10955	early nodulin bind
1169	130	5.5	253	2	S53619	major prion protei	1242	127.5	5.4	1872	2	S36152	MHC class III hist
1170	130	5.5	331	2	F70820	hypothetical glyci	1243	127.5	5.4	1940	2	F75393	hypothetical prote
1171	130	5.5	334	2	S53490	RNA-binding protei	1244	127	5.4	228	2	T49891	glycine-rich prote
1172	130	5.5	448	2	S05355	hypothetical prote	1245	127	5.4	241	2	S71048	major prion protei
1173	130	5.5	563	2	A36054	mucin homolog - bo	1246	127	5.4	253	1	UJHU	major prion protei
1174	130	5.5	622	2	G86371	hypothetical prote	1247	127	5.4	253	2	S53635	major prion protei
1175	130	5.5	625	2	T41603	alpha-amylase - fi	1248	127	5.4	253	2	S53614	major prion protei
1176	130	5.5	676	2	S61977	transcription fact	1249	127	5.4	253	2	I37032	major prion protei
1177	130	5.5	1618	2	S21424	nestin - human	1250	127	5.4	253	2	I61847	major prion protei
1178	130	5.5	1872	2	T30888	vitellogenin - Ath	1251	127	5.4	253	2	S53616	major prion protei
1179	130	5.5	3705	2	AD0123	probable autotrans	1252	127	5.4	298	2	A40616	34K antigen - Myco
1180	129.5	5.5	142	2	C33910	sal homeotic prote	1253	127	5.4	370	1	OZQOAV	c-Maf protein - mo
1181	129.5	5.5	287	2	T15779	hypothetical prote	1254	127	5.4	378	2	I57555	circumsporozoite p
1182	129.5	5.5	900	2	B87957	collagen 1 - Caeno	1255	127	5.4	409	2	A70647	probable PPE prote
1183	129.5	5.5	564	1	KRHUEA	keratin 6a, type I	1256	127	5.4	496	2	A54770	N-acetylglucosamin
1184	129.5	5.5	666	2	T05432	hypothetical prote	1257	127	5.4	579	2	E83144	hypothetical prote
1185	129.5	5.5	732	2	T08420	1-phosphatidylinos	1258	127	5.4	644	1	I40712	endo-1,4-beta-xyla
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1187	129.5	5.5	948	2	T26417	hypothetical prote	1260	127	5.4	719	2	S51007	hypothetical prote
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1189	129.5	5.5	4776	2	E95206	cell wall surface	1262	127	5.4	748	2	S19652	hypothetical prote
1190	129	5.5	155	2	S20846	glycine-rich prote	1263	127	5.4	1145	2	G87284	adenylate cyclase
1191	129	5.5	156	2	S41771	glycine-rich RNA-b	1264	127	5.4	1705	2	S51672	probable tape-meas
1192	129	5.5	201	2	G01204	twist protein homo	1265	127	5.4	1787	2	AG1360	hypothetical prote
1193	129	5.5	256	2	JU0268	major prion protei	1266	127	5.4	301	2	T21314	hypothetical prote
1194	129	5.5	256	2	S37149	prion protein - go	1267	126.5	5.4	342	2	S18649	homeotic protein H
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1197	129	5.5	456	1	KRHU5	keratin 15, type I	1270	126.5	5.4				

1271 126.5 5.4 742 2 JC7595 scavenger receptor  
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 1273 126.5 5.4 910 2 A34721 androgen receptor  
 1274 126.5 5.4 911 2 B34721 androgen receptor  
 1275 126.5 5.4 929 2 C96623 hypothetical prote  
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 1278 126.5 5.4 2059 2 D82671 surface protein XF  
 1279 126.5 5.4 2142 2 B35098 MHC class III hist  
 1280 126 5.3 144 2 S35716 glycine-rich prote  
 1281 126 5.3 199 2 S32224 acp-22 protein - y  
 1282 126 5.3 284 2 A35419 neurophil protein  
 1283 126 5.3 302 2 T15936 hypothetical prote  
 1284 126 5.3 305 2 S33690 fibrillarlin - fisa  
 1285 126 5.3 320 2 T09555 fibrillarlin - Arab  
 1286 126 5.3 334 2 A31920 collagen sqt-1 pre  
 1287 126 5.3 340 2 AB3401 hypothetical prote  
 1288 126 5.3 417 2 JC7092 Psul protein - fis  
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 1316 125 5.3 425 2 T11619 probable nucleopor  
 1317 125 5.3 438 2 D90734 probable tail fibe  
 1318 125 5.3 438 2 S62453 hypothetical prote  
 1319 125 5.3 440 2 S37303 sox-4 protein - mo  
 1320 125 5.3 466 2 T35164 probable secreted  
 1321 125 5.3 509 2 T09572 cdc2-like protein  
 1322 125 5.3 534 2 T39903 serine-rich protei  
 1323 125 5.3 570 2 S56132 cellulase (EC 3.2.  
 1324 125 5.3 635 2 F75477 hypothetical prote  
 1325 125 5.3 642 1 S34416 transcription fact  
 1326 125 5.3 712 2 B47021 pectic enzyme secr  
 1327 125 5.3 943 2 JC4081 sucrose/fructanase  
 1328 125 5.3 955 2 G64866 probable membrane  
 1329 125 5.3 1315 2 T05300 hypothetical prote  
 1330 124.5 5.3 177 2 S37749 collagen alpha 2(X  
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 1334 124.5 5.3 458 2 T31631 hypothetical prote  
 1335 124.5 5.3 481 2 A26483 bindin precursor -  
 1336 124.5 5.3 516 2 AC1540 ATP-dependent RNA  
 1337 124.5 5.3 682 2 JC7670 cathepsin-B mRNA 3  
 1338 124.5 5.3 687 2 F83671 hypothetical prote  
 1339 124.5 5.3 710 2 A31641 daughterless (da)  
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 1341 124.5 5.3 995 2 T32466 hypothetical prote  
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1344 124.5 5.3 1374 2 AE3259 extracellular seri  
 1345 124.5 5.3 1613 2 T06678 hypothetical prote  
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 1347 124.5 5.3 3591 1 S21010 filamentous hemagg  
 1348 124 5.2 254 2 A34759 prion protein - Ch  
 1349 124 5.2 285 2 T31503 hypothetical prote  
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 1351 124 5.2 452 2 I49595 cyokeratin 15 - m  
 1352 124 5.2 452 2 T30082 hypothetical prote  
 1353 124 5.2 459 2 T45911 hypothetical prote  
 1354 124 5.2 486 1 A57601 transcription fact  
 1355 124 5.2 562 2 T49788 related to merozoi  
 1356 124 5.2 580 2 S11890 serine proteinase  
 1357 124 5.2 784 2 AC1091 5'-nucleotidase, p  
 1358 124 5.2 787 2 T00798 hypothetical prote  
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 1360 124 5.2 1325 2 A64905 yckell polarity prot  
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 1362 124 5.2 1428 2 T13926 probable protein p  
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 1384 123.5 5.2 1403 2 S77624 mannanuron C-5-epi  
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 1393 123 5.2 483 2 A55033 keratin 12 - mouse  
 1394 123 5.2 511 2 S24345 Balbiani ring 1 pr  
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 1397 123 5.2 624 2 T02289 probable polygalac  
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 1399 123 5.2 841 2 C87331 ISCC2, transposase  
 1400 123 5.2 902 2 T26775 hypothetical prote  
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 1402 123 5.2 1334 2 T50568 probable multi-dom  
 1403 123 5.2 1560 2 T30282 calcium-binding pr  
 1404 122.5 5.2 160 2 T26289 hypothetical prote  
 1405 122.5 5.2 296 2 B39581 GRESAG protein 9u  
 1406 122.5 5.2 391 2 A49645 transcription fact  
 1407 122.5 5.2 437 2 A55682 keratin l3, type I  
 1408 122.5 5.2 532 2 B35621 spore germination  
 1409 122.5 5.2 626 2 F85295 hypothetical prote  
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Db 725 GGNSETGSGDGGAGGNGGAAGTGTGGDGLTGCTG 759

RESULT 2  
A70934  
hypothetical glycine-rich protein Rv0578c - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: A70934  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: A70934  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1306 <COL>  
A;Cross-references: UNIPROT:O53775; GB:AL021942; GB:AL123456; NID:g3242298; PIDN:CAA1744  
A;Experimental source: strain H37RV  
C:Genetics:  
A;Gene: Rv0578c  
C;Superfamily: collagen alpha 1(IV) chain

Query Match 18.6%; Score 439.5; DB 2; Length 1306;  
Best Local Similarity 30.9%; Pred. No. 8e-16;  
Matches 151; Conservative 34; Mismatches 194; Indels 109; Gaps 22;

QY 17 GSCEAGPLQSGRESSTGTN--IGALGHLGLDALSGVGKAIGK-----EAGGAAGSKV 67  
Db 567 GHGAAGAL-----GVNGGVGAGGHC-CD---PGVGGAGGGGSGSTPGANGACENTP 615

QY 68 SEA--LQQGTREAVGTGVRQVPFGAADALGNRVGE-AAHALGNTGHE----IGROAEDV 120  
Db 616 TSGGNGGNGRGADATGFGQTGASGGRGDDGLVNGGAGGAGSGSKGLPGLRLGNP- 674

QY 121 IRHGADAVRGSWGVPHSGAWTSGHGLFGSQGLGGQG-----CGNPG 166  
Db 675 ---GLDGGTGGNGGAGGSGGAWAGNGGTGGAGGTGGVGTGGSGSDGVNGSSAGADGHFG 731

QY 167 GLCTPWHVHGPNGSAGSFGMNPQG-----APWGOGNGGPPNPNTN-----TOG 210  
Db 732 GTGGVGTGKGDDGGDGGAPNVAGSQCPGAGGDDGTGCGVGGNGRGIDGADATAG 791

QY 211 AVAQPGYGVSRASNQNEGCTNPP-----PGSG-----CGSSNSGSGSGSGSGSGSNGD 262  
Db 792 ARQDGGAGGAGGKGRGGTGGPGGAGPAGTTGSGQAGGNGGSGGTGGDPDGGNGANGS 851

QY 263 --NNNGSSGSGSGSGSGSGSGSGSG-----GSS-----GSSSGNSG----- 298  
Db 852 VFTNNGITGGNGGNGNAGPSGAGSGGAGSTFGATGSSSIHVNGGNGGNGGNGDHALSG 911

QY 299 -GSRGDSGSSSSGSGTSGS--SSNGHSGS-----GNGHKPGCKPGNEARGSGESGI 349  
Db 912 NGAAGGNGGNGGNSLRGSGGAGHGGNGGNGNARGMGDDGTGCGACGNAGCQTGNGGAGN 971

QY 350 QGPRGQGVSSNMTREISKENR-----LIGSGSDNYRQGSWSGSGGDAVGGV---NTVNS 402  
Db 972 GDDGTGSDGNPCAITGSGGRGDDGGVGGQGSVAGDGDGGRGAGGTGGTGLRGTGTA 1031

QY 403 ETSPGMPN 410  
Db 1032 TGATGTFD 1039

RESULT 3  
T49109  
glycine-rich protein - Arabidopsis thaliana  
N;Alternate names: protein AT4g22020  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004

C;Accession: T49109  
R;Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Me submitted to the Protein Sequence Database, May 2000  
A;Reference number: Z25016  
A;Accession: T49109  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-396 <REV>  
A;Cross-references: UNIPROT:O65450; EMBL:AL022140; GSPDB:GN00062; ATSP:AT4g22020  
A;Experimental source: cultivar Columbia; BAC clone FIN20  
C:Genetics:  
A;Gene: ATSP:AT4g22020  
A;Map position: 4  
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8

Query Match 17.9%; Score 423; DB 2; Length 396;  
Best Local Similarity 33.2%; Pred. No. 2e-15;  
Matches 133; Conservative 22; Mismatches 169; Indels 76; Gaps 14;

QY 17 GSGEAGPLQSGRESSTGTNIGALGHLGLDALSGVGKAIGKEAGGAAGSKVSEALGQGT 76  
Db 63 GGG 122

QY 77 EAVGTGV-RQVPFGAADALGNRVGEAAHALGNTGHEIGROAEDVIRHGADAVRGSWQGV 135  
Db 123 SCAGAGVGGTTCGVGG 164

QY 136 PCHSGAWTSGHGLFGSQGLGGQGNPGGLGTPWHVHYPGNAGSFGMNPQGAPWQ 195  
Db 165 GAGAGVGGSSGAG--GG 214

QY 196 GGNGGPPNPFGTWTQGAQPGYGVSRASNQNEGCTNPPPSGSGSGSGSGSGSGSGSGS 255  
Db 215 GGGGG--GGGGGGGANGSGSGHGS-----GSGAGCGVSGAAGGGGGGGGGGGGG 258

QY 256 GGSN---GDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSGSGSGSGSGSGSGSGS 312  
Db 259 GSGSGKVGSGYGHGSGFGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 314

QY 313 STGSSSGNHGSGGGNGHKGPKGCKPGNEARGSGES-GIOGPRGQGVSSNMTREISKENRL 371  
Db 315 GNGKSGSGSGGG 356

QY 372 LGSGDNYRQGSWSGSG--GGDAVGG-----VNTVNSETSP 406  
Db 357 NCGGGVGFMGIGFGLGIGGGSGGTGTTLTGDKNSP 396

RESULT 4  
E70806  
hypothetical glycine-rich protein Rv3507 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: E70806  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: E70806  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1381 <COL>  
A;Cross-references: GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA17744.1; PID:g2924444  
A;Experimental source: strain H37RV  
C:Genetics:  
A;Gene: Rv3507  
C;Superfamily: collagen alpha 1(IV) chain

Query Match 17.6%; Score 415.5; DB 2; Length 1381;  
Best Local Similarity 29.9%; Pred. No. 1.5e-14;





QY 340 EARGSGSIOGPRGQGVSSNMREISKEGNRLILGSG-DNYRGQSGSWGSGGDAVGVN 398  
Db 713 EGGAGNSGCGTNGSGGAGGAG--GKGGTGGAGGSADNPTGAPGAGGAGGTGGAGAG 770  
QY 399 TVNSETSPG 407  
Db 771 GAGGATGTG 779

RESULT 7  
F70580  
hypothetical glycine-rich protein Rv2162c - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: F70580  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: F70580  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-532 <COL>  
A:Cross-references: UNIPROT:O06215; GB:AL123456; NID:g3261759; PIDN:CAB08665.  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: Rv2162c  
C:Superfamily: uncharacterized glycine-rich protein, PE motif containing

Query Match 17.1%; Score 404.5; DB 2; Length 532;  
Best Local Similarity 32.2%; Pred. No. 2.4e-14;  
Matches 138; Conservative 33; Mismatches 182; Indels 75; Gaps 17;  
QY 6 PLACLILALCLGSG-EAGPLQSGESTGTNIGALHGLGLDALSEGVGKA-----IGKEA 59  
Db 106 PTQTLRPLRIGNADGPGQNGGPG-GLLYGNGGAGGDTANPNGSGSAGLTONGG 164  
QY 60 GGAAGSKVSEALGGGTREAVGTGVRQVPGFGAADALG-----NRVGEAAHALNTGHEIG 114  
Db 165 AGGAGA---ATCAGGAGGNGWLYNGGPGGAAGLTAGGVSPAGGAGGAAGLWGH--- 217  
QY 115 RQADVTRHGADAVRGSQVPHSGAWETSGHGIFPGSOGLGCGQGNPGGLTGPWVH 174  
Db 218 -----GGAGGAGGSASGAPGAGGAGGGRGLLYGDGGAGGAG-GN-GSNGVTGVH 267  
QY 175 GYPNSAGSFGMNPQGAQPGWGGNGGPPNFGTN---TQGAVAQPGVGSVRASNQEGCT 230  
Db 268 GGNAGGAAGLIGNAGGDDGNGGLSNTGASGGAGGAGGAAIIGNGGDGGHGGHG 327  
QY 231 NPPPSGGSGSSNSGGSG-----SQSGSSGSGSNGDNNGSSSGSSSGSSSGSS 285  
Db 328 NSCGAGGAGGAGGAGGAGGHVGLIGNGGGAGGAGGNGNDN-----SSTLADAGSGGAGA 381  
QY 286 SGSSSGSSNSG--GSRGDSGSSSWGSSSTGS-----SSGNHGGSGGNGHK 331  
Db 382 AGNGGLFYNGGVGRGNGGFSFSACTSGGDDGIGGAGGIGGLIGSGGGGCGDGNNGQA 441  
QY 332 PGCEKPGNEARG--SGSSGIGQPRGQGVSSNMREISKEGNRLILGSG-DNYRGQSGSWGS 388  
Db 442 P-----TPNAGDGGAGGNARLIIDGGRG-----GNGEGGDPGPGVRGDDGNGGN 487  
QY 389 GGGDAVGG 396  
Db 488 GGNVAVIG 495

RESULT 8  
D70807  
hypothetical glycine-rich protein Rv3514 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: D70807  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: D70807  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1489 <COL>  
A:Cross-references: GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA17751.1; PID:g2924451  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: RV3514  
C:Superfamily: collagen alpha 1(IV) chain

Query Match 17.1%; Score 403; DB 2; Length 1489;  
Best Local Similarity 32.5%; Pred. No. 7.1e-14;  
Matches 137; Conservative 30; Mismatches 179; Indels 76; Gaps 19;  
QY 17 GSGEAGPLQSGESTGTNIGALHGLGLDALSEGVGKAICKEAGGAAGSKVSEALOGGTR 76  
Db 1090 GTGGTG---GVGGTGGDCGNA-GTCAGDPKGKGTGCTGTGCGGCGAGGSGGANFNGGTG 1144  
QY 77 EAVGTGVRQVPGFGAADALGNRVGEAA-----HALGNTGHEIGRQAEDEVTRHGADAVR 129  
Db 1145 GTGGTG-----GTGGKGMGGIAGDGGPGDGGNAGVGKGGTNG-----NGSGGT 1191  
QY 130 GSNQGVPHSGA-----METSQGHG--FGSGGLGGGQ-----GNPGLGLTPWVHG 175  
Db 1192 GTTGGAGGAGGAGLANTGTAGNAGIGDGGCGGNGGQDSSGLGGQPGFAGGPGGKG 1251  
QY 176 YPNSAGSFGMNPQGA--PWQGGNGGP-----PNFGTNTQGAVAQPGVGSVRASNQ 226  
Db 1252 GAGNAGTGTNGSGAGGAGGCGGAGGAGISFNSNGSGTGTGTGGVGGTG-GD--GGAAG 1308  
QY 227 EGTNPPPSGSG--GGSSNSGSGSQSGSSSGSGSNGDNNGSSSGSSSGSSSGSSSG 284  
Db 1309 TGAGDPKGKGTGCTGTGCGGSGGAGGSGGANFNGGTGCTGTGCGKGMGGIAGDGGPG 1368  
QY 285 SSGSSS-----GSSGN--SGSRGDSGSESSWSSTGSSGNHCGSGGNGHKPGCEKP 337  
Db 1369 GDGNAGVCGKGTNGSGSGTGTGTGGPGSGGATFGSGTGKGGAGGDDG--DGAD-- 1424  
QY 338 GNEARGSGESGIGQPRGQGVSSNMREISKEGNRLILG--GSGDNYRGQSGSWGSGGDAVGG 396  
Db 1425 GGAATGVDGDDGGGNG-----GNGGTGVSFPGILGAGGTGGLGGAGAGGG 1473  
QY 397 VN 398  
Db 1474 AD 1475

RESULT 9  
H70846  
hypothetical glycine-rich protein Rv3345c - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: H70846  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: H70846  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1538 <COL>

D<sub>b</sub> 333 GGGGTGGLLFNGGAGGH-GAAAGNGL--AAGNGVSSGGGGAGGTGG-----AGDGGGA 384

Qy 231 NPPSGGGSSNSGG-----GSGSQSGSSGSGSNGDNNNGSSSGSSSSG-----;





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2005, 00:04:15 ; Search time 179 Seconds  
(without alignments)  
1258.742 Million cell updates/sec

Title: US-10-063-561-52

Perfect score: 2363

Sequence: 1 MKFQGPLACLLALCLGSGE.....KLGFINWDAINKDQRSSRIP 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2363	100.0	440	2	Q6UCX7 homo sapien
2	1996	84.5	476	2	Q6E0U4
3	1043	44.1	517	2	Q6E0U6 mus musculus
4	1038.5	43.9	508	2	Q6P253 mus musculus
5	1030	43.6	493	2	Q6S239 mus musculus
6	546.5	23.1	407	2	Q6C4L6 mus musculus
7	486	20.6	1553	2	Q6FPR0
8	471	19.9	1274	2	Q6CHN8
9	460.5	19.5	1938	2	Q7TW50
10	450.5	19.1	1079	2	Q6MW7
11	439.5	18.6	1306	2	Q7D9L6
12	439.5	18.6	1306	2	Q6MX28
13	439.5	18.6	1306	2	Q7U107
14	433	18.3	725	2	Q7SEPT7
15	430	18.2	1391	2	Q6C6W0
16	428	18.1	528	2	Q63WJ8
17	426.5	18.0	1815	2	Q6CF66
18	426	18.0	512	2	Q62HK1
19	423	17.9	396	2	Q654D0
20	420.5	17.8	1384	2	Q8V1Z1
21	415.5	17.6	1381	2	Q6MW9
22	412.5	17.5	484	2	Q6MWY1
23	412.5	17.5	1360	2	Q7TW4
24	406	17.2	1901	1	PG54 MYCTU
25	404.5	17.1	532	2	Q7D7F8
26	403	17.1	1224	2	Q6CN84
27	403	17.1	1489	2	Q6MW6
28	400.5	16.9	992	2	Q7TW8
29	400.5	16.9	1538	2	Q6MW70
30	399.5	16.9	853	2	Q79F55
31	399	16.9	786	2	O18740 canis famil

32	398	16.8	850	2	Q7U0P1
33	397.5	16.8	743	2	Q6RHW0
34	397.5	16.8	763	2	Q7U0R0
35	397.5	16.8	1217	2	Q8V1Y9
36	397.5	16.8	1460	2	Q7TWC3
37	397.5	16.8	1507	2	Q8VJ23
38	397	16.8	897	2	Q6Q294
39	396.5	16.8	1715	2	Q8VIZ0
40	395	16.7	714	2	Q6MMW8
41	395	16.7	749	2	Q7TWK6
42	395	16.7	1660	2	Q79PD4
43	395	16.7	1685	2	Q7D721
44	393	16.6	626	2	Q7TWM2
45	392.5	16.6	923	2	Q79FU3
46	392.5	16.6	923	2	Q7U0X8
47	392	16.6	731	2	Q6MWX5
48	392	16.6	775	2	Q8VJ15
49	392	16.6	1329	2	Q79FP2
50	392	16.6	1408	2	Q8VK17
51	392	16.6	5263	1	FBOH_BOMMO
52	391	16.5	2249	2	Q9NHW4
53	390.5	16.5	635	2	Q8VK71
54	389.5	16.5	1408	2	Q7U022
55	388	16.4	1150	2	Q7TYG8
56	387.5	16.4	619	2	Q91PQ9
57	386	16.3	778	1	PG46 MYCTU
58	385.5	16.3	518	2	Q67WR0
59	383.5	16.2	767	2	Q79FT0
60	383	16.2	641	1	EBN1_EBV
61	383	16.2	641	2	Q777E1
62	381.5	16.1	738	2	Q8VK15
63	381.5	16.1	741	2	Q79FP1
64	381.5	16.1	774	2	Q7U0P7
65	381	16.1	390	2	Q9M3Y2
66	380.5	16.1	749	2	Q7D974
67	380.5	16.1	837	2	Q79FY9
68	380.5	16.1	2401	2	Q7RF52
69	379.5	16.1	628	2	Q8VJ19
70	379.5	16.1	1618	2	Q6FQ10
71	379	16.0	465	1	GRP2_PHAVU
72	378.5	16.0	490	2	Q7VSE6
73	378	16.0	588	2	Q6MWX7
74	378	16.0	617	2	Q46172
75	376.5	15.9	749	2	Q79FV7
76	375	15.9	914	1	WA22 MYCTU
77	374	15.8	831	2	Q7U2D6
78	373.5	15.8	584	2	Q7D580
79	373.5	15.8	584	2	Q7TW48
80	373.5	15.8	667	2	Q7D8W7
81	373.5	15.8	667	2	Q79FT3
82	373.5	15.8	1382	2	Q6BN56
83	373	15.8	871	2	O44358
84	372	15.7	694	2	Q7D724
85	372	15.7	909	2	Q7U1D3
86	371.5	15.7	671	2	Q7U0R1
87	371	15.7	400	2	Q8GTL0
88	371	15.7	615	2	Q6MX26
89	371	15.7	615	2	Q7TXQ0
90	371	15.7	644	2	Q8WSW4
91	371	15.7	747	1	SPD1_NEPCL
92	370.5	15.7	491	2	Q79FP3
93	369.5	15.6	491	2	Q7U027
94	369.5	15.6	795	2	Q7U020
95	369.5	15.6	1428	2	O44341
96	369	15.6	557	2	Q6BVD0
97	369	15.6	622	2	Q8VKN3
98	367.5	15.6	608	2	Q7U2C0
99	367.5	15.6	608	2	Q7U125
100	366.5	15.5	877	2	Q7U2D7
101	366	15.5	408	2	Q43688
102	366	15.5	610	2	Q9VSV8
103	366	15.5	691	2	Q9B1U3
104	365.5	15.5	496	2	Q79G09

Q7u0p1	mycobacteri
Q6rhw0	mus musculu
Q7u0r0	mycobacteri
Q8viy9	mycobacteri
Q7tWC3	mycobacteri
Q8vj23	mycobacteri
Q6q294	agelenopais
Q8vizo	mycobacteri
Q6mmw8	mycobacteri
Q7twk6	mycobacteri
Q79pd4	mycobacteri
Q7d721	mycobacteri
Q7tWm2	mycobacteri
Q79fu3	mycobacteri
Q7u0x8	mycobacteri
Q6mwX5	mycobacteri
Q8vj15	mycobacteri
Q79fp2	mycobacteri
Q8vk17	mycobacteri
P05790	bombyx mori
Q8nhw4	nephila cla
Q8vk71	mycobacteri
Q7u022	mycobacteri
Q7tyg8	mycobacteri
Q91pq9	cynomolgus
P71933	mycobacteri
Q67wr0	oryza sativ
Q79ft0	mycobacteri
P03211	epstein-bar
Q777e1	human herpe
Q8vk15	mycobacteri
Q79fp1	mycobacteri
Q7u0p7	mycobacteri
Q9m3y2	tritium ae
Q7d974	mycobacteri
Q79fy9	mycobacteri
Q7rf52	plasmodium
Q8vj19	mycobacteri
Q6fq10	candida gla
P10496	phaseolus v
Q7vep6	mycobacteri
Q6mwX7	mycobacteri
Q46172	nephila cla
Q79fv7	mycobacteri
Q06794	mycobacteri
Q7u2d6	mycobacteri
Q7d580	mycobacteri
Q7d8w7	mycobacteri
Q79ft3	mycobacteri
Q6bn56	debaromyce
O44358	nephila cla
Q7d724	mycobacteri
Q7u1d3	mycobacteri
Q7u0r1	mycobacteri
Q8gtl0	oryza sativ
Q6mx26	mycobacteri
Q7txq0	mycobacteri
Q8wsw4	nephila cla
P19837	nephila cla
Q79fp3	mycobacteri
Q7u027	mycobacteri
Q7u020	mycobacteri
O44341	halotis ru
Q6bvd0	debaromyce
Q8vkn3	mycobacteri
Q7u2c0	mycobacteri
Q7u125	mycobacteri
Q7u2d7	mycobacteri
Q43688	vigna ungui
Q9vsv8	drosofila
Q9b1u3	dolomedea t
Q79g09	mycobacteri

105	365.5	15.5	496	2	Q7U2U5	Q7u2u5 mycobacteri	178	342	14	5	515	1	PG34 MYCTU	O50594 mycobacteri
106	365.5	15.5	533	2	Q8VKR5	Q8vkr5 mycobacteri	179	341.5	14.5	1468	2	Q9GUB5	Q9gub5 gallaria me	
107	365	15.4	576	2	P71664	P71664 mycobacteri	180	341	14.4	674	2	Q681A9	Q681a9 arabidopsis	
108	365	15.4	591	2	Q6MX50	Q6mx50 mycobacteri	181	340.5	14.4	452	2	Q7U0U49	Q7u0u49 mycobacteri	
109	365	15.4	663	2	Q8VJC0	Q8vjc0 mycobacteri	182	339.5	14.4	487	2	Q79G08	Q79g08 mycobacteri	
110	364.5	15.4	524	2	Q8J7U0	Q8j7u0 araneus ven	183	339	14.3	614	2	Q9LH97	Q9lh97 arabidopsis	
111	364.5	15.4	801	1	PG10 MYCTU	O53810 mycobacteri	184	339	14.3	937	1	HYR1 CANAL	P46591 candida alb	
112	364.5	15.4	907	2	O44359	O44359 nephila cla	185	338	14.3	429	2	Q817T9	O817t9 araneus ven	
113	364	15.4	421	2	Q9DERY1	Q9dey1 cyprinus ca	186	337	14.3	270	2	Q700C3	Q700c3 arabidopsis	
114	364	15.4	609	2	Q79FV3	Q79fv3 mycobacteri	187	337	14.3	290	2	Q7Y218	Q7y218 arabidopsis	
115	364	15.4	606	2	Q8VKC5	Q8vkc5 mycobacteri	188	337	14.3	840	2	Q95YF6	Q95yf6 patinopecte	
116	364	15.4	626	2	Q9NHW1	Q9nhw1 nephila ina	189	337	14.3	1002	2	Q9BIU8	Q9biu8 argiope tri	
117	363.5	15.4	349	1	GRP ARATH	P27483 arabidopsis	190	336.5	14.2	338	2	Q8VJ24	Q8vj24 mycobacteri	
118	363	15.4	639	2	Q79FU9	Q79fu9 mycobacteri	191	335	14.2	581	2	Q7U1U2	Q7ulu2 debaryomyce	
119	363	15.4	650	2	Q8VJW1	Q8vjw1 mycobacteri	192	334.5	14.2	531	2	Q6BZJ0	Q6bzj0 arabidopsis	
120	363	15.4	1114	2	O6CCAI	O6ccai yarrowia li	193	334	14.1	255	2	Q9SIH2	Q9sih2 arabidopsis	
121	362.5	15.3	561	2	Q8VKR1	Q8vkr1 mycobacteri	194	334	14.1	284	2	Q73E49	Q73e49 bacillus ce	
122	362.5	15.3	2850	1	HORN HUMAN	Q86vz3 homo sapien	195	334	14.1	498	1	PG33 MYCTU	O50615 mycobacteri	
123	362	15.3	486	1	LORI_MOUSE	P18165 mus musculu	196	333.5	14.1	501	2	Q66RZ1	O66rz1 mycobacteri	
124	361.5	15.3	422	2	Q6Z142	Q6z142 oryza sativ	197	333	14.1	466	2	Q7TZG4	O7tzg4 mycobacteri	
125	361	15.3	540	2	Q7TZI3	Q7tzi3 mycobacteri	198	332.5	14.1	342	2	Q9VKG8	Q9vkr8 drosophila	
126	360.5	15.3	342	2	Q6HNZ6	Q6hnz6 bacillus th	199	332.5	14.1	356	2	Q6NNY8	Q6nnys mycobacteri	
127	360	15.2	562	2	Q79FQ7	Q79fq7 mycobacteri	200	332.5	14.1	491	1	PG36 MYCTU	O6cd35 yarrowia li	
128	360	15.2	562	2	Q7U0B1	Q7u0b1 mycobacteri	201	332.5	14.1	501	2	Q7TZH0	O19318 caenorhabdi	
129	360	15.2	586	2	Q7D8J2	Q7d8j2 mycobacteri	202	332.5	14.1	563	2	Q6J6N0	O6j6n0 araneus ven	
130	359.5	15.2	342	2	Q63GI1	Q63gi1 bacillus ce	203	331.5	14.0	622	2	Q8VKJ6	Q8vkj6 mycobacteri	
131	359.5	15.2	773	2	Q7U160	Q7u160 mycobacteri	204	330	14.0	447	2	Q9BIV1	Q9biv1 argiope aur	
132	359.5	15.2	1011	2	Q7D877	Q7d877 mycobacteri	205	329.5	13.9	513	2	Q61067	O61067 plasmodium	
133	359.5	15.2	1011	2	Q79FL8	Q79fl8 mycobacteri	206	329.5	13.9	504	2	Q7TXZ9	Q7txz9 mycobacteri	
134	359.5	15.2	1018	2	Q7T2U3	Q7t2u3 mycobacteri	207	329.5	13.9	2174	2	Q6CD35	O6cd35 yarrowia li	
135	359	15.2	463	1	PG20 MYCTU	O53416 mycobacteri	208	329	13.9	549	2	Q19318	O19318 caenorhabdi	
136	359	15.2	854	2	Q9BIU4	Q9biu4 dolomedes c	209	325.5	13.8	439	2	Q6MWV6	O6mwv6 mycobacteri	
137	358.5	15.2	486	2	Q9AR23	Q9ar23 oryza sativ	210	325.5	13.8	452	2	Q9LW52	Q9lw52 arabidopsis	
138	358.5	15.2	958	2	O17434	O17434 nephila cla	211	324.5	13.7	1458	2	Q910B9	Q910b9 oncorhynch	
139	358	15.2	359	2	Q6Z498	Q6z498 oryza sativ	212	323.5	13.7	436	2	Q8VIX6	O8vix6 mycobacteri	
140	358	15.2	774	2	Q868B4	Q868b4 caenorhabdi	213	323.5	13.7	1729	2	Q9U617	O9u617 drosophila	
141	357	15.1	760	2	Q6PY84	Q6py84 kukulcania	214	323	13.7	268	2	Q9FIQ2	O9fiq2 arabidopsis	
142	357	15.1	766	2	Q6CV63	Q6cv63 kluyveromyc	215	322.5	13.6	355	2	Q7VEL2	O7vel2 mycobacteri	
143	357	15.1	1884	2	Q9NHW2	Q9nhw2 nephila ina	216	322	13.6	1189	2	Q21535	O21535 caenorhabdi	
144	356	15.1	281	2	Q22843	Q22843 caenorhabdi	217	321.5	13.6	431	2	Q692G4	Q692g4 nephila cla	
145	356	15.1	603	2	Q7U079	Q7u079 mycobacteri	218	320.5	13.6	756	2	Q8J1W4	O8j1w4 claviceps p	
146	355.5	15.0	922	2	Q6BTJ4	Q6btj4 debaryomyce	219	320.5	13.6	1071	2	Q7YU48	O7yu48 drosophila	
147	355	15.0	291	2	Q39337	Q39337 brasica na	220	320.5	13.6	1713	2	Q9VTR6	O9vtr6 drosophila	
148	355	15.0	831	2	Q7U159	Q7u159 mycobacteri	221	320	13.5	594	2	Q6MX30	O6mx30 mycobacteri	
149	355	15.0	868	2	Q7U2D8	Q7u2d8 mycobacteri	222	320	13.5	620	2	Q9V7U0	Q9v7u0 drosophila	
150	354.5	15.0	340	2	O811B8	O811b8 bacillus ce	223	320	13.5	1953	2	Q9B1T7	Q9b1t7 nephila ina	
151	353	14.9	588	2	Q9IPQ8	Q9ipq8 cynomolgus	224	318	13.5	1464	2	Q6P9I2	O6p9i2 xenopus lae	
152	353	14.9	624	2	Q7TZL0	Q7tzl0 mycobacteri	225	317	13.4	2655	2	Q964F4	O964f4 antheraea y	
153	352.5	14.9	384	1	GRP1_PETHY	P09789 petunia hyb	226	316	13.4	546	2	Q7TY98	O7ty98 mycobacteri	
154	352	14.9	603	1	PG24 MYCTU	Q10637 mycobacteri	227	316	13.4	1036	2	Q6RX21	O6fx21 candida gla	
155	351.5	14.9	895	2	Q6FPM8	Q6fpm8 candida gla	228	315	13.3	302	2	Q9SL09	O9sl09 arabidopsis	
156	351	14.9	316	2	Q6FHY3	Q6fhy3 homo sapien	229	315	13.3	462	2	Q9NHW3	O9nhw3 nephila cla	
157	351	14.9	957	1	PG03 MYCTU	P56877 mycobacteri	230	314.5	13.3	543	1	PG44 MYCTU	O50630 mycobacteri	
158	350.5	14.8	461	2	Q79FC3	Q79fc3 mycobacteri	231	314	13.3	304	2	Q7XJ17	O7xj17 lycopersico	
159	350.5	14.8	476	2	Q7D6W4	Q7d6w4 mycobacteri	232	314	13.3	367	2	Q6XP6	O6xp6 anophelae g	
160	350.5	14.8	879	2	Q8VKD2	Q8vkd2 mycobacteri	233	314	13.3	387	2	Q692G3	O692g3 nephila cla	
161	350	14.8	316	1	LORI HUMAN	P23490 homo sapien	234	314	13.3	521	2	Q6V5C3	O6v5c3 arabidopsis	
162	349	14.8	618	2	Q79FK9	Q79fk9 mycobacteri	235	313.5	13.3	3659	2	Q98LN6	O98lne rhizobium l	
163	349	14.8	882	2	Q79FV6	Q79fv6 mycobacteri	236	313	13.2	1449	2	Q910C0	O910c0 oncorhynch	
164	347.5	14.7	464	2	Q7TY83	Q7ty83 mycobacteri	237	312.5	13.2	252	1	GRP1 PHAVU	P10495 phaseolus v	
165	347.5	14.7	544	2	Q46171	Q46171 nephila cla	238	310.5	13.1	775	2	Q6BGF1	O6bgl1 debaryomyce	
166	346	14.6	648	2	Q9BIU7	Q9biu7 argiope tri	239	310	13.1	321	2	Q69XV3	O69xv3 oryza sativ	
167	346	14.6	974	1	GLH2_CABEL	Q96619 caenorhabdi	240	309.5	13.1	265	2	Q69K59	O69ks9 oryza sativ	
168	345	14.6	672	1	PHX5_MOUSE	P08399 mus musculu	241	309.5	13.1	509	2	Q7TYG7	O7tyg7 mycobacteri	
169	345	14.6	966	1	FIB1_PETMA	P02674 petromyzon	242	309	13.1	454	2	Q8VUD7	O8vud7 mycobacteri	
170	344.5	14.6	797	2	Q7U1D4	Q7u1d4 mycobacteri	243	308.5	13.1	251	2	Q9UVE7	O9uve7 yarrowia li	
171	344	14.6	525	2	Q79FB3	Q79fb3 mycobacteri	244	308.5	13.1	2639	2	Q76786	O76786 antheraea t	
172	344	14.6	681	2	Q9BIU9	Q9biu9 argiope tri	245	308	13.0	271	2	Q08529	O08529 nicotiana t	
173	344	14.6	783	2	Q7D9C6	Q7d9c6 mycobacteri	246	308	13.0	2496	1	HORN_MOUSE	O8vh48 mus musculu	
174	344	14.6	783	2	Q79FW8	Q79fw8 mycobacteri	247	307	13.0	526	2	Q6WEQ9	O6weq9 plasmodium	
175	343	14.5	538	2	Q7U2T0	Q7u2t0 mycobacteri	248	306.5	13.0	419	1	CSP_PLACM	O06767 mytilus edu	
176	342.5	14.5	575	2	Q86P83	Q86p83 drosophila	249	306.5	13.0	904	2	Q76271	O76271 caenorhabdi	
177	342.5	14.5	636	2	Q16987	Q16987 araneus dia	250	306	12.9	284	2	Q21073	O21073 caenorhabdi	



251 Q6FX23 12.9 1034 2 Q6FX23 Q6fx23 candida gla  
 252 Q6I417 12.9 267 2 Q6I417 Q6i417 bacillus an  
 253 Q9FJ63 12.9 343 2 Q9FJ63 Q9fj63 arabadopsis  
 254 Q9I332 12.9 511 2 Q9I332 Q9i332 cercopitheca  
 255 Q16161 12.9 902 2 Q16161 Q16161 mytilus edu  
 256 Q8MW55 12.9 905 2 Q8MW55 Q8mw55 mytilus gal  
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 258 Q6C7Y4 12.9 404 2 Q6C7Y4 Q6c7y4 yarrowia li  
 259 Q7S737 12.8 1884 2 Q7S737 Q7s737 neopospora  
 260 Q93486 12.8 678 2 Q93486 Q93486 oncorhynchus  
 261 Q8Y293 12.8 426 2 Q8Y293 Q8y293 ralsstonia s  
 262 Q9PF60 12.8 592 2 Q9PF60 Q9pf60 xylella fas  
 263 Q9STW7 12.8 388 2 Q9STW7 Q9stw7 oryza sativ  
 264 Q7SX03 12.7 388 2 Q7SX03 Q7sx03 brachydanio  
 265 Q14593 12.7 393 1 Q14593 Q14593 plasmodium  
 266 Q7PT93 12.7 1666 2 Q7PT93 Q7pt93 anopheles g  
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 272 Q26639 12.7 3198 2 Q26639 Q26639 strongyloce  
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 275 Q41187 12.6 210 2 Q41187 Q41187 arabadopsis  
 276 Q8MYJ1 12.6 262 2 Q8MYJ1 Q8myj1 dictyosteli  
 277 Q94CI8 12.6 284 2 Q94CI8 Q94ci8 lycopersico  
 278 Q44367 12.6 922 2 Q44367 Q44367 mytilus edu  
 279 Q92U08 12.6 2174 2 Q92U08 Q92u08 rhizobium m  
 280 Q6P82 12.6 214 2 Q6P82 Q6p82 kukulcania  
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 284 Q8T215 12.5 480 2 Q8T215 Q8t215 dictyosteli  
 285 Q7UN71 12.5 1047 2 Q7UN71 Q7un71 rhodopirell  
 286 Q9SPN6 12.5 486 2 Q9SPN6 Q9spn6 hordeum vul  
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 290 Q8U0U3 12.5 894 2 Q8U0U3 Q8u0u3 oncorhynchus  
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 292 Q7Y215 12.5 614 2 Q7Y215 Q7y215 arabadopsis  
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 294 Q7XDV2 12.4 222 2 Q7XDV2 Q7xdv2 oryza sativ  
 295 Q9VGH5 12.4 586 2 Q9VGH5 Q9vgh5 drosophila  
 296 Q93560 12.4 794 2 Q93560 Q93560 sagittaria  
 297 Q9FHF2 12.4 256 2 Q9FHF2 Q9fhf2 mycobacteri  
 298 Q8I275 12.4 257 2 Q8I275 Q8i275 bacillus an  
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 303 Q8VPM9 12.3 821 2 Q8VPM9 Q8vpm9 micrococccus  
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 316 Q6PY83 12.2 185 2 Q6PY83 Q6py83 kukulcania  
 317 Q6ALH2 12.2 2363 2 Q6ALH2 Q6alh2 desulfotale  
 318 Q70BL5 12.1 2795 2 Q70BL5 Q70bl5 paracentrot  
 319 Q18758 12.1 13288 2 Q18758 Q18758 sus scrofa  
 320 Q6RH33 12.1 857 2 Q6RH33 Q6rh33 dinocampus  
 321 Q7ZX33 12.1 399 2 Q7ZX33 Q7zx33 xenopus lae  
 322 Q94FP9 12.1 543 2 Q94FP9 Q94fp9 arabadopsis

324 286 12.1 563 2 Q9BIT5 Q9bit5 nephelia ina  
 325 286 12.1 2112 2 Q9VEL9 Q9vel9 drosophila  
 326 285.5 12.1 1370 2 Q6C3B8 Q6c3b8 yarrowia li  
 327 285 12.1 227 2 Q6Z8R3 Q6z8r3 oryza sativ  
 328 285 12.1 250 2 Q92P84 Q92p84 rhizobium m  
 329 284 12.0 293 2 Q9DEX9 Q9dex9 cyprinus ca  
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 331 284 12.0 543 2 Q94FQ0 Q94fq0 arabadopsis  
 332 283.5 12.0 379 2 Q692G2 Q692g2 nephelia cla  
 333 283 12.0 464 2 Q7XDI5 Q7xd15 oryza sativ  
 334 283 12.0 464 2 Q9FWK8 Q9fwk8 oryza sativ  
 335 283 12.0 689 2 Q8BSK0 Q8bsk0 mus musculu  
 336 283 12.0 1051 2 Q26055 Q26055 paracentrot  
 337 283 12.0 1160 2 Q8R564 Q8r564 mus musculu  
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 344 283 12.0 1987 2 Q99PB3 Q99pb3 mus musculu  
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 346 282.5 12.0 1447 2 Q9IB91 Q9ib91 xenopus lae  
 347 282 11.9 338 2 Q60354 Q60354 homo sapien  
 348 282 11.9 394 2 Q7SHJ4 Q7shj4 neopospora  
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 353 281 11.9 827 2 Q7PZ88 Q7pz88 anopheles g  
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 355 281 11.9 1439 2 Q97406 Q97406 halictis di  
 356 280.5 11.9 476 2 Q80890 Q80890 herpesvirus  
 357 280.5 11.9 1449 2 Q6N215 Q6n215 brachydanio  
 358 280 11.8 444 2 Q9BIU6 Q9biu6 argiope tri  
 359 280 11.8 1380 1 DHX3\_MOUSE P04133 mus musculu  
 360 280 11.8 1466 1 CAL3\_HUMAN P02461 homo sapien  
 361 279.5 11.8 1449 2 Q640B2 Q640b2 xenopus tro  
 362 278.5 11.8 526 1 FUS\_HUMAN P35637 homo sapien  
 363 278.5 11.8 526 2 Q8TER3 Q8ter3 homo sapien  
 364 278.5 11.8 929 2 Q9NBL3 Q9nbl3 drosophila  
 365 278.5 11.8 929 2 Q9NBW0 Q9nbw0 drosophila  
 366 278.5 11.8 939 2 Q9NRH9 Q9nrh9 drosophila  
 367 278.5 11.8 939 2 Q9NHQ0 Q9nhq0 drosophila  
 368 278.5 11.8 2780 2 Q6BLF5 Q6blf5 debaryomyce  
 369 278.5 11.8 2880 2 Q9V8E6 Q9v8e6 drosophila  
 370 278.5 11.8 2302 2 Q9N693 Q9n693 drosophila  
 371 278 11.8 220 2 Q93367 Q93367 brassica ol  
 372 278 11.8 270 2 Q61764 Q61764 mus musculu  
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 374 277.5 11.7 230 2 Q7XDU2 Q7xd2 oryza sativ  
 375 277.5 11.7 621 2 Q8VJK6 Q8vjk6 mycobacteri  
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 378 277.5 11.7 1449 2 Q6PEI9 Q6pei9 brachydanio  
 379 277.5 11.7 1449 2 Q802B5 Q802b5 xenopus lae  
 380 277 11.7 256 2 Q24568 Q24568 zea mays (m  
 381 277 11.7 335 2 Q6I199 Q6i199 drosophila  
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 383 277 11.7 1447 2 Q6U1J5 Q6u1j5 brachydanio  
 384 276.5 11.7 682 2 Q22537 Q22537 caenorhabdi  
 385 276.5 11.7 748 2 Q636W5 Q636w5 bacillus ce  
 386 276.5 11.7 1372 1 CA21\_RAT P02466 rattus norv  
 387 276.5 11.7 2332 2 Q6ALH4 Q6alh4 desulfotale  
 388 276 11.7 1366 2 Q15177 Q15177 homo sapien  
 389 276 11.7 1366 2 Q7Z5S6 Q7z5s6 homo sapien  
 390 275 11.6 193 2 Q7YWK8 Q7ywk8 caenorhabdi  
 391 275 11.6 950 2 Q9VK59 Q9vk59 drosophila  
 392 275 11.6 1156 1 GLH4\_CAEEL Q76743 caenorhabdi  
 393 274.5 11.6 929 2 Q9NGW5 Q9ngw5 drosophila  
 394 274.5 11.6 1376 2 Q7SSH8 Q7ssh8 neopospora  
 395 274 11.6 460 2 Q6C0R1 Q6c0r1 yarrowia li  
 396 274 11.6 593 1 K1CJ\_HUMAN P13645 homo sapien

397	274	11.6	730	2	Q9ZU23	O9zu23 arabidopsis	470	263.5	11.2	2147	2	Q98MG8	Q98mg8 rhizobium 1
398	274	11.6	889	2	Q7Q5L2	Q7q5l2 anopheles g	471	263	11.1	435	2	Q7Z152	Q7z152 caenorhabdi
399	274	11.6	3016	2	Q7Q5L2	P73590 synchocyst	472	263	11.1	907	2	Q26312	Q26312 strongyloce
400	273	11.6	970	2	Q7Q6V4	Q7q6v4 anopheles g	473	263	11.1	1097	2	Q6C029	Q6c029 yarrowia li
401	273	11.6	1168	2	Q6HF99	Q6hf99 bacillus th	474	263	11.1	1752	2	Q07265	Q07265 strongyloce
402	273	11.6	1491	2	Q91718	O91718 xenopus lae	475	262.5	11.1	410	2	Q7ZUE3	Q7zue3 brachydanio
403	273	11.6	1491	2	Q7ZTM4	Q7ztm4 xenopus lae	476	262.5	11.1	645	2	Q79FW4	Q79fw4 mycobacteri
404	272.5	11.5	604	2	Q9L252	O9l252 streptomyc	477	262.5	11.1	645	2	Q7ULC5	Q7ulc5 mycobacteri
405	272.5	11.5	1372	1	CA21_MOUSE	Q01149 mus musculu	478	262.5	11.1	646	2	Q7D9B9	Q7d9b9 mycobacteri
406	272.5	11.5	1445	2	Q93251	Q93251 rana catesb	479	262.5	11.1	685	2	Q6IG02	Q6ig02 rattus norv
407	272.5	11.5	2104	2	Q8IKG1	Q8ikg1 plasmodium	480	262.5	11.1	1049	1	CA13_BOVIN	P04258 bos taurus
408	272.5	11.5	2310	2	Q9GRA9	O9gra9 drosophila	481	262.5	11.1	2038	1	FSH_DROME	P13709 drosophila
409	272	11.5	375	1	SANT_PLAFV	P09593 plasmodium	482	262	11.1	245	2	Q6BYG2	Q6byg2 debaryomyce
410	271.5	11.5	370	2	Q79FF0	Q79ff0 mycobacteri	483	262	11.1	1549	2	Q60444	Q60444 cricetus
411	271.5	11.5	370	2	Q7U007	Q7u007 mycobacteri	484	261.5	11.1	815	2	Q632W4	Q632w4 bacillus ce
412	271.5	11.5	375	2	Q7D8E3	Q7d8e3 mycobacteri	485	261.5	11.1	1110	2	Q8IRN6	Q8irn6 drosophila
413	271	11.5	681	2	Q8YTC9	O8ytc9 anabaena sp.	486	261.5	11.1	2038	2	Q9W3L3	O9w3l3 drosophila
414	271	11.5	1364	1	CA21_BOVIN	P02465 bos taurus	487	261	11.0	1226	2	Q7UL12	Q7ul12 rhodopirell
415	270.5	11.4	854	2	Q7TYP1	O7typ1 mycobacteri	488	260.5	11.0	1321	2	Q7Z202	Q7z202 bacillus ce
416	270.5	11.4	1027	1	CAFF_RIFPA	P30754 rifia pach	489	260	11.0	359	2	O8IG99	O8ig99 drosophila
417	270.5	11.4	1226	2	Q7Q3B9	Q7q3b9 anopheles g	490	260	11.0	722	2	Q76B22	Q76b22 bombyx mori
418	270.5	11.4	1366	1	CA21_HUMAN	P08123 homo sapien	491	260	11.0	730	2	Q26052	Q26052 paracentroc
419	270	11.4	779	2	Q76B23	O76b23 bombyx mori	492	260	11.0	1366	1	CA21_CANFA	O46392 canis fami
420	270	11.4	854	2	Q09238	O09238 pseudocorti	493	260	11.0	1486	2	Q71717	Q71717 xenopus lae
421	270	11.4	1035	2	Q76C74	Q76c74 saccharomyc	494	260	11.0	1486	2	Q7ZTI6	Q7zt16 xenopus lae
422	270	11.4	1366	2	Q6N964	Q6n964 rhodopsu	495	259.5	11.0	261	2	Q9ZWM2	Q9zwm2 cucumis sat
423	270	11.4	1713	2	Q8TGE1	Q8tge1 saccharomyc	496	259.5	11.0	399	2	Q9BIT8	Q9bit8 latrodectus
424	270	11.4	1844	2	Q7S6Q1	Q7s6q1 neurospora	497	259.5	11.0	1186	2	Q76B21	Q76b21 bombyx mori
425	269.5	11.4	360	2	Q9BIU0	O9biu0 latrodectus	498	259.5	11.0	1222	2	CA13_MOUSE	O8k173 mus musculu
426	269.5	11.4	443	2	Q9GUB4	O9gub4 galleria me	499	259.5	11.0	1464	1	CA13_MOUSE	P08121 mus musculu
427	269	11.4	361	2	Q79FE6	Q79fe6 mycobacteri	500	259.5	11.0	1464	2	Q7TT32	Q7tt32 mus musculu
428	269	11.4	382	2	Q7D777	Q7d777 mycobacteri	501	259.5	11.0	1464	2	O8BKY2	O8bky2 mus musculu
429	269	11.4	410	2	Q16988	Q16988 araneus dia	502	259.5	11.0	1464	2	O8BLW4	O8blw4 mus musculu
430	269	11.4	422	2	Q803K3	O803k3 brachydanio	503	259	11.0	263	2	Q6ZLW9	Q6zlw9 oryza sativ
431	269	11.4	1025	2	Q7WIW0	Q7wiw0 bordetella	504	259	11.0	441	2	Q26062	Q26062 plasmodium
432	268.5	11.4	259	2	Q02049	O02049 caenorhabdi	505	259	11.0	517	2	Q8CFQ9	Q8cfq9 mus musculu
433	268.5	11.4	333	2	Q6BC34	Q6bc34 patinopecte	506	259	11.0	684	2	P90679	P90679 arenicola m
434	268.5	11.4	557	2	Q8BQ46	Q8bq46 mus musculu	507	259	11.0	886	2	Q9VKR7	Q9vkr7 drosophila
435	268.5	11.4	584	2	Q6CA50	Q6ca50 yarrowia li	508	259	11.0	3145	2	O98MG7	O98mg7 rhizobium 1
436	268	11.3	183	1	GRP2_ORYSA	P29834 oryza sativ	509	258.5	10.9	1309	2	O812N4	O812n4 bacillus ce
437	268	11.3	647	2	Q6H1W5	Q6h1w5 drosophila	510	258	10.9	138	2	Q964C4	Q964c4 encaphalito
438	268	11.3	241	2	Q6H519	Q6h519 bacillus an	511	258	10.9	208	2	Q9ZRV2	Q9zrv2 ciccr ariet
439	268	11.3	870	2	Q6FPN0	Q6fpn0 candida gla	512	258	10.9	394	1	THVD_CLAFS	Q9uv14 claviceps f
440	268	11.3	1055	2	Q6HCP4	Q6hcf4 bacillus th	513	258	10.9	604	2	Q6BQ06	Q6bq06 debaryomyce
441	267.5	11.3	429	2	Q76966	Q76966 podocoryne	514	257.5	10.9	386	1	RB87_DROME	P48810 drosophila
442	267.5	11.3	1207	2	Q9PVP5	Q9pvp5 brachydanio	515	257.5	10.9	503	2	Q734G5	Q734g5 bacillus ce
443	266.5	11.3	561	2	Q7TPC1	Q7tpc1 mus musculu	516	257.5	10.9	518	1	FUS_MOUSE	P56959 mus musculu
444	266.5	11.3	987	2	Q89CB5	O89cb5 bradyrhizob	517	257.5	10.9	584	2	Q8N175	Q8n175 homo sapien
445	266	11.3	243	2	Q98DS7	O98ds7 rhizobium 1	518	257.5	10.9	735	2	Q7Z009	Q7z009 anagasta ku
446	266	11.3	342	2	Q8SX59	O8sx59 drosophila	519	257	10.9	385	2	Q9VFT2	Q9vft2 drosophila
447	266	11.3	586	2	Q8EXJ2	Q8exj2 leptospira	520	257	10.9	433	2	O61152	O61152 plasmodium
448	266	11.3	683	2	Q9PDW2	Q9pdw2 xylella fas	521	257	10.9	632	2	Q7TX52	Q7tx52 mycobacteri
449	266	11.3	1088	2	Q69UP6	Q69up6 oryza sativ	522	257	10.9	686	2	O8VJ65	O8vj65 mycobacteri
450	265.5	11.2	175	2	Q9LSN6	O9lsn6 arabidopsis	523	257	10.9	998	2	O8CFM4	O8cfm4 mus musculu
451	265.5	11.2	265	2	Q69PC6	Q69pc6 oryza sativ	524	257	10.9	1160	2	Q14046	Q14046 homo sapien
452	265.5	11.2	461	2	Q6V5F7	Q6v5f7 capsella ru	525	257	10.9	1352	2	Q90YJ0	Q90yj0 brachydanio
453	265.5	11.2	568	2	Q9NL38	Q9nl38 pinctada ma	526	256.5	10.9	508	2	Q7KHL0	Q7khl0 drosophila
454	265.5	11.2	614	2	Q7TYR8	Q7tyr8 mycobacteri	527	256.5	10.9	809	2	O93485	O93485 oncornynch
455	265.5	11.2	615	2	Q7D7A1	Q7d7a1 mycobacteri	528	256.5	10.9	1352	2	Q61QX2	Q61qx2 brachydanio
456	265	11.2	331	2	Q692G6	Q692g6 nephila cla	529	256	10.8	421	2	O93119	O93119 antheraea p
457	265	11.2	717	2	Q75FL0	Q75fl0 leptospira	530	256	10.8	429	2	O61150	O61150 plasmodium
458	265	11.2	1119	2	Q75DC8	Q75dc8 ashaya goss	531	256	10.8	436	2	Q967T8	Q967t8 antheraea p
459	264.5	11.2	297	2	Q7XDU7	Q7xd7 oryza sativ	532	256	10.8	743	2	Q686B2	Q686b2 vibriophage
460	264.5	11.2	536	1	FAEB_PIREQ	O9y871 piromyces e	533	256	10.8	1487	2	Q77753	Q77753 canis fami
461	264.5	11.2	1820	2	Q91907	O91907 pagrus majo	534	255.5	10.8	501	2	Q86X94	Q86x94 homo sapien
462	264	11.2	227	2	Q84W21	O84w21 arabidopsis	535	255.5	10.8	592	1	RB56_HUMAN	Q92804 homo sapien
463	264	11.2	741	2	Q6RCF4	O6rcf4 vibriophage	536	255.5	10.8	1369	2	Q6V5D4	Q6v5d4 olinarabido
464	264	11.2	818	2	Q812Y5	O812y5 bacillus ce	537	255	10.8	357	2	Q6V5F6	Q6v5f6 capsella ru
465	264	11.2	1163	2	Q8N6U4	Q8n6u4 homo sapien	538	255	10.8	632	2	O9N2N7	O9n2n7 hemice
466	263.5	11.2	561	2	Q7W7Z1	Q7w7z1 bordetella	539	255	10.8	1052	2	Q7YZ84	Q7yz84 plasmodium
467	263.5	11.2	763	1	GLH1_CABEL	P34689 caenorhabdi	540	254.5	10.8	413	2	Q8IME3	Q8ime3 drosophila
468	263.5	11.2	1412	2	Q8MUF5	O8muf5 hydra atten	541	254.5	10.8	496	2	Q7KRL6	Q7krl6 drosophila
469	263.5	11.2	1418	2	Q9W7R9	O9w7r9 cynops pyrr	542	254.5	10.8	502	2	Q7KRL7	Q7krl7 drosophila

543	254.5	10.8	700	2	Q8CIT9	Q8cit9 mus musculus
544	254	10.7	1419	2	Q63123	Q63123 rattus norv
545	254	10.7	1487	2	Q14047	Q14047 homo sapien
546	254	10.7	1745	1	CA35_HUMAN	CA35_HUMAN
547	254	10.7	1747	1	Q26640	Q26640 strongyloce
548	253.5	10.7	396	2	Q03136	Q03136 plasmodium
549	253.5	10.7	401	1	CSP_PLACG	CSP_PLACG
550	253.5	10.7	509	2	Q875B1	Q875B1 podospora a
551	253.5	10.7	539	2	Q8MQG9	Q8mqg9 caenorhabdi
552	253.5	10.7	660	2	Q86D04	Q86d04 caenorhabdi
553	253.5	10.7	1492	2	Q6P422	Q6p422 xenopus tro
554	253	10.7	818	2	Q9N190	Q9n190 bos taurus
555	253	10.7	1217	2	Q17240	Q17240 bombyx mori
556	252.5	10.7	1418	1	CA12_HUMAN	CA12_HUMAN
557	252.5	10.7	386	2	Q24486	Q24486 homo sapien
558	252.5	10.7	496	2	Q7KA80	Q7ka80 drosophila
559	252	10.7	582	2	Q7D5C5	Q7d5c5 mycobacteri
560	252	10.7	582	2	Q7TW98	Q7tw98 mycobacteri
561	252	10.7	1497	2	Q61431	Q61431 mus musculu
562	252	10.7	1583	2	Q6C398	Q6c398 yarrowia li
563	251.5	10.6	343	2	Q01914	Q01914 phytophthor
564	251.5	10.6	490	2	Q9SUW9	Q9suw9 arabidopsis
565	251.5	10.6	810	2	Q9ES29	Q9es29 mus musculu
566	251.5	10.6	860	1	ELS_MOUSE	ELS_MOUSE
567	251.5	10.6	860	2	Q8C9J8	Q8c9j8 mus musculu
568	251.5	10.6	1723	2	Q9GQB1	Q9gqb1 hydra atten
569	251	10.6	125	2	Q964C1	Q964c1 encephalito
570	251	10.6	232	2	Q7S4R3	Q7s4r3 neurospora
571	251	10.6	315	2	Q8IGP8	Q8igp8 drosophila
572	251	10.6	425	2	Q61151	Q61151 plasmodium
573	251	10.6	429	1	CSP_PLAMA	CSP_PLAMA
574	251	10.6	429	2	Q61144	Q61144 plasmodium
575	251	10.6	429	2	Q61148	Q61148 plasmodium
576	251	10.6	429	2	Q62597	Q62597 plasmodium
577	251	10.6	671	1	CA11_RAT	CA11_RAT
578	251	10.6	1420	2	Q6FW4	Q6fw4 candida gla
579	251	10.6	1453	2	Q63079	Q63079 rattus norv
580	250.5	10.6	360	2	Q16985	Q16985 araneus dia
581	250.5	10.6	540	2	Q7NL21	Q7nl21 gloebacter
582	250.5	10.6	585	2	Q8NN98	Q8nn98 corynebacte
583	250	10.6	315	2	Q7KRL5	Q7krl5 drosophila
584	250	10.6	326	2	Q854M0	Q854m0 mycobacteri
585	250	10.6	603	2	Q8VJ66	Q8vj66 mycobacteri
586	250	10.6	813	2	Q636W4	Q636w4 bacillus ce
587	250	10.6	1497	2	Q7TMS0	Q7tms0 mus musculu
588	250	10.6	1570	2	Q6INP8	Q6inp8 xenopus lae
589	249.5	10.6	395	2	Q7M3X0	Q7m3x0 plasmodium
590	249.5	10.6	589	2	Q7TX53	Q7tx53 mycobacteri
591	249.5	10.6	940	2	Q00405	Q00405 homo sapien
592	249.5	10.6	1033	1	IF2_STRCO	IF2_STRCO
593	249	10.5	516	2	Q9XE70	Q9xe70 streptomyce
594	249	10.5	590	2	Q6MX04	Q6mx04 mycobacteri
595	249	10.5	773	2	Q95TR3	Q95tr3 drosophila
596	249	10.5	1215	2	Q9W2K4	Q9w2k4 drosophila
597	248.5	10.5	2465	2	Q8CB66	Q8cb66 yarrowia li
598	248.5	10.5	507	2	Q8IB33	Q8ib33 antheraea m
599	248.5	10.5	710	2	Q8VWMD1	Q8vwd1 streptomyce
600	248.5	10.5	1011	2	Q7VX87	Q7vx87 bordetella
601	248.5	10.5	1016	2	Q9XTX5	Q9xtx5 caenorhabdi
602	248.5	10.5	1442	2	Q62031	Q62031 mus musculu
603	248.5	10.5	1442	2	Q62033	Q62033 mus musculu
604	248.5	10.5	1459	1	CA12_MOUSE	CA12_MOUSE
605	248.5	10.5	1459	2	Q62032	Q62032 mus musculu
606	248	10.5	117	2	Q964C2	Q964c2 encephalito
607	248	10.5	343	2	Q81761	Q81761 arabidopsis
608	248	10.5	385	1	RO32_XENLA	RO32_XENLA
609	248	10.5	425	2	Q61147	Q61147 plasmodium
610	247.5	10.5	279	2	Q57148	Q57148 human herpe
611	247.5	10.5	347	2	Q01916	Q01916 phytophthor
612	247.5	10.5	399	1	CAZ_DROME	CAZ_DROME
613	247.5	10.5	481	2	Q97641	Q97641 equus cabal
614	247.5	10.5	1418	2	Q28396	Q28396 equus cabal
615	247.5	10.5	1419	2	Q80VY3	Q80vy3 mus musculu
Q80X38	mus musculu					
Q641K3	mus musculu					
Q9JLI2	mus musculu					
Q8VKM3	mycobacteri					
Q6MX44	mycobacteri					
Q7U270	mycobacteri					
Q61146	plasmodium					
Q6PCL3	mus musculu					
Q11087	mus musculu					
Q81079	mus musculu					
Q9X917	canis fami					
Q89340	suid herpes					
Q9CR91	m mus muscu					
Q9CE77	drosophila					
Q9V7B7	mus musculu					
P12105	gallus gall					
Q7XD75	oryza sativ					
Q79F13	mycobacteri					
P13941	rattus norv					
Q23062	caenorhabdi					
Q12906	h interleuk					
Q8AW17	brachydanio					
O80815	arabidopsis					
P17139	caenorhabdi					
Q61245	mus musculu					
P02457	gallus gall					
Q76045	homo sapien					
P02452	homo sapien					
O8N473	homo sapien					
Q9J104	rattus norv					
Q89UQ1	bradyrhizob					
Q7PGN6	anopheles g					
O8MS22	drosophila					
O82K53	streptomyce					
Q7TW10	mycobacteri					
Q42626	brassica na					
Q8SX80	drosophila					
O6LH98	bacillus th					
O6LAN8	homo sapien					
O96472	theileria t					
O7YXC8	caenorhabdi					
Q9W4M4	drosophila					
O22432	pinus taeda					
O03797	schistosoma					
O67WQ9	oryza sativ					
O9FM47	arabidopsis					
O7XJJ6	chlamydomon					
Q96QC0	homo sapien					
P05997	homo sapien					
O6GQ57	mus musculu					
P08120	drosophila					
O9VMV4	drosophila					
O7XDR9	oryza sativ					
Q9GZC7	trypanosoma					
Q93424	caenorhabdi					
O61145	plasmodium					
P02453	bos taurus					
O80WR4	mus musculu					
Q7XDR7	oryza sativ					
Q9SUX1	arabidopsis					
O6CE66	yarrowia li					
O8AW11	brachydanio					
Q96QB3	homo sapien					
O9BIU1	gasteracant					
Q07138	microciona					
Q7TXZ3	mycobacteri					
Q7Q3C5	anopheles g					
O8T9H1	drosophila					
O43539	lilium long					
O61149	plasmodium					
Q28009	bos taurus					
Q10778	mycobacteri					
FP21_MYCTU						
Q7XZU9	hordeum vul					

689	240	10.2	1348	2	Q7PVX1	Q7pyx1 anophelēs g	762	234	9.9	237	2	Q6DX9	Q6dxx9 plasmodium
690	239.5	10.1	469	2	Q81KL9	Q8lk19 bacillus an	763	234	9.9	301	2	Q01927	Q01927 phycophthor
691	239.5	10.1	538	2	Q8NOR6	Q8n0r6 turbo marmo	764	234	9.9	309	2	Q8V6M8	Q8v6m8 halovirus h
692	239.5	10.1	663	2	Q812Y6	Q812y6 streptomycē	765	234	9.9	339	2	Q84LH8	Q84lh8 solanum tub
693	239.5	10.1	706	2	Q41972	Q41972 murid herpe	766	234	9.9	1626	2	Q8NFW1	Q8nfw1 homo sapien
694	239.5	10.1	727	2	Q41973	Q41973 murid herpe	767	234	9.9	1655	2	Q24754	Q24754 drosophila
695	239.5	10.1	774	2	Q41971	Q41971 murid herpe	768	233.5	9.9	165	1	GRP1_ORYSA	P25074 oryza sativ
696	239.5	10.1	812	2	Q06452	Q06452 ephydatia m	769	233.5	9.9	171	2	Q04139	P00439 aradidopsis
697	239.5	10.1	1669	1	CA14_MOUSE	P02463 mus musculus	770	233.5	9.9	180	2	P91207	P91207 caenorhabdi
698	239	10.1	584	2	Q62EE4	Q62ee4 burkholderi	771	233.5	9.9	811	2	Q9AD50	Q9ad50 streptomycē
699	239	10.1	826	2	Q8KON6	Q8kon6 mus musculus	772	233.5	9.9	966	2	Q01385	Q01385 neospora
700	239	10.1	1041	2	Q66S51	Q66s51 oikopleura	773	233.5	9.9	1617	2	Q6MGB2	Q6mgb2 rattus norv
701	239	10.1	2165	2	Q8NPD5	Q8nfd5 homo sapien	774	233.5	9.9	2936	2	Q7VRK8	Q7vrk8 canis famil
702	238.5	10.1	121	2	Q964C5	Q964c5 encephalito	775	233	9.9	237	2	Q6DXZ7	Q6dxz7 plasmodium
703	238.5	10.1	212	1	EGG1_SCHJA	P19470 schistosoma	776	233	9.9	296	2	Q8RUS0	Q8rus0 aradidopsis
704	238.5	10.1	267	2	Q9B088	P9b088 mycobacteri	777	233	9.9	373	1	R031_XENLA	P51968 xenopus lae
705	238.5	10.1	387	2	Q7M3W9	Q7m3w9 plasmodium	778	233	9.9	536	2	Q6DKB4	Q6dkb4 xenopus lae
706	238.5	10.1	387	2	Q7M3W9	Q7m3w9 plasmodium	779	233	9.9	658	2	Q6FRG1	Q6frg1 candida gla
707	238.5	10.1	450	1	SWP1_ENCCU	Q9xv1 encephalito	780	233	9.9	783	2	Q9XAI1	Q9xai1 streptomycē
708	238.5	10.1	615	2	Q9VYL7	Q9vy17 drosophila	781	233	9.9	864	1	ELS_RAT	Q93172 rattus norv
709	238.5	10.1	689	2	Q75EH4	Q75eh4 ashbya goss	782	232.5	9.8	253	2	Q7ADR2	Q7adr2 oryza sativ
710	238.5	10.1	1420	2	Q90W37	Q90w37 gallus gall	783	232.5	9.8	290	2	Q21294	Q21294 caenorhabdi
711	238	10.1	963	2	Q9UVL2	Q9uvl2 neospora	784	232.5	9.8	342	1	CUS36_MANSE	Q6frg1 candida gla
712	238	10.1	1011	2	Q6CF27	Q6cf27 yarrowia li	785	232.5	9.8	388	2	Q9VR7	Q9vr7 drosophila
713	238	10.1	1736	1	CA2B_HUMAN	P13942 homo sapien	786	232.5	9.8	652	2	Q86NR7	Q86nr7 drosophila
714	238	10.1	1806	1	CA1B_HUMAN	P12107 homo sapien	787	232.5	9.8	2109	2	P79787	P79787 gallus gall
715	238	10.1	1991	2	Q7RTD0	Q7rtd0 plasmodium	788	232	9.8	329	2	Q9BEY0	Q9bey0 cyprinus ca
716	238	10.1	2037	2	Q9PVZ2	Q9pvz2 xenopus lae	789	232	9.8	460	1	CYS7_DICDI	Q94504 dictyostell
717	237.5	10.1	185	2	Q7XDT6	Q7xdt6 oryza sativ	790	232	9.8	463	2	Q9GVL3	Q9gvl3 felis silve
718	237.5	10.1	247	2	Q6DX38	Q6dx38 plasmodium	791	232	9.8	797	2	Q9GVL3	Q9gvl3 hydra magni
719	237.5	10.1	349	2	Q9BIV0	Q9biv0 argiope aur	792	232	9.8	913	2	Q6C979	Q6c979 yarrowia li
720	237.5	10.1	495	2	Q71RFP0	Q71rpf0 ovine herpe	793	231.5	9.8	239	2	Q9BMN2	Q9bmn2 plasmodium
721	237.5	10.1	940	2	Q7YR38	Q7yr38 pan troglod	794	231.5	9.8	244	2	Q9LYF08	Q9lyf08 aradidopsis
722	237.5	10.1	1362	1	CA21_CHICK	P02467 gallus gall	795	231.5	9.8	487	2	Q9ZB39	Q9zb39 ureaplasma
723	237.5	10.1	1831	2	Q7Q1Y4	Q7q1y4 anophelēs g	796	231.5	9.8	544	2	Q6BU19	Q6bul19 debaryomyce
724	237.5	10.1	2944	2	Q63R70	Q63r70 mus musculus	797	231.5	9.8	925	2	Q767K9	Q767k9 sus scrofa
725	237	10.0	309	2	Q9FNR1	Q9fnr1 aradidopsis	798	231.5	9.8	1475	2	Q9XEP3	Q9xep3 sorghum bic
726	237	10.0	365	2	Q61P29	Q6ip29 xenopus lae	799	231	9.8	185	2	Q948R3	Q948r3 oryza sativ
727	237	10.0	490	2	Q9V948	Q9v948 drosophila	800	231	9.8	221	2	Q65514	Q65514 aradidopsis
728	237	10.0	535	2	Q7WLD1	Q7wld1 bordetella	801	231	9.8	237	2	Q6DXZ8	Q6dxz8 plasmodium
729	237	10.0	642	2	Q6G364	Q6g364 bartonella	802	231	9.8	237	2	Q6DXZ9	Q6dxz9 plasmodium
730	237	10.0	854	2	Q8IVT9	Q8ivt9 homo sapien	803	231	9.8	237	2	Q6DY01	Q6dy01 plasmodium
731	237	10.0	1024	2	Q6FLA5	Q6fla5 candida gla	804	231	9.8	237	2	Q7XLA1	Q7xla1 oryza sativ
732	237	10.0	3409	2	Q6SSE6	Q6sse6 chlamydomon	805	231	9.8	350	2	Q8C2H8	Q8c2h8 mus musculu
733	236.5	10.0	247	2	Q6DX44	Q6dx44 plasmodium	806	231	9.8	373	2	Q9P639	Q9p639 neospora
734	236.5	10.0	717	2	Q6MI66	Q6mi66 bdellovibri	807	231	9.8	413	2	Q7D7A7	Q7d7a7 mycobacteri
735	236.5	10.0	747	1	CA12_BOVIN	P02459 bos taurus	808	231	9.8	413	2	Q7TYS4	Q7tys4 mycobacteri
736	236.5	10.0	961	2	Q7RW88	Q7rw88 neospora	809	231	9.8	422	2	Q94KD0	Q94kd0 aradidopsis
737	236.5	10.0	977	2	Q8X005	Q8x005 neospora	810	231	9.8	501	2	Q6GLD1	Q6glld1 xenopus tro
738	236.5	10.0	1733	1	VNUA_PRIVKA	P33485 pseudorabie	811	231	9.8	536	2	Q7ZXQ2	Q7zxq2 xenopus lae
739	236.5	10.0	1736	1	CA2B_MOUSE	Q64739 mus musculus	812	231	9.8	898	2	Q8K588	Q8k588 mus musculu
740	236	10.0	504	2	Q6FL65	Q6fl65 candida gla	813	231	9.8	911	2	Q812A1	Q812a1 mus musculu
741	236	10.0	518	2	Q8MQ08	Q8mq08 caenorhabdi	814	231	9.8	1758	1	CA24_CABEL	P17140 caenorhabdi
742	236	10.0	524	2	Q02123	Q02123 caenorhabdi	815	230.5	9.8	284	2	Q6EEZ3	Q6eez3 euprostheno
743	236	10.0	888	2	Q90796	Q90796 gallus gall	816	230.5	9.8	485	2	Q9UV68	Q9uv68 neocallimas
744	236	10.0	1827	2	Q8U0M5	Q8uums oryzaia lac	817	230.5	9.8	643	2	Q87E00	Q87e00 xylella fas
745	235.5	10.0	228	2	Q6DY00	Q6dy00 plasmodium	818	230.5	9.8	859	2	Q8IRV3	Q8irv3 drosophila
746	235.5	10.0	643	1	K2C1_HUMAN	P02464 homo sapien	819	230.5	9.8	887	2	Q9M4V1	Q9m4v1 drosophila
747	235.5	10.0	682	2	Q9VRM2	Q9vrm2 drosophila	820	230.5	9.8	1300	2	Q36421	Q36421 alcelaphine
748	235.5	10.0	1714	2	Q7Z515	Q7z515 homo sapien	821	230.5	9.8	2096	2	Q7TWN7	Q7twn7 mycobacteri
749	235	9.9	448	2	Q18265	Q18265 caenorhabdi	822	230.5	9.8	3157	2	Q6MWN9	Q6mwn9 mycobacteri
750	235	9.9	568	2	Q6E1Z0	Q6eiz0 canis famil	823	230	9.7	115	1	SEB1_GALME	Q96614 gallieria me
751	235	9.9	839	2	Q9RX57	Q9rx57 deinococcus	824	230	9.7	1023	2	Q7Q3C0	Q7q3c0 anophelēs g
752	235	9.9	891	2	Q8OV58	Q8ov58 mus musculus	825	230	9.7	1778	1	N189_SCHPO	Q9uk4 schizosacch
753	235	9.9	1269	2	Q7T227	Q7t227 gallus gall	826	229.5	9.7	160	2	Q94669	Q94669 plasmodium
754	234.5	9.9	207	1	EGG2_SCHJA	P19469 schistosoma	827	229.5	9.7	167	2	Q7QIN7	Q7qin7 anophelēs g
755	234.5	9.9	419	2	Q42638	Q42638 brassica ol	828	229.5	9.7	175	2	Q7XDT1	Q7xdt1 oryza sativ
756	234.5	9.9	438	2	Q7M3U7	Q7m3u7 parvalinell	829	229.5	9.7	294	2	Q16986	Q16986 araneus dia
757	234.5	9.9	455	2	Q28495	Q28495 macaca mula	830	229.5	9.7	398	2	Q7Q1A7	Q7q1a7 anophelēs g
758	234.5	9.9	2109	1	PGCA_CHICK	P07898 gallus gall	831	229.5	9.7	539	2	Q7TWN9	Q7twn9 mycobacteri
759	234.5	9.9	2585	2	Q23587	Q23587 caenorhabdi	832	229.5	9.7	569	1	K1CJ_MOUSE	P02535 mus musculu
760	234.5	9.9	2944	1	CA17_HUMAN	Q02388 homo sapien	833	229.5	9.7	585	2	Q7QB9	Q7qby9 anophelēs g
761	234	9.9	237	2	Q26166	Q26166 plasmodium	834	229.5	9.7	708	2	Q7ZWN8	Q7zwn8 xenopus lae

835	229.5	9.7	740	2	Q73J82	Q73j82 treponema d	908	225	9.5	767	2	Q7PM40	Q7pm40 anopheles g
836	229.5	9.7	824	2	Q81B45	Q81b45 bacillus ce	909	225	9.5	1196	1	ICEV_PSEXS	Q33479 pseudomonas
837	229.5	9.7	853	2	Q8VQZ0	Q8vqz0 myxococcus	910	225	9.5	1746	2	Q7PVR9	Q7pvr9 anopheles g
838	229.5	9.7	857	2	Q85783	Q85783 myxococcus	911	224.5	9.5	174	2	Q9LTP5	Q9ltp5 arabidopsis
839	229	9.7	162	2	Q9M0B4	Q9m0b4 arabidopsis	912	224.5	9.5	235	2	Q9LI22	Q9liz2 oryza sativ
840	229	9.7	192	2	Q7XDT3	Q7xdt3 oryza sativ	913	224.5	9.5	442	2	Q7PVR2	Q7puk2 anopheles g
841	229	9.7	391	2	Q8S216	Q8s216 triticum ae	914	224.5	9.5	561	2	Q8BVU3	Q8bv3 mus musculus
842	229	9.7	570	2	Q8RSI6	Q8rsi6 uncultured	915	224.5	9.5	775	2	Q8BVU3	Q8f342 streptomyce
843	228.5	9.7	197	2	Q8ATP3	Q8atp3 pennisetum	916	224.5	9.5	801	2	Q8T5G4	Q8t5g4 anopheles g
844	228.5	9.7	228	2	Q6DXV0	Q6dxv0 plasmidium	917	224.5	9.5	830	2	Q7PVR8	Q7pvr8 anopheles g
845	228.5	9.7	429	1	D848_YEAST	P18899 saccharomyc	918	224.5	9.5	910	1	ILF3_RAT	Q9jil3 rattus norv
846	228.5	9.7	560	2	Q50275	Q50275 mycoplasma	919	224	9.5	167	2	Q63115	Q63115 rattus norv
847	228.5	9.7	561	2	Q41664	Q41664 homo sapien	920	224	9.5	387	2	Q6S7B1	Q6s7b1 arabidopsis
848	228.5	9.7	800	2	Q8NU13	Q8nu13 xenopus lae	921	224	9.5	404	2	O22791	O22791 arabidopsis
849	228.5	9.7	2523	2	Q8TJ88	Q8tj88 methanosarc	922	224	9.5	447	2	Q9YTJ3	Q9ytj3 ateline her
850	228.5	9.7	5146	2	Q9VXR3	Q9vrx3 drosophila	923	224	9.5	544	2	Q8I6C4	Q8i6c4 drosophila
851	228	9.6	189	2	Q7XDS0	Q7xdso oryza sativ	924	224	9.5	625	2	Q6IMF3	Q6imf3 rattus norv
852	228	9.6	196	2	O22638	O22638 zea mays (m	925	224	9.5	681	2	Q6AZQ8	Q6azq8 xenopus lae
853	228	9.6	238	2	Q7TQ07	Q7tq07 plasmodium	926	224	9.5	1115	2	Q6PFB1	Q6pfb1 mus musculus
854	228	9.6	690	2	Q73T97	Q73t97 mycobacteri	927	224	9.5	1497	1	CA1G_HUMAN	Q9umd9 homo sapien
855	228	9.6	738	2	Q82YD4	Q82yd4 streptomyce	928	224	9.5	1691	2	Q9ESQ1	Q9esq1 mus musculus
856	228	9.6	738	2	Q90779	Q90779 gallus gall	929	224	9.5	2310	2	Q9W2U7	Q9w2u7 drosophila
857	228	9.6	1684	2	Q8TNB6	Q8tnb6 white spot	930	223.5	9.5	339	2	Q6CAL8	Q6cal8 yarrowia li
858	228	9.6	1684	2	Q8VAAL	Q8vaal white spot	931	223.5	9.5	572	2	F71187	F71187 enterobacte
859	228	9.6	1684	2	Q8ILK9	Q8ilk9 white spot	932	223.5	9.5	572	2	Q936Y6	Q936y6 pseudomonas
860	227.5	9.6	116	2	Q8NI04	Q8ni04 plasmodium	933	223.5	9.5	572	2	Q6UP53	Q6up53 alicaligenes
861	227.5	9.6	228	2	Q6TQ08	Q6tq08 plasmodium	934	223.5	9.5	572	2	Q76M30	Q76m30 comamonas a
862	227.5	9.6	237	2	Q6DY02	Q6dy02 plasmodium	935	223.5	9.5	572	2	Q7X3E2	Q7x3e2 uncultured
863	227.5	9.6	277	2	Q7PMW8	Q7pmw8 anopheles g	936	223.5	9.5	631	2	Q9N1P1	Q9n1p1 bos taurus
864	227.5	9.6	372	2	Q7Z008	Q7z008 anagata ku	937	223.5	9.5	659	2	Q8MT98	Q8mt98 drosophila
865	227.5	9.6	431	2	Q7QCQ9	Q7qcq9 anopheles g	938	223.5	9.5	824	2	Q69YT0	Q69yto homo sapien
866	227.5	9.6	726	2	Q81ZX1	Q81zx1 streptomyce	939	223.5	9.5	974	2	Q9UVL3	Q9uvl3 neurospora
867	227.5	9.6	1130	2	Q6CIH1	Q6cih1 kluveromyce	940	223.5	9.5	978	2	P91777	P91777 pacifastacu
868	227.5	9.6	1297	2	Q6VBI9	Q6vbi9 candida gla	941	223.5	9.5	1075	2	Q86X41	Q86x41 homo sapien
869	227.5	9.6	1997	2	Q7RXD0	Q7rxdo neurospora	942	223.5	9.5	1427	2	Q8GIZ2	Q8giz2 mycoplasma
870	227	9.6	236	2	Q4AFQ5	Q4afq5 arabidopsis	943	223.5	9.5	1855	2	Q80ZF0	Q80zf0 rattus norv
871	227	9.6	371	2	O45114	O45114 caenorhabdi	944	223	9.4	192	2	Q92WM7	Q92wm7 zea mays (m
872	227	9.6	536	2	Q8I6B9	Q8i6b9 drosophila	945	223	9.4	441	2	Q6G4M7	Q6g4m7 bartonella
873	227	9.6	544	2	Q8I6C5	Q8i6c5 drosophila	946	223	9.4	544	2	Q8I6C3	Q8i6c3 drosophila
874	227	9.6	645	2	Q63P58	Q63p58 burkholderi	947	223	9.4	911	1	ILF3_MOUSE	Q9zlx4 mus musculus
875	227	9.6	703	1	CA28_HUMAN	P35067 homo sapien	948	223	9.4	1001	2	Q05164	Q05164 saccharomyc
876	227	9.6	1148	1	ICEK_PSEXS	Q30611 pseudomonas	949	223	9.4	1200	1	ICEN_PSESY	P06620 pseudomonas
877	227	9.6	1210	1	ICEN_PSEBFL	P09815 pseudomonas	950	222.5	9.4	228	2	Q6TOR2	Q6tor2 plasmodium
878	227	9.6	1622	2	Q7G9F9	Q7g9f9 vibrio para	951	222.5	9.4	655	2	Q8IRV2	Q8irv2 drosophila
879	226.5	9.6	228	2	Q6DY45	Q6dy45 plasmodium	952	222.5	9.4	739	-2	Q70575	Q70575 mus musculus
880	226.5	9.6	252	2	Q7VEJ9	Q7vej9 prochloroco	953	222.5	9.4	1063	2	Q9CH86	Q9ch86 lactococcus
881	226.5	9.6	469	1	CS66_WHEAT	P46526 triticum ae	954	222.5	9.4	1260	2	Q9UGY9	Q9ugy9 homo sapien
882	226.5	9.6	637	2	Q9D2R8	Q9d2r8 mus musculus	955	222.5	9.4	1761	2	O18407	O18407 drosophila
883	226.5	9.6	641	2	Q17740	Q17740 caenorhabdi	956	222.5	9.4	2523	2	Q6MWY2	Q6mwY2 mycobacteri
884	226.5	9.6	1022	1	CA26_CHICK	P15988 gallus gall	957	222	9.4	363	2	Q9FGH5	Q9fgh5 arabidopsis
885	226.5	9.6	1709	2	Q86L43	Q86l43 dictyosteli	958	222	9.4	365	1	ROA1_XENLA	P17130 xenopus lae
886	226	9.6	189	2	Q9UEH6	Q9ueh6 oryza sativ	959	222	9.4	504	2	Q7QUT6	Q7qut6 anopheles g
887	226	9.6	1621	2	Q9H4R9	Q9h4r9 homo sapien	960	222	9.4	544	2	Q8I081	Q8i081 drosophila
888	226	9.6	1669	1	CA14_HUMAN	P02462 homo sapien	961	222	9.4	552	2	Q6MMW0	Q6mmw0 mycobacteri
889	226	9.6	1691	1	CA64_HUMAN	Q14031 homo sapien	962	222	9.4	552	2	Q7TW76	Q7tw76 mycobacteri
890	226	9.6	544	2	Q8I072	Q8i072 drosophila	963	222	9.4	623	2	Q8VIY0	Q8viy0 mycobacteri
891	226	9.6	834	2	Q8W056	Q8w056 oryza sativ	964	222	9.4	676	2	Q6DE50	Q6de50 xenopus lae
892	226	9.6	1600	2	Q9UEH6	Q9ueh6 homo sapien	965	222	9.4	946	2	Q857Y4	Q857y4 mycobacteri
893	226	9.6	1621	2	Q9H4R9	Q9h4r9 homo sapien	966	222	9.4	1519	2	Q7Z3C4	Q7z3c4 homo sapien
894	226	9.6	1691	1	CA14_HUMAN	P02462 homo sapien	967	221.5	9.4	100	2	Q964C3	Q964c3 encephalito
895	226	9.6	1691	1	CA64_HUMAN	Q14031 homo sapien	968	221.5	9.4	173	2	Q41191	Q41191 arabidopsis
896	226	9.6	2189	2	Q9BI05	Q9bi05 eimeria ten	969	221.5	9.4	193	2	Q9VWM4	Q9vwm4 drosophila
897	225.5	9.5	265	2	Q6DDA7	Q6dda7 xenopus tro	970	221.5	9.4	228	2	Q6T0R0	Q6t0r0 plasmodium
898	225.5	9.5	751	2	Q9RLN9	Q9rln9 mus musculus	971	221.5	9.4	228	2	Q6T0R5	Q6t0r5 plasmodium
899	225.5	9.5	770	2	Q6BIY3	Q6biy3 debaryomyce	972	221.5	9.4	349	2	Q6C605	Q6c605 yarrowia li
900	225.5	9.5	809	2	Q76869	Q76869 drosophila	973	221.5	9.4	503	2	Q9HEH4	Q9neh4 neurospora
901	225.5	9.5	1113	1	N116_YEAST	Q02630 saccharomyc	974	221	9.4	273	2	Q65X75	Q65x75 oryza sativ
902	225.5	9.5	1338	2	Q7TWFO	Q7twp0 mycobacteri	975	221	9.4	310	2	Q90612	Q90612 gallus gall
903	225.5	9.5	1474	2	Q86G87	Q86g87 pseudoplusi	976	221	9.4	544	2	Q8I6C0	Q8i6c0 drosophila
904	225	9.5	325	2	Q8INH0	Q8inh0 drosophila	977	221	9.4	544	2	Q8I6C1	Q8i6c1 drosophila
905	225	9.5	544	2	Q8I6C8	Q8i6c8 drosophila	978	221	9.4	544	2	Q8I6C6	Q8i6c6 drosophila
906	225	9.5	572	2	Q63IU2	Q63iu2 burkholderi	979	221	9.4	561	2	Q9CXH6	Q9cxh6 mus musculus
907	225	9.5	624	2	Q8NIV1	Q8niv1 neurospora	980	221	9.4	575	2	Q9SBI7	Q9sb17 hordeum vul

981	221	9.4	594	2	Q67Q95	Q67g95 symbiobacte	1054	217	9.2	718	2	Q91TR1	Q91tr1 tupalid her
982	221	9.4	758	2	Q6TSC0	Q6tec0 crasostrea	1055	217	9.2	1045	2	Q801S8	Q801e8 xenopus lae
983	220.5	9.3	141	2	Q9BJP8	Q9bjp8 plasmodium	1056	216.5	9.2	212	2	Q949P9	Q949f9 oryza sativ
984	220.5	9.3	316	2	Q19111	Q19111 caenorhabdi	1057	216.5	9.2	244	2	Q6V5C2	Q6v5c2 arabidopsis
985	220.5	9.3	618	2	Q79F80	Q79f80 mycobacteri	1058	216.5	9.2	290	2	Q26FT54	Q26f54 paracentrot
986	220.5	9.3	618	2	Q7U0K5	Q7u0k5 mycobacteri	1059	216.5	9.2	419	2	Q6FT22	Q6ft22 candida gla
987	220.5	9.3	636	2	Q8VK65	Q8vk65 mycobacteri	1060	216.5	9.2	674	1	CA1A_BOVIN	P23206 bos taurus
988	220.5	9.3	645	1	K22E_HUMAN	P35908 homo sapien	1061	216.5	9.2	837	2	Q81B46	Q81b46 bacillus ce
989	220	9.3	192	2	Q7XDS2	Q7xd82 oryza sativ	1062	216.5	9.2	1019	1	CA26_HUMAN	P12110 homo sapien
990	220	9.3	202	2	Q8MML4	Q8mml4 dictyosteli	1063	216.5	9.2	1019	2	Q6P0Q1	Q6p0q1 homo sapien
991	220	9.3	332	2	Q6C1Z7	Q6c1z7 yarrowia li	1064	216.5	9.2	2090	1	N214_HUMAN	P35658 homo sapien
992	220	9.3	413	2	Q9HEJ0	Q9hej0 neurospora	1065	216.5	9.2	2091	2	Q75R47	Q75r47 homo sapien
993	220	9.3	568	2	Q8CD80	Q8cd80 mus musculu	1066	216	9.1	191	2	Q7XDR5	Q7xdr5 oryza sativ
994	220	9.3	572	2	Q9AUG8	Q9aug8 comamonas t	1067	216	9.1	405	2	Q6MWT4	Q6mmt4 bdellovibri
995	220	9.3	595	2	Q7XJ24	Q7xj24 oryza sativ	1068	216	9.1	405	2	Q19414	Q19414 caenorhabdi
996	220	9.3	954	2	Q8WXV8	Q8wxv8 homo sapien	1069	216	9.1	569	2	Q6CH78	Q6ch78 yarrowia li
997	220	9.3	954	2	Q96P44	Q96p44 homo sapien	1070	216	9.1	1838	1	CA15_HUMAN	P23008 homo sapien
998	220	9.3	957	2	Q9H0V3	Q9h0v3 homo sapien	1071	216	9.1	1838	1	Q88207	Q88207 mus musculu
999	220	9.3	1206	2	Q869X8	Q869x8 dictyosteli	1072	216	9.1	2090	2	Q9W2T1	Q9w2t1 drosophila
1000	220	9.3	1333	2	Q8PD38	Q8pd38 xanthomonas	1073	216	9.1	2093	2	Q15010	Q15010 homo sapien
1001	220	9.3	1740	2	Q9HCJ0	Q9hcj0 homo sapien	1074	215.5	9.1	102	2	Q964C0	Q964c0 encaphalito
1002	219.5	9.3	207	2	Q43522	Q43522 lycopersico	1075	215.5	9.1	424	2	Q6H9M8	Q6h9m8 erwinia pyr
1003	219.5	9.3	214	2	Q6H3Y0	Q6h3y0 oryza sativ	1076	215.5	9.1	520	1	MRCO_HUMAN	Q9uew3 homo sapien
1004	219.5	9.3	262	2	Q6CBL5	Q6cbl5 yarrowia li	1077	215.5	9.1	1034	2	Q8K229	Q8k229 mus musculu
1005	219.5	9.3	311	2	Q8V6M2	Q8v6m2 halovirus h	1078	215.5	9.1	2132	1	PGCA_MOUSE	Q61282 mus musculu
1006	219.5	9.3	339	2	Q8I097	Q8i097 drosophila	1079	215	9.1	200	1	GRP_HORVU	P17816 hordeum vul
1007	219.5	9.3	684	1	CA39_HUMAN	Q14050 homo sapien	1080	215	9.1	232	2	Q94FR1	Q94fr1 arabidopsis
1008	219.5	9.3	1191	2	Q6PCK7	Q6pck7 xenopus lae	1081	215	9.1	250	2	Q9VX64	Q9vx64 drosophila
1009	219	9.3	191	2	Q7XDR3	Q7xdr3 oryza sativ	1082	215	9.1	340	2	Q6WEQ0	Q6weq0 boechera dr
1010	219	9.3	193	2	Q70592	Q70592 rattus norv	1083	215	9.1	448	2	Q7XDS3	Q7xds3 oryza sativ
1011	219	9.3	294	2	Q6MGT3	Q6mgt3 bdellovibri	1084	215	9.1	479	2	O06292	Q06292 mycobacteri
1012	219	9.3	342	2	Q9LH90	Q9lh90 arabidopsis	1085	215	9.1	479	2	Q7U280	Q7u280 mycobacteri
1013	219	9.3	345	2	Q7TDH1	Q7tdh1 halovirus h	1086	215	9.1	541	2	Q9MA97	Q9ma97 arabidopsis
1014	219	9.3	368	2	Q8MPJ9	Q8mpj9 plasmodium	1087	215	9.1	566	2	Q91VL4	Q91vl4 mus musculu
1015	219	9.3	379	1	ROA3_MOUSE	Q8bg05 mus musculu	1088	215	9.1	575	2	Q9SPA7	Q9spa7 hordeum vul
1016	219	9.3	379	1	ROA3_RAT	Q6urk4 rattus norv	1089	215	9.1	594	2	Q7WKH2	Q7wkh2 bordetella
1017	219	9.3	413	2	Q64939	Q64939 lophopyrum	1090	215	9.1	635	2	Q6UD62	Q6ud62 uncultured
1018	219	9.3	473	2	Q84WQ1	Q84wq1 arabidopsis	1091	215	9.1	669	2	Q7UE67	Q7ue67 rhodopirell
1019	219	9.3	544	2	Q816B7	Q816b7 drosophila	1092	215	9.1	1029	1	CA26_MOUSE	Q02788 mus musculu
1020	219	9.3	544	2	Q816B8	Q816b8 drosophila	1093	215	9.1	1319	1	MN1_HUMAN	Q10571 homo sapien
1021	219	9.3	544	2	Q816C2	Q816c2 drosophila	1094	215	9.1	1405	2	Q8KMK1	Q8kmk1 mycoplasma
1022	219	9.3	716	2	Q825D6	Q825d6 streptomyc	1095	215	9.1	1567	1	ICEN_XANCT	P18127 xanthomonas
1023	219	9.3	734	2	Q61VJ4	Q61vj4 ciona intes	1096	215	9.1	1690	1	CA44_HUMAN	P53420 homo sapien
1024	219	9.3	775	2	Q82CQ3	Q82cq3 streptomyc	1097	215	9.1	1838	2	Q15094	Q15094 homo sapien
1025	219	9.3	1053	2	Q92Q54	Q92084 mus musculu	1098	215	9.1	3848	2	P94772	P94772 erwinia chr
1026	219	9.3	1212	2	Q8OU93	Q8ou93 mus musculu	1099	214.5	9.1	191	2	Q7XDR8	Q7xdr8 oryza sativ
1027	219	9.3	2303	2	Q7QCA2	Q7qca2 anopheles g	1100	214.5	9.1	241	2	Q6V5D7	Q6v5d7 ollimarabido
1028	218.5	9.2	297	2	Q8HEH5	Q8heh5 dictyosteli	1101	214.5	9.1	373	2	Q9U2I7	Q9u2i7 caenorhabdi
1029	218.5	9.2	370	2	Q95TX4	Q95tx4 drosophila	1102	214.5	9.1	465	2	Q9RXC3	Q9rcx3 deinococcus
1030	218.5	9.2	378	1	ROA3_HUMAN	P51991 homo sapien	1103	214.5	9.1	558	2	Q6BI51	Q6bi51 debaryomyce
1031	218.5	9.2	497	2	Q7K536	Q7k536 drosophila	1104	214.5	9.1	589	2	Q9JL16	Q9jll6 mus musculu
1032	218.5	9.2	589	2	Q66043	Q66043 cercopithe	1105	214.5	9.1	678	2	Q6P467	Q6p467 homo sapien
1033	218.5	9.2	612	2	Q7X678	Q7x678 chlamydomon	1106	214.5	9.1	778	2	Q86BH1	Q86bh1 drosophila
1034	218.5	9.2	705	2	Q04310	Q04310 arabidopsis	1107	214.5	9.1	792	2	Q8MT89	Q8mt89 drosophila
1035	218.5	9.2	1218	2	Q6VBJ4	Q6vbj4 candida gla	1108	214.5	9.1	970	2	Q8VBY1	Q8vby1 rattus norv
1036	218.5	9.2	1416	2	Q6VBZ3	Q6vbz3 candida gla	1109	214.5	9.1	1018	2	Q9WBV6	Q9wbv6 pseudomonas
1037	218.5	9.2	1535	2	Q62D27	Q62d27 burkholderi	1110	214	9.1	301	2	Q8WSZ3	Q8wsz3 nephila cla
1038	218.5	9.2	1580	2	Q8BLX7	Q8blx7 mus musculu	1111	214	9.1	399	2	Q9WSZ3	Q9wsz3 rhizobium l
1039	218.5	9.2	1940	2	Q9VMV5	Q9vmv5 drosophila	1112	214	9.1	594	2	Q7W927	Q7w927 bordetella
1040	218	9.2	284	2	Q9BIS8	Q9bis8 tetragnatha	1113	214	9.1	627	1	K2C1_MOUSE	P04104 mus musculu
1041	218	9.2	481	2	Q8VKM5	Q8vkm5 mycobacteri	1114	214	9.1	699	2	Q6P1C4	Q6p1c4 mus musculu
1042	218	9.2	763	2	Q7Q1W5	Q7qlw5 anopheles g	1115	214	9.1	911	1	CA1B_BOVIN	Q28083 bos taurus
1043	218	9.2	2119	2	Q86XD3	Q86xd3 homo sapien	1116	214	9.1	1275	2	Q76602	Q76602 caenorhabdi
1044	217.5	9.2	218	2	Q8SV22	Q8sy22 drosophila	1117	214	9.1	1332	2	Q8SZ27	Q8sz27 drosophila
1045	217.5	9.2	355	2	Q9L8W2	Q9l8w2 mycoplasma	1118	214	9.1	1332	2	Q86S06	Q86s06 drosophila
1046	217.5	9.2	384	2	Q9L8V9	Q9l8v9 mycoplasma	1119	214	9.1	1375	2	Q86S05	Q86s05 drosophila
1047	217.5	9.2	1521	2	Q8CHS9	Q8chs9 mus musculu	1120	214	9.1	1461	2	Q8MKQ2	Q8mkq2 drosophila
1048	217.5	9.2	1666	2	Q8LPE8	Q8lpe8 chlamydomon	1121	214	9.1	1472	2	Q9V358	Q9v358 drosophila
1049	217.5	9.2	1752	2	Q7QBX5	Q7qbx5 anopheles g	1122	214	9.1	1756	2	Q7PMG9	Q7pmg9 anopheles g
1050	217.5	9.2	1880	2	Q18465	Q18465 hirudo medi	1123	214	9.1	1840	2	Q60467	Q60467 cricetus
1051	217	9.2	391	2	Q8GX10	Q8gx10 arabidopsis	1124	214	9.1	2447	2	Q6SF13	Q6sf13 uncultured
1052	217	9.2	575	2	Q40042	Q40042 hordeum vul	1125	213.5	9.0	195	2	Q6MWV0	Q6mwv0 mycobacteri
1053	217	9.2	632	2	Q6C5E6	Q6c5e6 yarrowia li	1126	213.5	9.0	575	2	Q8CIF9	Q8cif9 mus musculu

1127	213.5	9.0	687	1	DSPP_RAT	Q62598 rattus norv	1200	209.5	8.9	2333	1	PGCA_CANFA	Q28343 canis famli
1128	213.5	9.0	695	2	Q9XUQ0	Q9xug0 caenorhabd	1201	209.5	8.9	3080	2	Q9V602	Q9v602 drosophila
1129	213.5	9.0	959	1	N100_YEARST	Q02629 saccharomyc	1202	209.5	8.9	3109	2	Q9BMQ0	Q9bmq0 drosophila
1130	213.5	9.0	1653	2	Q63M66	Q63m66 burkholderi	1203	209.5	8.9	3276	2	Q9W321	Q9w321 drosophila
1131	213.5	9.0	1670	1	CA34_HUMAN	Q01955 homo sapien	1204	209	8.8	288	2	Q6L8H1	Q6l8h1 homo sapien
1132	213.5	9.0	1840	2	Q9JIO3	Q9ji03 rattus norv	1205	209	8.8	457	2	Q7UUX5	Q7uux5 mycobacteri
1133	213.5	9.0	2415	1	FGCA_HUMAN	P16112 homo sapien	1206	209	8.8	554	2	Q8S7B5	Q8s7b5 oryza sativ
1134	213	9.0	193	2	Q7XD70	Q7xdt0 oryza sativ	1207	209	8.8	554	2	Q7XFL8	Q7xf18 oryza sativ
1135	213	9.0	218	2	Q6K574	Q6k5t4 oryza sativ	1208	209	8.8	610	2	Q6FU80	Q6fuo0 candida gla
1136	213	9.0	368	2	Q8MPK1	Q8mpk1 plasmodium	1209	209	8.8	799	2	Q8BNS7	Q8bns7 mus musculu
1137	213	9.0	457	2	Q9VC50	Q9vc90 drosophila	1210	209	8.8	847	2	Q69T67	Q69t67 oryza sativ
1138	213	9.0	529	2	Q43509	Q43509 homo sapien	1211	209	8.8	934	2	Q9GMD3	Q9gmd3 bos taurus
1139	213	9.0	529	2	Q8IZU4	Q8izu4 homo sapien	1212	209	8.8	1707	1	CA24_MOUSE	P08122 mus musculu
1140	212.5	9.0	189	2	Q66K53	Q66k53 homo sapien	1213	209	8.8	2573	2	Q7SAE9	P15989 neurospora
1141	212.5	9.0	220	1	SER2_GALME	Q96615 gallieria me	1214	209	8.8	3137	1	CA36_CHICK	P15989 gallus gall
1142	212.5	9.0	829	2	Q94C88	Q94c88 arabidopsis	1215	208.5	8.8	194	2	Q96853	Q96853 schistosoma
1143	212.5	9.0	857	2	Q69Z83	Q69z83 mus musculu	1216	208.5	8.8	353	2	Q7QFF4	Q7qff4 anopheles g
1144	212.5	9.0	882	2	Q80VW9	Q80vw9 mus musculu	1217	208.5	8.8	377	2	Q42627	Q42627 brassica na
1145	212.5	9.0	950	2	Q86SC8	Q86sc8 ciona intes	1218	208.5	8.8	442	1	CYS4_DICDI	P54639 dictyosteli
1146	212.5	9.0	1035	2	Q6FU56	Q6fu56 candida gla	1219	208.5	8.8	491	2	Q6EI03	P90534 dictyosteli
1147	212.5	9.0	1804	2	Q9ZVV0	Q9zvv0 arabidopsis	1220	208.5	8.8	809	2	P90534	Q48848 arabidopsis
1148	212.5	9.0	1835	2	Q9IAU4	Q9iau4 gallus gall	1221	208	8.8	201	2	Q48848	Q9bpx6 plasmodium
1149	212.5	9.0	1845	2	Q80UA8	Q80ua8 mus musculu	1222	208	8.8	370	2	Q9BPK6	Q9bpx6 plasmodium
1150	212.5	9.0	2285	2	Q9HBU5	Q9hbj5 homo sapien	1223	208	8.8	370	2	Q9BPK8	Q9bpx8 plasmodium
1151	212.5	9.0	2551	2	Q8CY18	Q8cy18 streptococc	1224	208	8.8	377	2	Q26116	Q6fxh4 candida gla
1152	212.5	9.0	2572	2	Q7PRV6	Q7prv6 anopheles g	1225	208	8.8	394	2	Q6FX84	Q7qdl5 anopheles g
1153	212	9.0	347	2	Q9XT25	Q9xt25 bos taurus	1226	208	8.8	436	2	Q7QDL5	Q7qdl5 anopheles g
1154	212	9.0	390	1	CS12_WHEAT	P46525 triticum ae	1227	208	8.8	457	2	Q79FU0	Q79fu0 mycobacteri
1155	212	9.0	568	2	Q6NUV1	Q6nuv1 brachydanio	1228	208	8.8	529	2	Q7YR44	Q7yrr4 pan troglod
1156	212	9.0	619	2	Q7PQ47	Q7pq47 anopheles g	1229	208	8.8	588	2	Q9QEK6	Q9qek6 cynomolgus
1157	212	9.0	633	2	Q6EIX21	Q6eix21 canis famli	1230	208	8.8	680	1	CA1A_MOUSE	Q14055 homo sapien
1158	212	9.0	645	2	Q9KXB9	Q9kxb9 escherichia	1231	208	8.8	689	1	CA29_HUMAN	Q9esq2 mus musculu
1159	212	9.0	907	2	Q26675	Q26675 theileria a	1232	208	8.8	1691	2	Q9ESQ2	Q9esq2 mus musculu
1160	212	9.0	975	2	Q6FUW3	Q6fuw3 candida gla	1233	208	8.8	1691	2	Q63ZW6	Q63zw6 mus musculu
1161	212	9.0	1023	2	Q7RT42	Q7rt42 plasmodium	1234	207.5	8.8	186	2	Q9DEX8	Q9dex8 cyprinus ca
1162	212	9.0	1046	2	Q8K388	Q8k388 mus musculu	1235	207.5	8.8	236	2	Q6V5H3	Q6v5h3 arabidopsis
1163	212	9.0	3056	2	Q7USQ0	Q7usq0 rhodospirell	1236	207.5	8.8	332	2	Q69ZG1	Q69z21 nephila cia
1164	211.5	9.0	193	2	Q9D6J0	Q9d6j0 mus musculu	1237	207.5	8.8	334	2	Q9JKB4	Q9jkb4 mus musculu
1165	211.5	9.0	226	2	Q7QCJ2	Q7qcj2 anopheles g	1238	207.5	8.8	365	1	ROAL_DROME	P07909 drosophila
1166	211.5	9.0	248	2	Q8VIW6	Q8viw6 mycobacteri	1239	207.5	8.8	389	1	SERI_BOWMO	P07856 bombyx mori
1167	211.5	9.0	286	2	Q9UIG9	Q9ulg9 drosophila	1240	207.5	8.8	428	2	Q8H3M9	Q8h3m9 erwinia sp.
1168	211.5	9.0	394	2	Q9VVC3	Q9vvc3 drosophila	1241	207.5	8.8	476	2	Q8VKAS	Q8vks5 mycobacteri
1169	211.5	9.0	431	2	Q7NIB7	Q7nib7 photorhabdu	1242	207.5	8.8	522	2	Q9P9G7	Q9p9g7 methanococc
1170	211.5	9.0	457	2	Q7TVR9	Q7tyr9 mycobacteri	1243	207.5	8.8	603	2	Q6FLA7	Q6fla7 candida gla
1171	211.5	9.0	480	2	Q8IGI0	Q8igi0 drosophila	1244	207.5	8.8	632	2	Q8CJT6	Q8cjt6 streptomyce
1172	211.5	9.0	957	2	Q641F3	Q641f3 xenopus lae	1245	207.5	8.8	662	2	Q8VHY3	Q8vhy3 mus musculu
1173	211	8.9	253	2	Q9BIT4	Q9bit4 nephila sen	1246	207.5	8.8	981	2	Q8MQ11	Q8mq11 drosophila
1174	211	8.9	286	2	Q9VB86	Q9vb86 drosophila	1247	207	8.8	208	2	Q25949	Q25949 plasmodium
1175	211	8.9	367	2	Q7QEF9	Q7qef9 anopheles g	1248	207	8.8	303	2	Q82BN1	Q82bn1 streptomyce
1176	211	8.9	371	1	ROAL_HUMAN	P09651 homo sapien	1249	207	8.8	313	2	Q9SYZ5	Q9syz5 arabidopsis
1177	211	8.9	643	2	Q68ED0	Q68ed0 mus musculu	1250	207	8.8	314	2	Q9FGY2	Q9fgy2 arabidopsis
1178	211	8.9	890	2	Q7087	Q77087 alvinella p	1251	207	8.8	405	2	Q23057	Q23057 caenorhabdi
1179	211	8.9	967	2	Q08294	Q08294 saccharomyc	1252	207	8.8	448	2	Q716P3	Q716p3 mycobacteri
1180	210.5	8.9	255	2	Q69ZG5	Q69z25 nephila cia	1253	207	8.8	529	2	Q63TRS	Q63tr5 burkholderi
1181	210.5	8.9	428	2	Q6XDB9	Q6xdb9 erwinia pyr	1254	207	8.8	645	2	Q776P1	Q776p1 bacterioph
1182	210.5	8.9	471	2	Q9UAY0	Q9uay0 caenorhabdi	1255	207	8.8	645	2	Q7Y2W1	Q7y2w1 stx2 conver
1183	210.5	8.9	509	2	Q7Z010	Q7z010 plodia inte	1256	207	8.8	645	2	Q7Y3C2	Q7y3c2 stx1 conver
1184	210.5	8.9	623	2	Q7SZR6	Q7szr6 brachydanio	1257	207	8.8	645	2	Q9XJK8	Q9xjk8 bacterioph
1185	210.5	8.9	624	2	Q6NUX1	Q6nux1 brachydanio	1258	207	8.8	645	2	Q8YAX7	Q8yax7 escherichia
1186	210.5	8.9	941	2	Q85Y78	Q85y78 mycobacteri	1259	207	8.8	680	1	CA1A_HUMAN	Q03652 homo sapien
1187	210.5	8.9	1488	2	Q8NPK0	Q8npk0 corynebacte	1260	207	8.8	824	2	Q7QJH6	Q7qjh6 anopheles g
1188	210.5	8.9	3190	2	Q01368	Q01368 drosophila	1261	207	8.8	1306	2	Q93N36	Q93n36 pantoea ana
1189	210	8.9	192	2	Q7XDR7	Q7xd7 oryza sativ	1262	207	8.8	1336	2	Q6RZ41	Q6rz41 homo sapien
1190	210	8.9	430	2	Q95RR2	Q95rr2 drosophila	1263	207	8.8	1516	2	Q6RZ39	Q6rz39 homo sapien
1191	210	8.9	459	2	Q6FB76	Q6fb76 acinetobact	1264	207	8.8	1751	2	Q6RZ40	Q6rz40 homo sapien
1192	210	8.9	1315	2	Q8QHLU5	Q8qhl9 xenopus lae	1265	207	8.8	2124	1	FGCA_RAT	P07897 rattus norv
1193	209.5	8.9	302	2	Q84Q60	Q84q60 arabidopsis	1266	206.5	8.7	322	2	Q8G4E5	Q8g4e5 bifidobacte
1194	209.5	8.9	319	2	Q6C4B0	Q6c4b0 yarrowia li	1267	206.5	8.7	342	1	ROAL_SCHAM	R21522 schistocerc
1195	209.5	8.9	595	2	Q82K69	Q82k69 streptomyce	1268	206.5	8.7	434	2	Q7N1B8	Q7n1b8 photorhabdu
1196	209.5	8.9	597	2	Q640K4	Q640k4 xenopus lae	1269	206.5	8.7	456	2	Q6CAZ4	Q6caz4 yarrowia li
1197	209.5	8.9	688	1	CA29_MOUSE	Q07643 mus musculu	1270	206.5	8.7	504	2	Q6J4Y8	Q6j4y8 gallus gall
1198	209.5	8.9	688	2	Q8K2W0	Q8k2w0 mus musculu	1271	206.5	8.7	528	2	Q81ZU5	Q81zu5 homo sapien
1199	209.5	8.9	920	2	Q78EC6	Q78ec6 mus sp. typ	1272	206.5	8.7	528	2	Q81ZU6	Q81zu6 homo sapien

1273	206.5	8.7	528	2	Q8NSP3	Q8n5p3 homo sapien	1346	203.5	8.6	456	2	Q638E4	Q638e4 bacillus ce
1274	206.5	8.7	573	2	Q8K7M7	Q8k7m7 streptococ	1347	203.5	8.6	476	2	Q9VA86	Q9va86 drosophila
1275	206.5	8.7	597	2	Q7P8S59	Q7p8s59 anopheles g	1348	203.5	8.6	486	1	CDSN_HUMAN	Q151i7 homo sapien
1276	206.5	8.7	647	2	Q9PT10	Q9pt10 oncorhynchus	1349	203.5	8.6	500	2	Q9NP52	Q9np52 homo sapien
1277	206.5	8.7	691	2	Q66L59	Q66l59 brachydanio	1350	203.5	8.6	513	2	Q85K1F9	Q85k1f9 mus musculu
1278	206.5	8.7	1025	1	CA16_MOUSE	Q44857 mus musculu	1351	203.5	8.6	943	2	Q8BK12	Q8bk12 mus musculu
1279	206	8.7	202	2	Q25952	Q25952 plasmodium	1352	203.5	8.6	1124	2	Q63UH1	Q63uh1 burkholderi
1280	206	8.7	370	2	Q8MPK2	Q8mpk2 plasmodium	1353	203.5	8.6	1335	2	Q6NVE4	Q6nve4 mus musculu
1281	206	8.7	374	2	Q75JC9	Q75jc9 dictyosteli	1354	203.5	8.6	1533	2	Q98HJ2	Q98hj2 rhizobium l
1282	206	8.7	447	2	Q9SIA8	Q9sia8 arabisopsis	1355	203	8.6	196	2	Q8FZF2	Q8fzf2 methanosarc
1283	206	8.7	713	2	Q9GV24	Q9gv24 sarcophaga	1356	203	8.6	223	2	Q9C6Y9	Q9c6y9 arabisopsis
1284	206	8.7	770	2	Q7WHU6	Q7whu6 bordetella	1357	203	8.6	260	2	Q8ISA8	Q8isa8 plasmodium
1285	206	8.7	1257	2	Q14654	Q14654 homo sapien	1358	203	8.6	277	2	Q9GQP0	Q9gqp0 plasmodium
1286	206	8.7	1322	1	ICEN_PANAN	P20469 pantocea ana	1359	203	8.6	439	2	Q8S7B4	Q8s7b4 oryza sativ
1287	205.5	8.7	406	2	Q23288	Q23288 arabisopsis	1360	203	8.6	439	2	Q7XFL9	Q7xfl9 oryza sativ
1288	205.5	8.7	411	2	Q8W034	Q8w034 arabisopsis	1361	203	8.6	499	2	Q9NRH4	Q9nrh4 homo sapien
1289	205.5	8.7	424	2	Q6H9M6	Q6h9m6 erwinia pyr	1362	203	8.6	526	2	Q6IFW6	Q6ifw6 rattus norv
1290	205.5	8.7	428	2	Q82FT8	Q82ft8 streptomyc	1363	203	8.6	637	2	Q7Q5C7	Q7q5c7 anopheles g
1291	205.5	8.7	518	1	MTCO_MOUSE	Q60754 mus musculu	1364	203	8.6	680	2	P93658	P93658 brassica na
1292	205.5	8.7	561	2	Q961F4	Q961f4 homo sapien	1365	203	8.6	690	2	Q6K2M1	Q6k2m1 oryza sativ
1293	205.5	8.7	592	2	Q90W75	Q90w75 oncorhynchus	1366	203	8.6	813	2	Q8GFF3	Q8gff3 streptomyc
1294	205.5	8.7	680	2	Q8BSX1	Q8bsx1 mus musculu	1367	203	8.6	825	1	SE5_RAT	Q63003 rattus norv
1295	205.5	8.7	1028	2	Q7Z645	Q7z645 homo sapien	1368	203	8.6	1034	1	ICEN_PANAN	Q47879 pantocea ana
1296	205.5	8.7	1112	2	Q7RN90	Q7rn90 plasmodium	1369	203	8.6	1253	1	DSP_P_HUMAN	Q9nz44 homo sapien
1297	205	8.7	164	2	Q7XDT8	Q7xdt8 oryza sativ	1370	203	8.6	2149	2	Q6XL68	Q6xl68 bos taurus
1298	205	8.7	177	2	Q26577	Q26577 schistosoma	1371	203	8.6	2364	1	PGCA_BOVIN	P13608 bos taurus
1299	205	8.7	187	2	Q8L3S8	Q8l3s8 zea mays (m	1372	203	8.6	2365	2	Q6XL67	Q6xl67 bos taurus
1300	205	8.7	207	2	Q25701	Q25701 plasmodium	1373	202.5	8.6	425	2	Q8WSL2	Q8ws12 plasmodium
1301	205	8.7	224	2	Q94FP7	Q94fp7 arabisopsis	1374	202.5	8.6	431	2	Q8GLD8	Q8gld8 bacillus th
1302	205	8.7	224	2	Q94FP8	Q94fp8 arabisopsis	1375	202.5	8.6	456	2	Q7UJ76	Q7uj76 rhodopirell
1303	205	8.7	368	2	Q8MPK0	Q8mpk0 plasmodium	1376	202.5	8.6	667	2	Q8XR8	Q8xr8 ralatonia s
1304	205	8.7	393	2	Q8MPK3	Q8mpk3 plasmodium	1377	202.5	8.6	677	1	CA29_CHICK	P12108 gallus gall
1305	205	8.7	640	2	Q6KQAQ4	Q6kaq4 mus musculu	1378	202.5	8.6	771	2	Q63LV4	Q63lv4 burkholderi
1306	205	8.7	775	2	Q7M2X5	Q7m2x5 oryctolagus	1379	202.5	8.6	831	2	Q62B18	Q62b18 burkholderi
1307	205	8.7	1012	2	Q62KN5	Q62kn5 burkholderi	1380	202.5	8.6	1028	1	CA16_HUMAN	P12109 homo sapien
1308	205	8.7	1036	2	Q6CWM9	Q6cwm9 kluyveromyc	1381	202.5	8.6	1456	2	Q6C4S5	Q6c4s5 yarrowia li
1309	205	8.7	1084	2	Q01212	Q01212 homo sapien	1382	202.5	8.6	3176	1	CA36_HUMAN	P12111 homo sapien
1310	205	8.7	1131	2	Q75DJ5	Q75dj5 ashbya goss	1383	202	8.5	324	2	Q7SD1	Q7sdb1 neurospora
1311	205	8.7	1301	2	Q6P3M9	Q6p3m9 xenopus tro	1384	202	8.5	348	2	Q75CJ3	Q75cj3 ashbya goss
1312	205	8.7	1417	2	Q9HVN6	Q9hvn6 pseudomonas	1385	202	8.5	430	1	NU42 YEAST	P49686 saccharomyc
1313	205	8.7	1516	1	CA1H_HUMAN	P39060 homo sapien	1386	202	8.5	464	2	Q8WSL4	Q8ws14 plasmodium
1314	205	8.7	1603	1	CA1F_HUMAN	Q7092 homo sapien	1387	202	8.5	488	2	Q6RBZ1	Q6rbz1 chlamydomon
1315	205	8.7	1610	2	Q92KQ8	Q92kq8 rhizobium m	1388	202	8.5	571	2	Q6H086	Q6h086 fremyella d
1316	205	8.7	2189	2	Q8IKV6	Q8ikv6 plasmodium	1389	202	8.5	692	2	Q8XT20	Q8xt20 ralatonia s
1317	205	8.7	2351	2	Q8PCQ5	Q8pcq5 xanthomonas	1390	202	8.5	700	2	Q9VXH1	Q9vxh1 drosophila
1318	204.5	8.7	279	2	Q6C3L2	Q6c3l2 yarrowia li	1391	202	8.5	733	2	Q9ADN4	Q9adn4 streptomyc
1319	204.5	8.7	280	2	Q91VQ2	Q91vq2 mus musculu	1392	202	8.5	742	2	Q8IR16	Q8ir16 drosophila
1320	204.5	8.7	443	1	Q28243	Q28243 canis famil	1393	202	8.5	749	2	Q82FQ7	Q82fq7 streptomyc
1321	204.5	8.7	483	1	MRCO_MESAU	Q9wub9 mesotricetu	1394	202	8.5	1432	2	Q9FPR8	Q9fpr8 chlamydomon
1322	204.5	8.7	611	2	Q6Z4M4	Q6z4m4 oryza sativ	1395	201.5	8.5	231	2	Q7SQN8	Q7sqn8 triticum ae
1323	204.5	8.7	654	2	Q9BX50	Q9bx50 homo sapien	1396	201.5	8.5	233	2	Q9BIT6	Q9bit6 nephila ina
1324	204.5	8.7	1019	1	CA16_CHICK	P20785 gallus gall	1397	201.5	8.5	393	2	Q18880	Q18880 caenorhabdi
1325	204.5	8.7	1310	2	Q6DFR4	Q6dfr4 xenopus tro	1398	201.5	8.5	425	2	Q6WMT5	Q6wmt5 bdellovibri
1326	204	8.6	177	1	EGG2_SCHMA	P12796 schistosoma	1399	201.5	8.5	433	2	Q9VEF5	Q9vef5 drosophila
1327	204	8.6	177	1	EGG3_SCHMA	P13396 schistosoma	1400	201.5	8.5	531	2	Q97468	Q97468 drosophila
1328	204	8.6	177	1	Q7XDR4	Q7xd4 oryza sativ	1401	201.5	8.5	531	2	Q8SXP8	Q8sxp8 drosophila
1329	204	8.6	131	2	Q43308	Q43308 arabisopsis	1402	201.5	8.5	555	2	Q6ZQR0	Q6zqr0 homo sapien
1330	204	8.6	228	2	Q95Z54	Q95z54 plasmodium	1403	201.5	8.5	623	2	Q8K2U8	Q8k2u8 mus musculu
1331	204	8.6	247	2	Q95Q50	Q95q50 anopheles g	1404	201.5	8.5	888	2	Q8QW00	Q8q419 gallus gall
1332	204	8.6	364	2	Q18453	P18453 heterodera	1405	201.5	8.5	1344	2	Q93419	Q93419 mus musculu
1333	204	8.6	476	2	CAFI_EPHMU	P18856 ephydacia m	1406	201.5	8.5	1671	2	Q7SE26	Q7se26 neurospora
1334	204	8.6	547	1	Q9L0T2	Q9l0t2 streptomyc	1407	201.5	8.5	1711	1	N214_DROME	Q9wlx4 drosophila
1335	204	8.6	717	2	Q9H4U3	Q9h4u3 homo sapien	1408	201	8.5	233	2	Q6WEQ8	Q6weq8 arabisopsis
1336	204	8.6	798	2	Q96JF7	Q96jf7 homo sapien	1409	201	8.5	302	2	Q9GQL8	Q9gql8 plasmodium
1337	204	8.6	832	2	Q6FPUB	Q6fpub candida gla	1410	201	8.5	302	2	Q9GQL9	Q9gql9 plasmodium
1338	204	8.6	866	2	Q67QD7	Q67qd7 symbiobacte	1411	201	8.5	317	2	Q9BH54	Q9bh54 plasmodium
1339	204	8.6	953	2	Q67QD7	Q67qd7 symbiobacte	1412	201	8.5	381	2	Q76450	Q76450 strongyloce
1340	204	8.6	1146	1	CA1G_CHICK	Q90584 gallus gall	1413	201	8.5	422	2	Q6H9N0	Q6h9n0 erwinia sp.
1341	204	8.6	1802	2	Q17163	Q17163 brugia mala	1414	201	8.5	433	2	Q69TP6	Q69tp6 oryza sativ
1342	204	8.6	1860	2	Q81ZC6	Q81zc6 homo sapien	1415	201	8.5	445	2	Q9VEB9	Q9veb9 drosophila
1343	203.5	8.6	262	2	Q767M8	Q767m8 sus scrofa	1416	201	8.5	690	2	Q8UGL8	Q8jgl8 brachydanio
1344	203.5	8.6	280	1	C36A_MANSE	Q8t634 manduca sex	1417	201	8.5	798	2	Q8SX18	Q8sx18 drosophila
1345	203.5	8.6	341	2	Q91ZR9	Q91zr9 mus musculu	1418	201	8.5	798	2	Q9VHP0	Q9vhp0 drosophila



1419	201	8.5	836	2	Q8S3T3	Q8e3t3 aegilops ta
1420	201	8.5	990	2	Q15206	Q15206 homo sapien
1421	201	8.5	1012	2	Q8XUM5	Q8xum5 ralatonia s
1422	201	8.5	1218	2	Q05331	Q05331 homo sapien
1423	201	8.5	1669	2	Q0QZ80	Q0qze80 mus musculu
1424	201	8.5	1712	1	CA24_HUMAN	P08572 homo sapien
200.5	201	8.5	239	2	Q69T79	Q69t79 oryza sativ
1426	200.5	8.5	312	2	O18097	O18097 caenorhabdi
1427	200.5	8.5	341	1	ROA2_MOUSE	Q88569 mus musculu
1428	200.5	8.5	341	2	Q9TTV2	Q9ttv2 saquinus oe
1429	200.5	8.5	353	1	ROA2_HUMAN	P22626 homo sapien
1430	200.5	8.5	538	2	Q8BPX3	Q8bpk3 mus musculu
1431	200.5	8.5	623	1	PNT1_DROME	P51022 drosophila
1432	200.5	8.5	663	2	Q7SEL6	Q7sel6 neurospora
1433	200.5	8.5	675	2	Q08000	Q08000 gallus gall
1434	200.5	8.5	678	2	Q8SCA4	Q8aca4 stx2 conve
1435	200.5	8.5	911	2	Q7PUV5	Q7puv5 anopheles g
1436	200.5	8.5	1271	2	Q7PC53	Q7pc53 microbubif
1437	200.5	8.5	1605	1	RRB1_MOUSE	Q99pl5 mus musculu
1438	200.5	8.5	2232	2	Q81FX6	Q81fx6 caenorhabdi
1439	200	8.5	125	2	Q69RC8	Q69rc8 oryza sativ
1440	200	8.5	313	2	Q692G0	Q692g0 nephila cla
1441	200	8.5	345	2	Q7ZWV4	Q7zwv4 xenopus lae
1442	200	8.5	523	2	Q7PYW0	Q7pyw0 anopheles g
1443	200	8.5	759	2	Q821J7	Q821j7 streptomyc
1444	200	8.5	1096	2	Q9SY83	Q9sy83 arabidopsis
1445	200	8.5	1258	1	ICEN_ERWHE	P16239 erwinia her
1446	200	8.5	1743	2	Q7PVF6	Q7pvr6 anopheles g
1447	200	8.5	3716	2	Q6MWX8	Q6mw8 mycobacteri
1448	199.5	8.4	212	2	Q9SFV8	Q9sfv8 arabidopsis
1449	199.5	8.4	214	1	GRP2_NICSY	P27484 nicotiana s
1450	199.5	8.4	269	2	Q6C117	Q6c117 yarrowia li
1451	199.5	8.4	341	2	Q9F2Q1	Q9f2q1 streptomyc
1452	199.5	8.4	393	2	Q26110	Q26110 plasmodium
1453	199.5	8.4	480	2	Q89EV2	Q89ev2 bradyrhizob
1454	199.5	8.4	482	2	Q6DCR4	Q6dcr4 xenopus lae
1455	199.5	8.4	493	2	Q7XES4	Q7xes4 oryza sativ
1456	199.5	8.4	519	2	Q8NCA5	Q8ncas homo sapien
1457	199.5	8.4	670	2	Q7SDQ7	Q7sdq7 neurospora
1458	199.5	8.4	673	2	Q14052	Q14052 homo sapien
1459	199.5	8.4	737	2	Q8RUT8	Q8rut8 chlamydomon
1460	199.5	8.4	790	2	Q22872	Q22872 caenorhabdi
1461	199.5	8.4	886	2	Q9NUB7	Q9nub7 homo sapien
1462	199.5	8.4	1022	2	Q22308	Q22308 caenorhabdi
1463	199.5	8.4	1599	2	Q854N0	Q854n0 mycobacteri
1464	199.5	8.4	1685	1	CA54_HUMAN	P29400 homo sapien
1465	199.5	8.4	1961	2	Q86GJ3	Q86gj3 drosophila
1466	199.5	8.4	1962	2	Q8NDV7	Q8ndv7 homo sapien
1467	199.5	8.4	7716	2	Q7UWZ8	Q7uwz8 rhodospirell
1468	199	8.4	173	1	EGG1_SCHMA	P06649 schistosoma
1469	199	8.4	183	2	Q9VRT3	Q9vri3 drosophila
1470	199	8.4	571	1	Q6CVL4	Q6cvl4 kluyveromyc
1471	199	8.4	585	1	RGA_DROME	Q4547 drosophila
1472	199	8.4	675	1	CA39_CHICK	P32017 gallus gall
1473	199	8.4	825	1	ICP0_HRV2H	P28284 human herpe
1474	199	8.4	826	2	P89473	P89473 human herpe
1475	199	8.4	1307	2	Q8JPF7	Q8jft7 xenopus lae
1476	198.5	8.4	157	2	Q9FCT4	Q9fct4 mycoplasma
1477	198.5	8.4	191	2	Q42448	Q42448 medicago sa
1478	198.5	8.4	264	2	Q9VYL8	Q9vy18 drosophila
1479	198.5	8.4	380	2	Q42637	Q42637 brassica ol
1480	198.5	8.4	388	2	Q95RA1	Q95ra1 drosophila
1481	198.5	8.4	465	2	O16001	O16001 hydra atten
1482	198.5	8.4	747	2	Q6NWS7	Q6nws7 brachydanio
1483	198.5	8.4	921	1	CA19_MOUSE	Q05722 mus musculu
1484	198.5	8.4	923	2	Q7Y1G5	Q7y1g5 oryza sativ
1485	198.5	8.4	979	2	Q919K3	Q919k3 gallus gall
1486	198.5	8.4	1329	2	Q7RZK3	Q7rzx3 neurospora
1487	198.5	8.4	1470	1	CA01_MOUSE	Q07563 mus musculu
1488	198	8.4	346	1	RO21_XENLA	P51989 xenopus lae
1489	198	8.4	386	2	Q8NL07	Q8nl07 xanthomonas
1490	198	8.4	393	2	Q26124	Q26124 plasmodium
1491	198	8.4	437	2	Q9VRB0	Q9vrB0 drosophila

## ALIGNMENTS

## RESULT 1

Q6UXC7	PRELIMINARY;	PRT;	440 AA.
ID	Q6UXC7		
AC	Q6UXC7;		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DR	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DE	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	KFGQ729.		
GN	ORFNames=UNQ729;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yaneura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment."		
RL	Genome Res. 13:2265-2270(2003).		
DR	EMBL; AY358412; AAQ8778.1; -.		
SQ	SEQUENCE 440 AA; 42208 MW; B4COAFD0CAAE18B0 CRC64;		
Query Match	100.0%;	Score 2363;	DB 2; Length 440;
Best Local Similarity	100.0%;	Pred. No. 1.7e-103;	
Matches 440;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	MKFGPLACLLALCLGSGEAGPLQGEESTGTNIGELGHGLDALSEGVGKRAIGKEAG	60
Db	1	MKFGPLACLLALCLGSGEAGPLQGEESTGTNIGELGHGLDALSEGVGKRAIGKEAG	60
Qy	61	GAAGSKVSEALGGTREAATGTVRQVPGFAGADALGNRVGEAAHALGNTGHEIGRAEDV	120
Db	61	GAAGSKVSEALGGTREAATGTVRQVPGFAGADALGNRVGEAAHALGNTGHEIGRAEDV	120
Qy	121	IRGADAVRGSWGQVPGHSGAWETSGGHGIFSGGGGLGGGQGNPGGLGTPTWHVHGPNS	180
Db	121	IRGADAVRGSWGQVPGHSGAWETSGGHGIFSGGGGLGGGQGNPGGLGTPTWHVHGPNS	180
Qy	181	AGSFGHNPQAGPAGQGGNGGPPNFGTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGGGG	240
Db	181	AGSFGHNPQAGPAGQGGNGGPPNFGTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGGGG	240
Qy	241	SSNSGGSGSQSGSSGGSGNDNNNGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSS	300
Db	241	SSNSGGSGSQSGSSGGSGNDNNNGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSS	300
Qy	301	RGDSGSESSWGSSTGSSSGNHGSGGGNGHKPKCEKPGNEARSGSGTQGFQGGVSSN	360
Db	301	RGDSGSESSWGSSTGSSSGNHGSGGGNGHKPKCEKPGNEARSGSGTQGFQGGVSSN	360

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Qy 361 MREISKEGNRLGGSGDNYRGQSSWGSAGDVGAVGNTVNSSETSPGMFNTDFWKNFKS 420
Db 361 MREISKEGNRLGGSGDNYRGQSSWGSAGDVGAVGNTVNSSETSPGMFNTDFWKNFKS 420
Qy 421 KLGFINWDINKDQSRIP 440
Db 421 KLGFINWDINKDQSRIP 440

RESULT 2
Q6E0U4 PRELIMINARY; PRT; 476 AA.
AC Q6E0U4;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Dermokine-beta.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15234001; DOI=10.1016/j.ygeno.2004.03.010;
RA Matsui T., Hayashi-Kisumi F., Kinoshita Y., Katahira S., Morita K.,
RA Miyachi Y., Ono Y., Imai T., Tanigawa Y., Komiya T., Tsukita S.;
RT "Identification of novel keratinocyte-secreted peptides dermokine-
RT alpha/-beta and a new stratified epithelium-secreted protein gene
RT complex on human chromosome 19q13.1.";
RL Genomics 84:384-397(2004).
DR EMBL; AY622965; AAT68269.1; -
SQ SEQUENCE 476 AA; 47010 MW; E2206CCB64AC4992 CRC64;

Query Match 84.5%; Score 1996; DB 2; Length 476;
Best Local Similarity 87.1%; Pred. No. 2.8e-86;
Matches 378; Conservative 2; Mismatches 0; Indels 54; Gaps 2;

Qy 1 MKFQGPLACLLALCLGSGEAGPLQSGESTGTNIGALGHGLDGLDSEGVGAIGKEAG 60
Db 1 MKFQGPLACLLALCLGSGEAGPLQSGESTGTNIGALGHGLDGLDSEGVGAIGKEAG 60
Qy 61 GAAGSKVSEALGQGTREAVGTGVRQVPGFCAADALGNRVGEAAHALGNTGHEIGROAEDV 120
Db 61 GAAGSKVSEALGQGTREAVGTGVRQVPGFCAADALGNRVGEAAHALGNTGHEIGROAEDV 120
Qy 121 IRHGADAVRGSWQVPGHSGAWETSGGHGIFGSGGLGGQGGNPGGLGTPWVHGYPGNS 180
Db 121 IRHGADAVRGSWQVPGHSGAWETSGGHGIFGSGGLGGQGGNPGGLGTPWVHGYPGNS 180
Qy 181 AGSFGMNPQAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASQNONEGCTNPPPSGGG 240
Db 181 AGSFGMNPQAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASQNONEGCTNPPPSGGG 240
Qy 241 SSNSGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 300
Db 241 SSNSGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 296
Qy 301 RGSQSGSSSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 360
Db 297 RGSQSGSSSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 346
Qy 361 MREISKEGNRLGGSGDNYRGQSSWGSAGDVGAVGNTVNSSETSPGMFNTDFWKNFKS 420
Db 347 -----NSETSPGMFNTDFWKNFKS 366
Qy 421 KLGFINWDINKDQ 434
Db 367 KLGFINWDINKNQ 380

RESULT 3
Q6E0U6 PRELIMINARY; PRT; 517 AA.
AC Q6E0U6;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Dermokine-beta.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15234001; DOI=10.1016/j.ygeno.2004.03.010;
RA Matsui T., Hayashi-Kisumi F., Kinoshita Y., Katahira S., Morita K.,
RA Miyachi Y., Ono Y., Imai T., Tanigawa Y., Komiya T., Tsukita S.;
RT "Identification of novel keratinocyte-secreted peptides dermokine-
RT alpha/-beta and a new stratified epithelium-secreted protein gene
RT complex on human chromosome 19q13.1.";
RL Genomics 84:384-397(2004).
DR EMBL; AY622963; AAT68267.1; -
SQ SEQUENCE 517 AA; 51660 MW; 61E2974EEB36650B CRC64;

Query Match 44.1%; Score 1043; DB 2; Length 517;
Best Local Similarity 48.9%; Pred. No. 1.3e-41;
Matches 231; Conservative 41; Mismatches 102; Indels 98; Gaps 13;

Qy 1 MKFQGPLACLLALCLGSGEAGPLQSGESTGTNIGALGHGLDGLDSEGVGAIGKEAG 60
Db 1 MKLQGSILACLLALCLGGAANPLHSGEGTGA-----SAAHGAGDAISHGIGEAVGQAK 56
Qy 61 GAAGSKVSEALGQGTREAVGTGVRQVPGFCAADALGNRVGEAAHALGNTGHEIGROAEDV 120
Db 57 EAASSGIQNALGQGHGEGGSTLLMGSRG-----DVFEHLRGEAAARSLGNAGNEIGROAEDI 112
Qy 121 IRHGADAVRGSWQVPGHSGAWETSGGHGIFGSGGLGGQGGNPGGLGTPWVHGYPGNS 180
Db 113 IROGVDAVH-----NAGSMGTSGHGAYGSGGAG--VQGNPGPGQGTWASG----- 157
Qy 181 AGSFGMNPQAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASQNONEGCTNPPPSGS 237
Db 158 -GNYGTNSLGGVGGGNGGGLNYETNAQGAQVAGYGTGVRGNQNSGCTNPPPSGSHS 216
Qy 238 ---GGGSSNSGG--GSGSQSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 286
Db 217 FNSNGSGSNDGSRGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 274
Qy 287 GSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 325
Db 275 GNSNSGNSGNSGSGSRDIETSNFDEGYSVSRGTGSRGGSG-----GSGSGSGSGSGSG 329
Qy 326 GNGHKGPKCEKPNKARGESGIGQFRGQGVSSNMREISKGNRLGGSGDNYRGQSGS 385
Db 330 GGN--KPECNPNNDVRMAGSGSQ-----GSGSGSGSGSGSGSGSGSGSGSGSGSG 357
Qy 386 WSGSGGDAVGVNTVNSSETSPGMFNTDFWKNFKSLGFINWDINKDQSRSS 437
Db 358 GGNIQKEAVNGLTNMSDASTLFPNIDNFWENLKSKTRFINWDINKGHAPS 409

RESULT 4
Q6P253 PRELIMINARY; PRT; 508 AA.
AC Q6P253;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE 1110014F24Rik protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RX Carninci P., Hayashizaki Y.;  
 RA "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP STRAIN=C57BL/6J; TISSUE=Head;  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP STRAIN=C57BL/6J; TISSUE=Head;  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RA The FANTOM Consortium;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP STRAIN=C57BL/6J; TISSUE=Head;  
 RC STRAIN=C57BL/6J; PubMed=11042159; DOI=10.1101/gr.145100;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP STRAIN=C57BL/6J; TISSUE=Head;  
 RC STRAIN=C57BL/6J; PubMed=11076861; DOI=10.1101/gr.152600;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP STRAIN=C57BL/6J; TISSUE=Head;  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK018753; BAC38319.1;  
 DR MGD; MGI:1920962; 1110014P24Rik.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 SQ SEQUENCE 407 AA; 42735 MW; 9D243DA7077983F6 CRC64;  
 Query Match 23.1%; Score 546.5; DB 2; Length 407;  
 Best Local Similarity 45.8%; Pred. No. 1.9e-18;  
 Matches 130; Conservative 29; Mismatches 86; Indels 39; Gaps 9;  
 QY 175 GYPCNSAGSGMPPQCAPWCGGNGPPNFTGTTCQAVAPGYSVRASNQNEGCTNPPPP 234

Db 34 GHPGQEQATMGLTLWALVVRVAMADHSTKMPRELWLSLGYGTVRGNQNSGCTNPPPP 93  
 QY 235 SCS-----GGSSNSGG-GSGSQSGSGSGNG-----DNNKSSSGSGSSSGSSGS 280  
 Db 94 SCSHESFNSGSGSNDGSRGSGSGSHGSGGSGGSGGSGGSGSS--SSSGNSGN 151  
 QY 281 SSGSGSGSGSGSGSGSGSG--GSRG-----DSGSESSWSSTGSSGNHSGSGGNGHKPG 333  
 Db 152 SNSGNSGNSGNSGNSGSGSGSDIETSPDEGYSVRGTGSGSGSGSGSGG--KPE 209  
 QY 334 CEKPGNEARGSGESGIGQPRGQGVSNMREISKEGNRLIGSGGDNRYRGSGSGSGGDA 393  
 Db 210 CNPFGNDVFMAGSGSQE-----SKSSHLLGGSHD-YQHGSGNGGNIQKEA 255  
 QY 394 VGGVTVNSETSPGMPNPDFTFWNPKSLGFINWDAINKDQRSS 437  
 Db 256 VNGLTMTNSDASTLPFNIDNFWENLKSRTFRFINWDAINKGHAPS 299  
 RESULT 7  
 Q6FPRO PRELIMINARY; PRT; 1553 AA.  
 AC Q6FPRO;  
 DT 05-JUL-2004 (Tremblrel. 27, Created)  
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
 DE Similarities with tr|Q08294 Saccharomyces cerevisiae YOL155c.  
 GN ORFNames=CAGLQJ01771g;  
 OS Candida glabrata CBS138.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxID=284593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CBS138;  
 RG Genolevures;  
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,  
 RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
 RA Boissarme A., Boyer J., Cattolico L., Confanier F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.L.;  
 RT "Genome evolution in yeasts.";  
 RL Nature 430:35-44(2004).  
 DR EMBL; CR380956; CAG60731.1;  
 SQ SEQUENCE 1553 AA; 145623 MW; A17810AE221D7480 CRC64;  
 Query Match 20.6%; Score 486; DB 2; Length 1553;  
 Best Local Similarity 33.6%; Pred. No. 3.9e-15;  
 Matches 143; Conservative 38; Mismatches 204; Indels 40; Gaps 10;  
 QY 17 GSGEAPLQSGGES---TGNTIGALGHLGDLSEGVGKALCKEAGGAGKSVSEALQ 73  
 Db 432 GSGSGSGTSG 491  
 QY 74 GTREAVGTGVRQP---GFGAADALGNRVGSAHALGNTGHEIGRQAEIVRHGADAVR 129  
 Db 492 GSGSGSGSGSGTGPBGSGSGSGTGPBGSGSGSGSGSGSGSGSGSGSGSGSGSG 551  
 QY 130 GSWQGVPHSGAWETSGGHGIGSGGGLG-----GQCGNPGGLGTPWVHGYPGNSAGSF 184  
 Db 552 GSGSGTSG 610  
 QY 185 GNPQCAPWCGGNGPPNFTGTTCQAVAPGYSVRASNQNEGCTNPPPSGSGGS --- 241

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Db 611 TCGSGSGSGSGSGSGSGSGSGTTCGSGSGSGSGSVSGSGSGTTCGSGSGSGSGSG 670
Qy 242 ----SNGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 291
Db 671 TCGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 730
Qy 292 GSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGE----- 346
Db 731 SGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGST 790
Qy 347 ----SGTCGFCGCGVSSNMREISKEGKRLGSGDNRGQSSWGSGDGVGVNTVNS 402
Db 791 PEGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 845
Qy 403 ETSFG 407
Db 846 GSNEF 850

RESULT 8
Q6CHN8
ID Q6CHN8 PRELIMINARY; PRT; 1274 AA.
AC Q6CHN8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Similarity (Fragment).
GN ORFNames=YAL10A06853g;
OS Yarrowia lipolytica CL1B99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CL1B99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Bolerame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissensbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CL1B99;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382127; CAG3749.1; -.
FT NON TER
SQ SEQUENCE 1274 AA; 116259 MW; 33583C8CE680B3E2 CRC64;

Query Match 19.9%; Score 471; DB 2; Length 1274;
Best Local Similarity 36.2%; Pred. No. 1.7e-14;
Matches 149; Conservative 27; Mismatches 168; Indels 68; Gaps 16;

Qy 17 GSGBAGPLOSSEES-----TGTNIGALGHGLDLSLSEGVGKAIGKEAGGAAGSKVSE 69
Db 881 GSGSGGDTSGNSGSGDGTSGNSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 932
Qy 70 ALGGTTEAVGTGVRVPGFAGAADALGNRVGEAAHALGNTGHEIGROAEDVIRHADAV 128
Db 933 --GDGTS---GNSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 981
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Qy 129 ----RGSMQGVPGHSGAWETSGHGIFGSGQGLG--GQGGNPGGLGTPTWVHGYPQNSAGSF 184
Db 982 GNGSGSGSGDGGSSNGSGSGDGTSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 1036
Qy 185 GMPPOGAPWQCGNGGPPNFTGTQGAQVAPGVGSVFAASNQNEBCTNPPPSGSGSGS--- 241
Db 1037 -----SGNGG-----SGSGSGSDSGSGSGSGSGSGSGSGSGSGSGSGSGSG 1080
Qy 242 SNGSGSGSGSGSGSGSGSGNDNNGSSG---GSNGSGSGSGSGSGSGSGSGSGSGSGSG 298
Db 1081 SDSGSGSGSGSG--SGSGSGSDSGSGSGSGSGSGSGSGSGSDSGSGSGSGSGSGSG 1139
Qy 299 GSREDSDSESWSGSTTSSSGNHGCGGNGHKGPCCKPGNEARGSG--ESGIQGFROGV 357
Db 1140 GSDSGSGSGSGSGSDSGSGSGSGSGSGSGSDSGSGSGSGSDSGSGSGSGSGSGSGSG 1199
Qy 358 SSNWREISKEGKRLGSGDNRGQSSWGSGDGVGVNTVNSETSPGMF 409
Db 1200 DSGSGSGSGSDSGSGSGS---GSNGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 1243

RESULT 9
Q7TWC0
ID Q7TWC0 PRELIMINARY; PRT; 1938 AA.
AC Q7TWC0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE PE-PGRS FAMILY PROTEIN.
GN Name=PE_PGRS55; OrderedLocusNames=Mb3541;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RL MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Eiglmeyer K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duchoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248346; CAD95727.1; -.
DR InterPro; IPR002202; HMG-CoA_red.
DR InterPro; IPR000084; PE_region_N.
DR InterPro; IPR002173; PfKB.
DR Pfam; PF00934; PE; 1.
DR ProDom; PD001223; PE_region_N; 1.
DR PROSITE; PS00318; HMG_COA_REDUCTASE_2; UNKNOWN_1.
DR PROSITE; PS00583; PFKE_KINASES_1; UNKNOWN_2.
KW Complete proteome.
SQ SEQUENCE 1938 AA; 152029 MW; 3C73A507FEB0F9C CRC64;

Query Match 19.5%; Score 460.5; DB 2; Length 1938;
Best Local Similarity 31.5%; Pred. No. 7.3e-14;
Matches 146; Conservative 36; Mismatches 173; Indels 109; Gaps 17;

Qy 17 GSGBAGPLOSSEESTGTNIGALGHGLDLSLSEGVGKAIGKEAGGAAGSKVSEALGGTR 76
Db 1218 GAGSGG-----NTSPGNGGQG-----GQGGSGGAGGAAG--AGGAGGANGTAGNGGQ 1266
Qy 77 EAVGTGVRVPGFAGAADALGNRVGEAAHALGNTGHEIGROAEDVIRHADAVRGSWGVP 136
Db 1267 GAGGTG-----GAGAASSATNGSGSGAGGTGGAGTGGGA-----GGGVGGAGGNG 1313
Qy 137 GH-----SGAWETSGHGIFGSGQGLGQ-----GQGNPPGGLGTP 171
Db 1314 GHGDDAGDGGNGANGNNRSGSGFLAGGTGAAGDGGQGGGAGGAGGAGGAGGT 1373
Qy 172 WHGYFGN-----SAGSCFMNPQAGWPWQGGNGGPPNFTNTQ--GAVAQPGYGSV 220
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[illegible]

RESULT 12

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Q6MX28
ID Q6MX28 PRELIMINARY; PRT; 1306 AA.
AC Q6MX28;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE PE-PGRS FAMILY PROTEIN.
DN
GN Name=PE_PGRS7; OrderedLocusNames=Rv0578c;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RC
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III,
RA Connor R., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Tekkaat F., Davies R.M., Devlin K., Felwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagella K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RL complete genome sequence.";
RL Nature 393:537-544(1998).
DR EMBL; BX842573; CAE55300.1; -.
DR TubercuList; Rv0578c; -.
DR InterPro; IPR002952; Eggshell.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR000084; PE_region_N.
DR InterPro; IPR002173; pFkB.
DR Pfam; PF00934; PE; 1.
DR PRINTS; PR01228; EGGSHELL.
DR PRODOM; PD001223; PE_region_N; 1.
DR PROSITE; PS00583; pFkB_KINASES_1; UNKNOWN_2.
DR PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1306 AA; 105964 MW; 843A30955FFFA56B6 CRC64;

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Query Match	18.6%	Score 439.5;	DB 2;	Length 1306;
Best Local Similarity	30.9%	Pred. No. 5.1e-13;		
Matches 151;	Conservative	34;	Mismatches 194;	Indels 109;
				Gaps 22;

Qy	17	GSBAGPLQSBESTGTN--IGBALHGLGDALSBGVKAIGK-----BAGGAAGSKV	67
Db	567	GHAAGAL-----GVNGGVGAGGHG-GD---PGVGGAGGCGSGSTPCANGAPGNT	615
Qy	68	SEA--LQCGTREAVGTCVRQVPFGAADALGNRVGE-AAHALGNTHGE----ICRQAE	120
Db	616	TSGGNGNGGRGADATCFGTGASGGRGGDGLVNGGAGGAGNGSKGLPGLRLGNP-	674
Qy	121	IRGADAVRSGVQVPHSHANETSGHG1FGSQGLCGOG-----QGNPG	166
Db	675	---GLDGGTCGNGGAGSGGAWAGNGGTGAGGTGGVGTGGSGSDGVNGSSAGADHGP	731
Qy	167	GLGTPVHWYPGNSAGSPGMNPOG-----APWQGGNGGPPNFTN-----TOG	210
Db	732	GTGCGVGTGKGGDGGDGAAPNGVAGSQCPGAGGDDGCTGGVGGNGGRJIDGADGATAG	791
Qy	211	AVAQPGVGSVRAQNQNEGTNPP-----PSGS-----CGSSNSGGGGSGSGSGSGSNGD	262
Db	792	ARGQDGAGGAGKGGRGTGTGPGGAGPAGTTGOSQAGGNGGSGGTGDPDGDGNGANGS	851
Qy	263	--NNNGSSSGSSSGSSSGSSGCGSSG-----GSS-----CGSSGNSG-----	298
Db	852	VFTNNGIGGNGGNAGPFGAGSGAGSTFCATGSSSSIHVNGGNGGNGDHALSG	911
Qy	299	SGRGDSGSESSWGSSTGS--SSNGHGGSG-----GGNHKPGCEKPGNEARGSGBSGI	349
Db	912	NGAAGNGGNGNGSLURGSGGAGGHGNGGNGASRGMGDGTGTGAGGACQIINGGGAGGN	971
Qy	350	QGFPGCGVSSNMREISKEGNR-----LLGSGDNYRGOGSSWGSGGDAVCGV--NTVNS	402
Db	972	GDDGTTGSDGNPCAITSGSGRGDGDGVGGCGGSGVADGDCRGGAGGTGCTGLRTTGA	1031
Qy	403	ETSPGMPN	410
Db	1032	TGATGTFD	1039

RESULT 13

ID	Q7UIQ7	PRELIMINARY;	PRT;	1306 AA.
AC	Q7UIQ7;			
DT	01-OCT-2003	(TrEMBLrel. 25, Created)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	PE-PGRS FAMILY PROTEIN.			
DE	Name=PE_PGRS7; OrderedLocusNames=Mb0593c;			
GN	Mycobacterium bovis.			
OS	Mycobacterium bovis.			
OC	Bacteria; Actinobacteria; Actinomycetales;			
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.			
NCBI_TaxID=1765;				
NCBI_TaxID=1765;				
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=AF2122/97.			
RC	MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;			
RX	Garnier T., Eglmeier K., Camus J.-C., Medina N., Mansoor H.,			
RA	Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,			
RA	Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,			
RA	Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;			
RA	"The complete genome sequence of Mycobacterium bovis";			
RT	Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).			
RL	EMBL; BX249336; CAD93455.1; -			
DR	InterPro; IPR000209; Pept_S8 S53.			
DR	InterPro; IPR000084; PE region_N.			
DR	InterPro; IPR002173; PfKb.			
DR	Pfam; PF00934; PE; 1.			
DR	ProDom; PD001223; PE region_N; 1.			
DR	PROSITE; PS00583; PFRB_KINASES_1; UNKNOWN 2.			
DR	PROSITE; PS00138; PFRB_TLASE_SER; UNKNOWN_1.			
DR	Complete proteome.			
DR	SEQUENCE 1306 AA; 105994 MW; 65628FBA01F4AD42 CRC64;			

Query Match 18.6%; Score 439.5; DB 2; Length 1306;

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Best Local Similarity 30.9%; Pred. No. 5.1e+13;
Matches 151; Conservative 34; Mismatches 194; Indels 109; Gaps 22;

QY 17 GSGEAGPLOSBERSTGTN--IGBALGHGLDALSEGVGAIKG-----EAGGAAGSKV 67
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 567 GHGAAGAL-----GVNGVGGAGGHG-GD---PGVGGAGGGSGSTPGANGAPGNTP 615
QY 68 SEA--LGGTREAATGTRVQVPPFGAADALGNRVB-AHALGNTGHE-----IGRQADV 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 616 TSGGNGGNGRGADATGFCGTGASGGRGGDGLVNGGAGGAGGSGKGLPGLGRGNP- 674
QY 121 IIRGADAVRSGWGVPHSGAWETSCHGTFSGGGGLGGG-----GQNP 166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 675 ---GLDGGTGGNGGAGGGGGAAGNAGTGGAGTGGVGGTGGSGSGVNGSSAGADGHPG 731
QY 167 GLGTPVWHYVPGNSAGSFGMNPQG-----APWQGGNGGPPNPFTN-----TQG 210
Db 732 GTGGVGTGCGKGGDGGGAAPNGVAGSQPGGAGDGGTGGVGGNGRGIDGADGATAG 791
QY 211 AVAQPVGVSRAVNQNEGCTNPP-----PSGS-----GGGSNSGGSGSGSGSGSGND 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 792 ARQDQAGGAGGKGRGGTGTGPGGAGPAGTTGSGAGGNGSGSGGTGDPGDDGNGANGS 851
QY 263 --NNCGSSGSGSGSGSGSGSGSGSG-----GSS-----GGSSGNSG----- 298
Db 852 VFTNNGIIGNGGNGGAGPAGSGAGSGAGSTFGATGSSSIHVNGGNGGNGGNDHALSG 911
QY 299 -GSRGDSGSSSGSGSGSGSGSGSGSGSG-----GNGHKPGCKPNEARGSGESGT 349
Db 912 NGAAGNGGNGGNGSLRGSGGAGGCHGNGGNGASRGMGDDGTGGAGNAGQIINGGAGGN 971
QY 350 QGPRGQGVSSNMREISKGNR-----LLGSGDNYRGQSGSWGSGGDAVGGV---NTVNS 402
Db 972 GSDGCTGSDGNPAGITGSGGRGGDGGVGGQGGVAGDGDGGRGAGGTGGTGLRGTTCG 1031
QY 403 ETSPPGFN 410
Db 1032 TGAATGFD 1039

RESULT 14
Q7SEP7 PRELIMINARY; PRT; 725 AA.
AC Q7SEP7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU02170.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Salitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gheer S.,
RA Kamal M., Kamysellis M., Mauceli E., Bieleke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Flamm M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Eboile D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an
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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data
DR EMBL; AABX01000029; EAAJ5293.1; -.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR002952; Eggshell.
DR PRINTS; PRO1228; EGGshell.
DR PROSITE; PS00070; ALDEHYDE DEHYDR CYS; UNKNOWN 1.
SQ SEQUENCE 725 AA; 63929 MW; 60F0003860219B9C CRC64;

Query Match 18.3%; Score 433; DB 2; Length 725;
Best Local Similarity 29.8%; Pred. No. 6.4e+13;
Matches 137; Conservative 46; Mismatches 173; Indels 104; Gaps 20;

QY 17 GSGEAGPLOSBERSTGTNIGBALGHGLDALSEGVGAIKGAGGAGSKVSEALGQGT 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185 GSG-LGGFAGAGAYGNGAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAG 243
QY 77 EAVGTGVRQVPPFG-----AADALGNRVGEAAHALGNTGHEIGRQADVIRHGADAV 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 N--GLGVNGIGLGNAGSLGDSGAYGNGAG-AGNAGNGG--LG----- 284
QY 129 RGSWQGV-PHSGAWETSCHG-IFGSQGLGGQGGNPGGLGTPVWHYVPGNSAGSGM 186
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 NGSGNGLGNGSGCANNGCGMDCSGMGAGGAGPG-GGAGGLGNG--ASGPGNGVGG 341
QY 187 NPQAPWQGGNGGPPNFTNTQGAQVAPGYSVRASINQNEGCTN-----PPSGSG 238
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 GAGGLGYSGGGPGGTSGNNGINAGNNGNAGNNGNAGNNGNAGNAGNAGNAGNAG 401
QY 239 GGSNSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 276
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 NNGN-NGNNGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAG 460
QY 277 -----SGSSSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 461 ICTPSPEAIVPGSAGNGGNGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 519
QY 326 GGNHKGPKCEKPNARGSGESGIQ-----FRGQGVSSNM-----RETSK- 367
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 NNGN-----GNDAGAGNGAPAPTPCTGSGSPSFLVLTITVTPQPARVVEKKQY 571
QY 368 GNRLLGGSDNYRGQSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 407
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 572 ANVMAYGGPDD--GAGAAPGSGSGSVAPGNGGNGSGSAPG 609

RESULT 15
Q6C6W0 PRELIMINARY; PRT; 1391 AA.
AC Q6C6W0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P08640 Saccharomyces cerevisiae YIR019c STA1
DE extracellular alpha-1.
GN ORFNames=YAL10E05819g;
OS Yarrowia lipolytica CUIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CUIB99;
RG Genolevures;
RA Lafontaine I., de Montigny J., March C., Neuvéglise C., Talla E.,
RA Goffard N., Franchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Barnay S., Bangeul S., Zattolico L., Confanioli F., de Barvar A.,
RA Boisrame A., Boyer J., Gattolico L., Confanioli F., Groppi A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Kachouri R.,
RA Hantraye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,
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